IMPROVEMENT OF COTTON FIBER MATURITY AND ASSESSMENT OF INTRA-PLANT FIBER VARIABILITY

A Dissertation

by

NAYANKUMAR KOTHARI NEHA

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

DOCTOR OF PHILOSOPHY

August 2012

Major Subject: Plant Breeding

Improvement of Cotton Fiber Maturity and Assessment of Intra-Plant Fiber Variability

IMPROVEMENT OF COTTON FIBER MATURITY AND ASSESSMENT OF INTRA-PLANT FIBER VARIABILITY

A Dissertation

by

NAYANKUMAR KOTHARI NEHA

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

DOCTOR OF PHILOSOPHY

Approved by:

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

August 2012

Major Subject: Plant Breeding

ABSTRACT

Improvement of Cotton Fiber Maturity and Assessment of Intra-Plant Fiber Variability.

(August 2012)

Nayankumar Kothari Neha, B.Sc., Gujarat University;

M.S., Texas Tech University

Chair of Advisory Committee: Dr. Steve Hague

The temporal system of fruiting on the cotton plant lends itself to bolls at different fruiting sites developing under different environmental conditions and with varied source-sink relationships. To investigate this, intra-plant fiber quality was assessed in four upland cultivars at College Station, Texas for three years and at Lubbock, Texas for two years. It was concluded that fiber quality steadily declines from the bottom sympodial branches towards the upper branches. 'FiberMax 832' had the best fiber quality among all cultivars but it also had the highest degree of variability within the plants. 'Half and Half' and 'Acala 1517-99' appear to have the least amount of intra-plant variability of fiber quality. Bolls from the bottom region of the plant have higher trash content compared to the upper region. To test the impact of fiber quality variability on boll sampling techniques employed, ten sampling protocols were compared against each other for three years in College Station, Texas, for two upland cultivars. Results suggest that randomized boll samples containing 50 bolls worked well to estimate

inherent fiber quality for most fiber traits while estimation of trash and lint percent was not predictable based on boll samples.

One of the problems associated with intra-plant fiber variability was the presence of immature fibers. In order to determine the potential for improvement of fiber maturity and standard fineness, five upland cotton (*Gossypium hirsutum* L.) genotypes were subjected to a diallel analysis at College Station, Texas, in 2011. Four cultivars that tend to produce fine and mature fibers and one cultivar that tends to produce coarse fibers were intermated in all combinations, without reciprocals. Estimates of general (GCA) and specific combining ability (SCA) for fiber maturity ratio and standard fineness based on Griffing's diallel Model I, Method 4 were calculated for AFIS and fiber micronaire, length and strength measurements for High Volume Instrument (HVI). Four parents had significant GCA effects and Acala 1517-99 was found to be the best parent for improving standard fineness followed by FiberMax 832 and 'Tamcot HQ-95'. Tamcot HQ-95 was the best parent to improve fiber maturity ratio while 'Deltapine 90' was the best parent to reduce fiber maturity ratio. The specific cross between Acala 1517-99 and Tamcot HQ-95 had the best performance. Diallel analysis indicated that fiber maturity ratio was influenced by non-additive gene effects more than additive gene effects while fiber standard fineness was highly influenced by additive gene effects.

Developing cultivars with optimal fiber standard fineness and maturity should be prioritized to address problems associated with neps and short fiber content and improve spinning performance of US cotton.

DEDICATION

This dissertation is dedicated to my parents. They taught me to follow my dreams and instilled the importance of education in my life. Without their love, support and sacrifice I would not be the person I am today.

I would also like to dedicate this dissertation to my loving husband. His encouragement and unconditional love has filled my life with happiness and laughter.

ACKNOWLEDGEMENTS

I take this wonderful opportunity to express my sincere appreciation and gratitude to Dr. Steve Hague, firstly, for accepting me as his Ph.D. student and secondly, for his patience, advice, supervision and invaluable guidance through my academic life at Texas A&M University. His kindness and encouragement has been the strongest support for me in the last four years. I would like to thank my committee members, Dr. Hequet, Dr. Smith, and Dr.Zhang, for their guidance and support throughout the course of this research. They have always made time to answer my questions with great patience which I truly appreciate.

I would also like to thank Dawn Deno, Nino Brown, Ben Beyer, student workers at the Cotton Improvement Lab and all my fellow graduate students who have helped me to complete this work. Without their help and support I would have never been able to complete this research. I would like to express my sincere gratitude to Cotton Incorporated and Texas Department of Agriculture for the financial support.

Finally, thanks to my mother and father for their prayers, love and encouragement. Thank you, Mom, for putting away your life for six months and being here to take care of me when I needed you the most. Thanks to my husband whose unfailing patience and love makes my life happy and joyous. Thank you to my wonderful daughter for making me smile every day since the day you entered my life. Thank you, Goldie, my wonderful dog and my best friend for always being there for me. Thanks to my sister, brother-in-law and my two wonderful nephews for their support and love.

NOMENCLATURE

USDA	United States Department of Agriculture
DPA	Days Post Anthesis
HVI	High Volume Instrument
H	Fineness
Hs	Standard Fineness
SFC (n)	Short Fiber Content by Number
SFC (w)	Short Fiber Content by Weight
MR	Maturity Ratio
IPS	Individual Plant Selection
AFIS	Advanced Fiber Information System
CSIRO	Commonwealth Scientific and Industrial Research Organization
GCA	General Combining Ability
SCA	Specific Combining Ability
PI	Plant Inventory
PVP	Plant Variety Protection
FBRI	Fiber and Biopolymer Research Institute
ANOVA	Analysis of Variance
Length (w)	Length by Weight from AFIS
Length (n)	Length by Number from AFIS
UHM	Upper Half Mean Length

UQL (w)	Upper Quartile Length by Weight from AFIS
UI	Uniformity Index
IFC	Immature Fiber Content
SCW	Secondary Cell Wall

TABLE OF CONTENTS

Page

CHAPTER Page

LIST OF FIGURES

Page

LIST OF TABLES

Page

CHAPTER I

INTRODUCTION

Cotton is grown throughout the world for fiber, oil products and proteins for animal feed. China, India and the U.S. are the largest producers of cotton. Other countries that produce large quantities of cotton include Argentina, Australia, Brazil, Egypt, Pakistan, Turkey and Uzbekistan. The U.S. is the largest exporter, 3rd largest producer and the 7th largest consumer of cotton. The majority of the US crop is planted in 17 southern states from Virginia to California. Major production regions include areas of the Texas High and Rolling Plains, the Mississippi Delta, California's San Joaquin Valley, central Arizona and southern Georgia (Cotton Incorporated, 2012).

The economic value of cotton lies in its yield and fiber quality. Improvement in both can be done with genetics and management practices (Anthony, 1999). For many years and to date, cotton breeders have been using data obtained from HVI for making important decisions in breeding programs. While HVI stays valuable commercially, advent in technology has introduced a number of new testing machines such as AFIS, Cottonscope® (Rodgers et al., 2012) and image analysis using fiber cross sections (Thibodeaux et al., 1999) which provide researchers with greater depth of information. Given the progressive nature of the spinning and textile industry, cotton plant breeders must strive to improve fiber quality to match international standards.

This dissertation follows the style and format of Crop Science.

One of the problems associated with cotton is the high degree of variability in fiber quality across different species, cultivars, within the same cultivars, within fields, across and within rows, within a plant and even within a single boll (Clouvel et al., 1998; Wilkins et al., 1999; Bednarz et al., 2006). The purpose of this research is to investigate the variability in fiber quality within a plant across sympodial branches to understand the growing habit, environmental impact and genetic influence with respect to fiber quality. Secondly, the impact of intra-plant fiber variability on efficiency of boll sampling techniques is evaluated to enable researchers to adequately sample bolls for fiber testing. Lastly, a diallel study has been conducted to address some of the causes of intra-plant fiber variability, such as the presence of immature fibers. This study introduces new fiber quality traits (fiber maturity and standard fineness) available from AFIS that might assist cotton plant breeders to make better decisions for improvement.

Fiber quality variability within plants is evaluated across four cultivars for three years in College Station, Texas and two years in Lubbock, Texas. Both locations are very different from each other in terms of growing conditions, cultivar adaptability and management practices. Fiber testing for this study is done using AFIS. Understanding problematic traits for spinners such as SFC and neps can be done with greater depth using AFIS. Fiber length given by HVI is weight biased thereby giving an overestimate of inherent fiber length. This can be accurately evaluated using AFIS length (n) and SFC (n) measurements. Distributions for fiber length, fineness and maturity ratio are also available to the breeders for further understanding fiber quality. All these traits have been addressed in this study.

Boll sampling techniques are compared in order to make appropriate recommendations for accurate fiber testing and analysis. It is imperative for researchers to adequately sample bolls when making decisions in breeding programs. Top bolls of cotton plants are often associated with immature fibers relative to the rest of the plant. If too many bolls are sampled from the upper regions of the plants, one may end up underestimating inherent fiber quality. If too many lower bolls are sampled, one may overestimate inherent fiber quality.

Fiber immaturity has been associated with neps, short fiber content and reduced strength (Hequet et al., 2006). The two studies conducted on intra-plant fiber variability and boll sampling techniques, showed that fiber maturity declines within the plants across all genotypes. The purpose of the diallel study conducted here is to evaluate the importance of AFIS as a selection tool for breeders because it provides fiber maturity data. AFIS also provides the information required for calculating fiber standard fineness. Standard fineness is a measurement of fiber fineness relative to fiber maturity ratio (Hequet et al., 2006). This trait relates very well with biological fineness of fibers. Selections based on fiber fineness relative to fiber maturity may prove to be effective in developing longer and stronger cultivars with reduced immaturity related problems.

Challenges for cotton plant breeders to improve yield and fiber quality can be met with multiple strategies using a multitude of tools and machines available. Fiber traits such as maturity and standard fineness need further research and breeding efforts for improvement. Problems associated with immature fibers have been recognized by the textile industry with greater severity over the last decade. This research addresses some

different techniques which may be included in breeding programs to improve fiber quality in the future.

Objectives

The objectives of this research are:

1. To determine variation of fiber quality within a plant using four diverse genotypes Acala 1577-99, FiberMax 832 (FM 832), Half and Half, and 'Texas Marker-1' (TM-1) grown at College Station and Lubbock, Texas.
2. To compare efficiency of different boll sampling protocols commonly used for fiber quality determination.
3. To utilize a diallel mating system involving five cultivars : 'Acala 1577-99', 'Deltapine 90' (DP 90), 'FiberMax 832' (FM 832), 'Half and Half' and 'Tamcot HQ-95' to estimate general combining ability (GCA) and specific combining ability (SCA) for fiber properties calculated from parents and F_1 progeny.

CHAPTER II

REVIEW OF LITERATURE

History

Cotton species are native to all continents except for Antarctica and speciation is thought to have begun 5-15 million years. There are about 50 known species in the cotton (Gossypium) genus. Four species independently have been domesticated for fiber production. Diploid species (26 chromosomes), *G.arboreum* and *G. herbaceum,* were domesticated in Asia and Africa and tetraploid species (52 chromosomes), *G.hirsutum* and *G.barbadense,* are believed to have originated in the Americas (Brubaker et al., 1999a; Brubaker et al., 1999b; Percy and Wendel, 1990; Wendel, 1989 and Wendel et al., 1992). Of these four species, *G.hirsutum* and *G.barbadense,* are cultivated in greater proportion compared to diploid types. Upland cotton, *G hirsutum*, is the most commonly produced species. It is thought to have arisen as a result of an interspecific hybridization between an A and D genome diploid species about 1-2 million years ago (Wendel, 1989). Since the first cotton crop was planted in 1621 in the United States, it has been an important part of the American agriculture industry (Smith, 1995; Ware 1936). Breeding efforts have been made for centuries to increase yield; however, commercial breeding only started in 1914 in South Carolina. At the time, fiber quality of cotton was assessed by fiber length because longer fibers spun with better efficiency and produced high quality textiles.

Historic events in cotton technology and management have played a major role in molding the breeding and textile industry as we see it today. Some of the historical events in the cotton industry involved the development of 'flying shuttle' for weaving by John Kay in 1738, the invention and later, improvement of the 'Spinning Jenny', the development of the cotton gin by Eli Whitney in 1794, the infestation and control/eradication of boll weevil and mechanical harvesting (Smith, 1995). The cotton gin was the catalyst that initiated the large US cotton industry. Three years before the gin was invented, U.S. production was 3,159 bales of cotton. Seven years after the gin was invented, US cotton production was 73,145 bales.

Insect pests were not a major problem for US cotton producers until the late 1800s when the Mexican boll weevil (*Anthonomus grandis*) migrated into Texas. In the early 20th century, crop losses were reported to be between 40-90% in some parts of the US. Various remedies were used to combat this pest including changes in planting patterns, row direction/width, physically removing and burning squares with weevil ovipositions, etc. It was eventually accepted that early maturing cultivars and prompt stalk destruction could reduce boll weevil damage. In the late 1970s, the National Boll Weevil Eradication Program was launched by USDA's Animal and Plant Health Inspection Service (APHIS) along the Virginia-North Carolina border, which expanded into Arizona, southern California and a portion of northwest Mexico. Later programs were launched in Oklahoma, New Mexico, the Mid-South, and Texas. Today the boll weevil has been functionally eradicated from Alabama, Tennessee, Missouri, Arkansas, Mississippi, California, Arizona, Oklahoma, and New Mexico. Texas and Louisiana

report some weevils which are expected to reduce/eradicate in the next few years (Cotton Incorporated, 2012).

Mechanical harvesters are an important component of cotton production. Manually harvesting cotton is extremely time consuming and requires extensive stoop labor. In 1926, a mechanical cotton stripper was successfully used in Lubbock, Texas. Mechanical harvesters improved cotton picking from 226.796 kg per day (handpicking) to thirteen bales per day (2830 kg) in 1937 using a cotton picker (Smith, 1995). As mechanical technology designed to improve harvesting and spinning efficiency became more common and began to cause substantial degradation to fiber quality, the textile industry demanded producers and hence plant breeders address issues to improve fiber quality.

In order to meet these new demands, cotton breeders began to develop high fiber quality and high-yielding cultivars to meet international quality standards for cotton fibers (Smith, 1995; Basra, 1999). Fiber quality was traditionally assessed by hand-classing in the USDA classing offices. The term "cotton classification" refers to the application of standardized procedures developed by USDA for measuring physical attributes of raw cotton that affect the quality of the finished product and/or manufacturing efficiency. Hand-classing was replaced by the development of the HVI (High Volume Instrument) testing in the late 1970s. By 1991, 100% of cotton was classed using HVI (Ghorashi, 2005). USDA classification currently consists of determinations of fiber length, length uniformity, strength, micronaire, color, leaf and extraneous matter. Extraneous matter is the only trait currently graded by humans.

Research and development of technology to rapidly measure other important fiber characteristics, such as fiber maturity, stickiness and short fiber content (SFC) is on-going (USDA, 2012 and Cotton Incorporated, 2012).

Growing Habit of Cotton

Cotton is dicotyledonous plant with indeterminate growing habit. Cotton plants are sensitive to growing temperature; however, under optimal conditions, the plant has a predictable growing pattern (Hearn, 1994 and Jones and Wells, 1997). Development occurs in five distinct phases inclusive of vegetative and reproductive stages. These developmental phases are germination and emergence, seedling establishment, leaf area and canopy development (vegetative stage), flowering and boll development (reproductive stage), and maturation. Germination and emergence occurs when the temperature at planting depth is at least 18.3^{o}C for three consecutive days. Emergence follows after five to seven days. The plant continues to grow and the first true leaf unfolds about seven to nine days after emergence depending on optimal temperature and growing conditions. Once the true leaf unfolds a new main stem leaf develops every 2.5 to 3 days. This is followed by a reproductive stage which involves flowering and boll set. This begins with the development of the first fruiting branch which has flower buds, commonly referred to as squares that appear approximately 30 days after planting in most fields. The fruiting pattern is vertical via main stem and horizontal via the extension of fruiting branches (sympodial branches). A new square appears every 2.5-3 days vertically and at an interval of 5-6 days horizontally on the fruiting branch. These

squares mature into an open flower in about 20 days which are typically self-pollinated in the absence of insect pollinators. These develop into bolls post-anthesis. Bolls grow for about 50 days post-anthesis (DPA) before opening and exposing seed cotton ready for harvest.

These fruiting positions are important to the breeder because within the first three fruiting branches are generally contained the majority of harvested seed cotton. (Bednarz et al., 2000; Jenkins et al., 1990). It has been shown with several cotton cultivars grown in the Mississippi Delta that 76% of the total yield occurs in the first fruiting position on sympodial branches, 18 to 21% of the yield occurs in the second fruiting position, and two to four percent of the yield is produced from all other fruiting positions on the sympodial branches (Jenkins et al., 1990). In a study conducted in California, it was reported that 76% of bolls retained through to maturity were on the first position of sympodial branches, and that six to eight percent of the bolls retained came from fruiting sites other than positions one and two on sympodial branches (Kerby and Hake, 1996).

Metabolic processes in cotton are temperature sensitive. This concept is explained by determining the growing degree days (GDD). The base temperature for this calculation has been set to 15.5^{o}C. GDD are calculated for each day after planting cotton. GDD for various stages in cotton development are, planting to emergence (45-130), emergence to first square (350-450), square to first bloom (250-500), bloom to open boll (910-950), early to late season (2550- 4600). Heat unit models provide a simple means for monitoring physiological development of crops and cultural practices.

These numbers can help growers to make accurate and timely decisions with respect to crop development in the season (Smith, 1995 and Fry and Butler, 1982).

Heritability

The phenotype is a product of the interaction between the encoding genes and the environment in which the genes are expressed. Based on the breeding objective, selections among desirable phenotypes are made by plant breeders. Because of the impact of the growing environment, the same species can react and perform differently when grown in multiple environments. This variation can mislead a breeder when making selections. Quantitative traits are difficult to select for in a breeding program compared to qualitative traits because of multiple genes interacting with the growing conditions (Acquaah, 2007; Fehr 1993)

The concept of reliability of a phenotypic value of a plant as a guide to the breeding value is called heritability of the metric trait (Acquaah, 2007). Heritability usually refers to the influence of genes on the trait being measured. Understanding this concept is important to plant breeding programs because it provides the breeder information on making decisions about the trait of interest. For example, heritability of a particular trait can determine if that trait can be effectively manipulated by a particular breeding method. It can also influence the selection methods used in a breeding program. Heritability is estimated as broad-sense and narrow-sense. Broad-sense heritability is estimated as the ratio of genetic variance by the total phenotypic variance whereas the narrow-sense heritability is derived from the ratio of additive variance to phenotypic

variance. Narrow-sense heritability usually has more applicability for a plant breeder of a self-pollinated crop because the additive component of genetic variance contributes to selection pressure applied (Acquaah, 2007; Fehr 1993; Allard, 1999; Poehlman, 2006).

Several studies have been conducted in cotton regarding heritability of traits such as fiber length, strength, fineness, micronaire and elongation as measured by HVI (High Volume Instrument), stelometer and other instruments. Studies also have been conducted on heritability of sticky cotton estimated by employing biochemical techniques to measure sugar content (Hague, 2008) The entry of the Advanced Fiber Information System (AFIS) in the research sector has facilitated the study of inheritance properties of traits such as short fiber content, maturity ratio, fineness, etc.; however, because of the expense and time associated with AFIS, the system has not been used as part of heritability studies as frequently as HVI (May, 1999; Ulloa, 2006).

Most inheritance studies have been conducted in relation with fiber length parameters. May and Jividen (1999) performed inheritance studies on various fiber parameters as measured by single and high volume- instruments. According to that study, heritability for fiber length (UHML) was 0.46 (single volume instrument) and 0.53 (HVI) and 2.5% span length was 0.21 (single volume instrument) and 0.34 (HVI). Parent-offspring regression heritability of fiber strength was 0.55 (stelometer) and 0.39 (HVI). These findings suggest breeding programs can improve fiber length and strength by using the appropriate tools and methods. Heritability for fiber micronaire was found to be 0.14 (single volume instrument) and 0.15 (HVI) indicating that improvement of micronaire will be a slow and frequently ineffective process. They also demonstrated the

heritability of AFIS measured parameters such as neps, short fiber content, immature fiber content and fineness. Fineness and immature fiber content were found to be significantly heritable, but short fiber content and neps were only moderately heritable traits.

Meredith (1996) showed heritability estimates (broad-sense) for short fiber content (by length and weight) as given by AFIS were 0.59-0.64 in $F_{2:3}$ progeny and $F_{2:6}$ progeny respectively. Ulloa (2006) showed that maturity ratio of fibers were highly heritable ($F_{2:3}$) 0.56 (narrow-sense) and 0.77 (broad-sense). This study also concluded that agronomic traits such as fiber lint percent, boll weight and seed weight were highly heritable. Contrary to the May and Jividen (1999) data, this study showed that fiber neps were moderately heritable (0.46-0.35). Pearson (1949) reported that cultivar variation was more important in explaining the variation in neps than the main effect of location and the cultivar x location interaction. It was suggested that research is needed to understand the expression of neps and other traits that may contribute to nep accumulation, such as maturity ratio, micronaire reading, fiber length and immature fiber content (Ulloa, 2006). Based on data from Ulloa (2006) and Meredith (1996), it can be inferred that traits such as short fiber content (SFC), maturity ratio, immature fiber content (IFC), fineness can be improved with selection. May (1999) suggested that bundle fiber strength, as measured by the stelometer, is a highly heritable trait with a heritability estimate of 0.90 (broad-sense).

Studies for fiber strength as measured by HVI suggest that strength can be improved by breeding programs. Myers and Bordelon (1995) used ten randomly selected

genotypes from a variety trial to estimate broad sense heritability and found lint yield (0.14) and fiber length uniformity (0.09) were lowly heritable traits. This study showed fiber micronaire had a heritability estimate of 0.00 indicating it was not a heritable trait under their experimental conditions. In contrast, May (1999) and Ulloa (2006) concluded that fiber micronaire, which is an estimate of fiber maturity and fiber fineness, was moderately to highly heritable and suggested micronaire can benefit from breeding programs and selection. Improving micronaire will not necessarily and simultaneously improve both fiber maturity and fineness. AFIS measurements have allowed researchers to separate measurements of fineness and maturity. Meredith (1996) reported variation in fiber maturity ratio was a result of environment, whereas fiber fineness was influenced by genes as well as environmental factors.

All the above mentioned studies consider genotype x environment (GxE) interaction and GxE variation to be of minimal importance with respect to its influence in estimating heritability or response to selection. Nevertheless, environment is an important factor in determining fiber maturity. Based on the data published by Wakelyn (2007) on cellulose deposition, fiber maturity is highly dependent on environmental factors. Verhalen and Murray (1969) concluded fiber length and strength were highly heritable traits that could be improved by using mass selection, whereas micronaire was sensitive to environmental factors and would need a pedigree breeding method for effective improvement. May (1999) reported environment was causing variation over genetic factors. Meredith (2003) showed variance associated with location contributed approximately 50% to the total variance observed for the USDA Regional High Quality

Tests performed for over 36 years. These studies suggest cotton breeders are faced with substantial challenges when making selections for fiber maturity.

Breeding Methods

Once heritability estimates for trait (s) of interest have been made, the breeder can then devise strategies concerning the type of breeding method that needs to be employed for crop improvement. A plethora of approaches and methods can be used by breeders to improve populations. One of the most important requirements of any method is to start with a genetically diverse parental material. This leads to genetic diversity in progeny, which can then be purified through a series of subsequent steps depending on the breeding method (Acquaah, 2007; Poehlman, 2006; Falconer and Mackay, 1996; Brown and Caligari, 2008). Some common methods used by cotton breeders are mass selection, recurrent selection and pedigree selection. There are modifications to these methods, for example single seed descent, which are often used. Jensen (1988) indicated mass selection was probably the first breeding method practiced in plants. In a study published by Ware (1950), it was mentioned a large amount of cultivars in the 19th and 20th century were originally derived from reselections of existing cultivars. Pedigree selection was first documented as a breeding practice in the late 1800's (Jensen, 1988). It is now the most widely used breeding method by both public (82%) and private (71%) cotton breeders (Bowman, 2000).

Acquaah (2007) described mass selection as a selection method from a biologically variable population. The purpose of mass selection is population

improvement through increasing the gene frequencies of desirable genes. Selection is based on plant phenotype and one generation per cycle is needed and can be employed once or multiple times (recurrent mass selection). There is no scope to increase genetic variability in this method of selection. The objective is to improve the average performance of the base population (Fehr, 1993). Recurrent selection involves a base population with diverse alleles and crosses involving the parents. These crosses are made to develop a genetically variable population which is then evaluated for improved and superior performance (Fehr, 1993). Selected plants are used to create improved populations. Selection pressure generally is low and the basis for selection is usually attributed to phenotypic traits. The objective of this method is to increase the number recombination events which may lead to genetic variability and ultimately enhanced traits (Fehr 1993).

The pedigree method was first described by H. H. Lowe in 1927 (Acquaah, 2007). This method involves meticulous record keeping by the breeder in terms of the population and its ancestry. The base population is crossed to generate an actively segregating progeny. Selections are made in subsequent generations for desired traits. The success of this method lies with the breeder's ability to identify and select superior phenotypes. Reselection is continued until the level of homozygosity within the population reaches the desired level. Documentation of the ancestry enables the breeder to identify parent-progeny back to the original early generation individually selected plant. Selections can be made as early as F_2 generation. Self-pollination is practiced in subsequent generations to create additional segregation and development of additional

homozygous alleles. The pedigree method allows for early generation testing (F2 onwards). In the cotton breeding community, early generation testing has been practiced (Bowman, 2000) with varying degrees of success (Jones and Smith, 2005). Typically the top 10-15% of the population is selected in a breeding program (Poehlman 2006; Fehr 1993). In cotton, selection pressure is high starting at the F_4 generation because subsequent yield trials require considerable resources including costly fiber testing. In most cases spinning tests, which require more than 10 kg of lint, need to be performed in later stages.

Diallel Mating System

Use of diallel mating systems has been used and documented in multiple crops including cotton. This mating system can evaluate yield, lint percentage, agronomic traits and fiber properties. (Berger et al., 2012; Joy et al., 2010; Ragsdale and Smith, 2007; Topal et al., 2004; Basal and Turgut, 2003; Al-Rawi and Kohel, 1969, Jensen, 1970; Griffing, 1956). Fehr (1993) describes two types of designs: nested design (type I) and factorial design (type II). Different mating systems and designs (diallel, nested designs) are frequently used in cotton research for estimating the general combining ability (GCA) and specific combining ability (SCA). GCA estimates the general performance of a cultivar with other cultivars mated and SCA determines parents that provide the best specific combination for a given trait (Hayman, 1954; Hayman 1960 and Griffing, 1956). Based on the GCA analysis we can estimate the parent's genetic ability to influence progeny for particular traits as a result of additive effects. It allows

for the selection of a parent which is a good general combiner (Griffing 1956). SCA identifies the specific combination of crosses that yield the best results.

The diallel mating design involves the mating of parents in all possible combinations. This technique can be used to estimate genetic variance parameters and heritability and to identify cultivars which may be useful as parents in a breeding program for trait improvement (Kearsey and Pooni, 1996).

Griffing (1956) described that the basic methods of the diallel analysis. Method 1 involves parents and all F_1 combinations including reciprocals. Method 2 is composed of the parents and all F_1 combinations without reciprocals. Method 3 consists of all F_1 combinations including reciprocal crosses but without parents, and Method 4 comprises only F1 combinations without reciprocals or parental lines. Each method can be evaluated as Model 1 or 2 (fix or random). Fixed effects are required when the parental lines are selected for the test.

Tools for Crop Improvement

Complex crossing schemes allow breeders to overcome linkage blocks and create novel allele combinations. Exotic cotton lines have been used as parents with elite upland cultivars introduce new traits, especially for host plant resistance, to increase the yield potential of cotton cultivars (Brubaker et al., 1999 and Stewart, 1995). Traits such as nematode (*Rotylenchus reniformis,* Linford and Oliveira; *Meloiodogyne incognita*, races 3 and 4) resistance, insect resistance, fiber quality, naked seed, glandless plants, heat/drought tolerance have been introduced into modern cultivars through intermating

with exotics (Stewart, 1995). Genetic linkage can be broken to separate undesirable traits from the trait of interest. Specially developed parents are also crossed to capitalize on the phenomenon of heterosis for cultivar development. Hybridization is thus used to develop F_1 hybrids. Crosses are also made to generate genetic variability and to maintain diversity in the gene pool. Lastly segregating populations derived from cross-pollinations between genetically diverse parents can be used to study inheritance pattern of traits of interest (Brown, 2008 ;Poehlman, 2006).

Another tool available to breeders is mutagenesis. H. Stubbe demonstrated the use of mutagenesis in producing mutants in tomato, soybean and other crops in 1928 (Acquaah, 2007). Auld et al., (2000) reported that improvement in cotton using mutagenesis was rarely practiced in comparison to other crops. Mutagenesis was shown to be a successful tool to create variability in diploid and tetraploid cottons (Auld et al., 2000). Lowery et al. (2007) described chemical mutagenesis of cotton using Sodium Azide and Ethyl Methane Sulfonate (EMS) to generate 'naked and tufted' seed.

Lastly, molecular tools hold great potential for improving cotton. The introduction of molecular markers into breeding programs has increased the development of improved varieties. This technology facilitates efficient selection of genomes with desirable traits (Rungis et al., 2005 ;Ribaut and Hoisington, 1998). QTLs (Quantitative Trait Loci) have been identified for fiber strength, length (Zhang et al., 2003; Zhang et al., 2004). Molecular breeding integrated with conventional phenotypic selection is increasingly being utilized for important traits in cotton (Cantrell and Xiao, 2008). Molecular markers are used extensively in marker-assisted technology and

dissection of quantitative trait loci (QTLs) that affect complex traits (Park et al., 2005). Recently Percy et al. (2012) developed a core set of Simple Sequence Repeats (SSR) markers for the characterization of gossypium germplasm. Markers are a powerful tool for identifying polymorphisms in genomes (Rungis et al., 2005). Different markers are available and widely accepted today such as SSR (Single Sequence Repeats), Single Nucleotide Polymorphism (SNP), Amplified Fragment Length Polymorphism (AFLP), and Restricted Fragment Length Polymorphisms (RFLP). PCR-based markers are the most preferred markers today (Lacape et al., 2003; Lacape et al., 2007). In order to contribute to the expanding genomic resources for cotton research and improvement, the Monsanto Corporation has facilitated uploading of unique SSR primer sequences, respective target clone sequence, and chromosome bin designation to the cotton database, which is available for general use in the cotton research community without restrictions (Xiao et al., 2009). Molecular markers have been used to study and understand cotton genomics and genetic diversity (Rana et al., 2005; Garcia et al., 2004). Several studies have been done on genetic mapping (Pearl et al., 2004; Zhang and Stewart, 2000) and DNA fingerprinting in cotton (Saha et al., 1998). Recently, functional markers were developed for identifying cellulose synthase genes. This was developed using in silico single nucleotide polymorphism (SNP) identification and Primer-BLAST designing gene-specific markers (Lin et al., 2012).

Fiber Development

Cotton fiber development occurs in overlapping phases namely: differentiation, initiation, elongation, secondary cell wall (SCW) development, and maturation. Fibers emerging from the seed can be of two types, linters and fuzz fibers. The initials of the lint begin their growth on the day or the day after flowering and those of the fuzz begin 5 or 6 days post-anthesis (dpa) and continue to the tenth or eleventh day. Cotton fibers are trichomes that initiate from the ovule epidermis. Differentiation of fiber cells occurs approximately – from three days prior to anthesis to the day of anthesis. It is followed by initiation and elongation, from a day prior to anthesis and generally up to approximately 20 dpa. However it has been shown that elongation can continue up to 45 dpa in long staple cotton (Naithani et al., 1982) or cease around 25 dpa in shorter staples (Jasdanwala et al., 1977). During the elongation phase, lint hair continues to grow and at this stage, the fiber length is set. The SCW begins to thicken at about 15 dpa and continues until about 50 dpa. After the completion of this stage, desiccation occurs and finally the boll opens. SCW starts to build up on the inner surface of the thin primary wall. The time scale of initial growth of SCW development depends on various factors, depending on growth conditions, genotype, and planting season. Generally, the build-up of the SCW is initially fairly rapid, but then the rate slows down a few days before boll opening. The free moisture inside the boll evaporates causing the fibers to dry and collapse. This gives a convoluted ribbon form to raw cotton fibers (Basra and Malik, 1984; Basra, 1999; Wilkins et al., 1999; Lord, 1981) (Table1).

Table 1: Development of cotton fibers

DEVELOPMENT STAGE	EVENT	TIME REQUIRED (DPA)
Differentiation	Differentiation of ovular epidermal cells for fiber initiation	-3dpa to 0dpa
Initiation	Fiber initials develop	0dpa to 6dpa
Elongation	Fibers increase in length	0dpa – 20dpa
Secondary Cell Wall (SCW) development	Development of secondary cell wall by the deposition of cellulose	15dpa to 50dpa
Dessication and Maturation	Evaporation of moisture within boll followed by boll opening	50 dpa to 65dpa

All these stages in fiber development impact the final configuration of the fiber in terms of its quality. Initials determine the amount of fibers produced (yield), elongation determines fiber length, and SCW development determines fiber maturity, fiber strength, micronaire and weight. All of these traits have an impact directly or indirectly on fiber yield.

Fiber Quality

Fiber properties such as length, length uniformity, short fiber content, strength, fineness and micronaire are important to cotton plant breeders and the textile industry. It

has been shown that fiber length and length distributions, strength, and fineness are the most important traits for the textile industry. The importance of fiber traits vary depending on the method of spinning used (Hsieh et al., 2000). Ring and rotor spinning give importance to fiber length, strength, fineness and uniformity ratio. However, rotor spinning is less sensitive to short fibers compared to ring spinning (Bradow and Davidonis, 2000).

Fiber length has been established for commercial upland cultivars 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 et al., 1996). Length uniformity is the ratio of the mean length of fibers to the upper mean half and expressed as a percentage (Anthony, 1999). Fiber strength is usually given by measuring the strength of a bundle of fibers of fixed mass. This is an important trait because the strength of a fiber bundle directly correlates with yarn strength (Hequet and Ethridge, 2000). Rotor spinning requires strong fibers for optimal processing (El Mogahzy, 2000). Stronger fibers are less susceptible to damage from rigorous cleaning treatments.

Fiber micronaire as measured by HVI is an accepted estimate of fineness and maturity by the cotton industry. The optimum range for cotton micronaire is between 3.7 and 4.2. This measurement is based on principles of air permeability of a test specimen of fixed mass contained in a holder of fixed dimensions explained by Lord (1981). It is measured with an airflow meter by placing 10 grams of cotton fiber into a cylinder and compressing it to a constant volume and setting the air pressure at 68.94kPa The rate of air flow through the cylinder is proportional to the inverse of the specific surface squared

because coarse fibers have less surface area per unit weight and air flows between these fibers more easily than between fine fibers. Accordingly, coarse fibers have high micronaire readings and fine fibers have low micronaire readings.

Fiber fineness is commonly defined by spinners as mass per unit length. Fineness allows for selection of fibers based on minimum number of fibers required to spin a particular sized yarn. (Wakelyn et al., 2007). The possible yarn count range for a specific cotton type is related directly to the fineness of the individual cotton fibers (Wakelyn et al., 2007). AFIS gives us the gravimetric fineness measurements also known as linear density of the fibers. Cottonscan® has been recently developed which gives a measurement of fiber fineness (Abbott et al., 2010). Fiber maturity is defined as the ratio of the area of the cell wall to the area of a circle having the same perimeter as the fiber section, also known as theta (θ).

Fiber maturity is a growth characteristic and represents the development of the secondary cell wall. All of the cotton fibers do not grow in the same manner (Lord, 1981). If growing conditions are favorable, most fibers are mature, i.e. have relatively thicker secondary cell walls. Individual fibers in the same boll of cotton also show variation in the cell wall thickness (Wilkins et al., 1999). Maturity measurements can be obtained by using the AFIS, Cottonscope® (Rodgers et al., 2012), Fourier transform infrared spectroscopy (FTIR) which have been used in the research setting, but not commercially available (Liu et al., 2011).

Variability in the quality of cotton fibers occurs because of a number of factors including fiber maturity. Thin secondary cell walls lead to immature fibers, which are

weak and process inefficiently at textile mills. Weak fibers break easily during fiber processing resulting in more short fibers and lower average fiber length. Immature fibers also get entangled easily leading to the formation of fiber neps. Immature fibers and neps have compromised dye uptake resulting in barre and white specks at the fabric level (Wakelyn et al., 2007;Ethridge and Simonton, 2004; Davidonis et al., 2003; Mangialardi, 1987).

Variability in Fiber Quality

Cotton fibers have a high-degree of variability in quality across different species, cultivars, within the same cultivars, within fields, across and within rows, within a plant and even within a single boll. (Clouvel et al., 1998; Davidonis et al., 1999; Wilkins et al., 1999; Davidonis et al., 2004; Bednarz et al., 2006;Kothari et al., 2008). This has an impact on the entire cotton industry because efficiency of spinning depends on set parameters for fiber quality standards.

Variability in fiber quality is affected by the plant's growing habit, environment, metabolic processes, soil quality, etc. Variability also has been reported in quality and yield because of variation in soil pH and organic matter (Johnson et al., 2002; Elms et al., 2001). Growing environment is probably one of the greatest causes of variability in fiber quality and yield within the same genotypes which can be attributed to rainfall, temperature and sunlight. Changes in temperature impact the metabolism of the plants which in turn affects boll development. This leads to unpredictable changes in the fiber quality within the developing bolls (Gipson and Joham, 1968; Gipson and Joham, 1969).

Typically higher temperatures result in faster metabolism in the plants. If high temperatures occur during fiber maturing phase, fiber quality can be adversely affected. This is because under normal growing conditions metabolism is slowed during the maturation phase. Sub-optimal temperatures negatively affect the SCW synthesis leading to formation of immature fibers (Haigler et al., 2009; Wang et al., 2009). Ultraviolet radiation leads to depolymerization of cellulose chains in the fibers leading to changes in the overall fiber quality (Morton and Hearle, 1997). Lack of rainfall leads to water stress, which leads to higher vegetative growth compared to boll set. When mineral and nutrition uptake from the soil is compromised during the fruiting stage, fiber quality of the bolls already set can be poor (Johnson et al., 1999).

The most common damaging nematodes afflicting cotton in the U.S. are southern root-knot (*Meloidogyne incognita*), reniform (*Rotylenchulus reniformis*) and Columbia lance (*Hoplolaimus columbus*). Southern root-knot nematode is found across the cotton belt in coarsely textured soil. Reniform nematode populations are highest in North Carolina to Texas. Columbia lance nematode is concentrated in the southeast region (Cotton Incorporated, 2012). Thrips (*Frankliniella spp.)* and aphids (*Aphis gossypii*) are typical early-season insects followed by bollworms (*elicoverpa armigera*), spidermites (*Tetranychus pacificus*) and white flies (*Bemisia tabaci*) (Boyd et al., 2004). Insects can impair yields and cause fiber quality issues (e.g. stickiness). Stink bugs (*Nezara viridula*) have been associated to boll rot and poor lint turnout (Toews et al., 2010). Thrips cause seedling damage and emergence issues during early growing season.

Cotton bollworms cause damage to squares and bigger bolls causing losses in yield and fiber quality (Herbert et al., 2009).

Aside from phenotypically controlled fiber quality, fiber analysis and textile processing introduce additional sources of variation. (Behery, 1993; Cranmer, 2004; MacAlister and Rogers, 2005; Faulkner, 2008). When cotton is harvested with a mechanical stripper, higher short fiber content is generated in comparison to cotton harvested with a mechanical cotton picker. (El Mogahzy and Chewning, 2001). Because of the amount of foreign matter, stripped cotton needs lint cleaning at the gin. This additional mechanical stress leads to more fiber breakage resulting in higher short fiber content and overall reduced fiber length in comparison to cotton that does not go through lint cleaners.

Ginning techniques for research projects are based on the amount of fiber to be ginned, testing methods and objectives of studies. There are three common ginning techniques used for research purposes: saw ginning, roller ginning and hand ginning. Various studies have shown fiber quality changes significantly based on the ginning mechanism applied to the same set of fibers being tested. Saw ginning tends to break more fibers than roller ginning while hand ginning tends to break fewer fibers than roller ginning (Robert et al., 2000; Hequet et al., 2006). Fiber breakage alters length distribution and short fiber content. Hand ginning is not an industrial process and is only used in research involving small samples of fiber. Commercial upland cotton is processed by saw gins. An advantage of saw ginning is the blending of cotton from various areas of the field and plants. Roller ginning is less effective in mixing the lint. In

research scenarios saw ginning, roller ginning and hand ginning are all commonly used. Laboratory scale gins almost never provide adequate mixing, hence it is important before fiber testing, to use a blender to mix the lint of the ginned samples because of the high variability seen within a plant (Hequet, 2006; Hequet and Ethridge, 2000).

Sampling techniques for cotton typically involve picking boll samples or sampling from the whole plot following machine harvest. Boll sampling is quick and effective as long as care is taken to harvest a random set of bolls from the testing area. This technique can compromise accuracy of data if the hand-picking method is biased. The plant usually has good quality bolls at the bottom fruiting positions and poor quality bolls at the upper branches. A proper sampling technique needs to be developed that ensures that sufficient number of bolls are picked from different fruiting positions of the plants that represent the actual fiber quality of the plot/row being tested.

Cotton Fiber Maturity

Fiber maturity is defined as the ratio of the area of the cell wall to the area of a circle having the same perimeter as the fiber section (θ). Fiber maturity is a growth characteristic and represents the development of the secondary cell wall. Fiber maturity directly or indirectly affects almost all other fiber properties. Immature fibers lead to low micronaire values, have weak SCW, and easily break. Excessive fiber breakage can occur during ginning and cleaning immature cotton fibers. Therefore, high SFC is generated in samples and fiber length is indirectly affected. Immature fibers lead to neps,

which lead to a lower quality fabric contaminated with white specks (Mangialardi, 1987; Davidonis et al., 2003; Ethridge and Simonton, 2004; Hequet and Abidi, 2010).

The reference method for the measurement of fiber maturity and fiber perimeter is the microscopic analysis of cotton fibers. This analysis can be performed on longitudinal fiber sections or on transverse fiber cross-sections. Considerable research has been conducted with image analysis technology to measure cotton maturity and other parameters from fiber cross sections (Matic-Leigh and Cauthen, 1994; Thibodeaux and Rajasekaran, 1999; Xu and Huang, 2004; Hequet et al., 2006). It has been shown that for a high-degree of accuracy in measuring fiber perimeter and relative wall thickness, image analysis of fiber cross-sections is one the best measuring techniques (Hequet et al., 2006). Wall thickness, fiber perimeter, maturity ratio (maturity), and degree of thickening are derived from the measured cross-sections of the fibers. The degree of thickening defined by θ is given as follows:

$$\theta = \frac{\text{Area of the cell wall}}{\text{Area of circle having same perimeter}}$$

Completely circular fibers, irrespective of their perimeter have value of θ equal to unity. Typical mature fibers have a moderately high value of θ. Immature fibers with little secondary wall thickening have a small value of θ. The degree of thickening θ may be regarded as a fundamental unbiased measure of fiber maturity, measuring the extent of the fiber wall relative to its maximum potential (Hequet et al., 2006).

Because of the time and expense involved with analysis using fiber cross sections, this study will use the AFIS maturity ratio measurements for estimating fiber maturity. AFIS also provides gravimetric fineness measurements which is the weight per unit length. This measurement is affected by the maturity of the fiber because immature fibers weigh less than more mature fibers. Hequet et al. (2006) reported standard fineness can be estimated from the AFIS maturity ratio and fineness measurements. This research group also determined the relationship of all equations that join fiber maturity ratio, θ (theta), gravimetric, and biological fiber fineness.

In terms of fiber maturity in a breeding program, May (1999) reviewed seventeen studies concerning fineness and fiber maturity. A majority of these studies showed that fiber maturity had a stronger environmental effect than a genetic effect, which challenges breeders.

Fiber Testing

HVI Testing

HVI is used commercially to grade cotton and measure essential properties of fibers. It is an invaluable system to the research sector because it provides an objective measure of fiber quality. HVI measurements are either equally accurate or better compared to single volume instruments used for fiber testing (May and Jividen, 1999). The micronaire measurement given by HVI is the accepted measure to estimate fiber maturity and fineness in the cotton industry. All HVI testing is performed under

standardized and controlled humidity and temperature conditions (65% relative humidity and 21^{o}C).

HVI measures length as the mean length and upper half mean length. UHML is the mean length by number of the longer one half of the fibers by weight. Length uniformity is a ratio of the mean length to the upper half mean length expressed as a percentage. The standard device currently used by HVI is a fiber comb with parallel needles attached with a spacing of 13needles/inch. The sample is placed in the fibrosampler so fibers protrude through holes. Fibers are picked up by the needles of the comb as the comb is moved over the sample. The fibers are then carded to produce a beard of parallel fibers. The density along the beard is then photo-electronically scanned from the base to the tip. The light attenuation is assumed to be related to the fiber mass between the lenses. Assuming that fibers have uniform linear density or fineness, the measured amount is proportional to the number of fibers. The sample density is then plotted against the distance from the comb. The HVI fiber-length data are converted into the percentage of the total number of fiber present at each length value and into other length parameters, such as mean length, UHML and length uniformity (Behery, 1993; Steadman, 1997).

HVI also gives fiber strength measurements. Strength is measured as the grams of force required to break a bundle of fibers with the bundle being equal to one tex unit (grams/tex). A tex is a unit equal to the weight in grams of 1,000 meters of fiber. Fiber strength is reported as kilonewton meter per kilogram (kN m kg-1) or grams/tex (Anthony, 1999) HVI strength values report the tenacity or specific strength of a fiber

bundle (Hequet et al., 2006). This measurement is for a given weight of fibers (bundle testing) and not measurements for individual fiber strength which might bring in a degree of bias to the obtained data.

AFIS Testing

AFIS works with aeromechanical processing of the fibers similar to opening and carding. Fibers are measured under conditions which are dynamically similar to real-world processing (Hequet and Ethridge 2000). The AFIS was developed to rapidly measure essential cotton fiber property distributions such as length, diameter, maturity and fineness (Bragg and Shofner, 1993). It gives the value of maturity ratio, neps, nep size, immature fiber content, short fiber content, and trash content.

AFIS uses about 5,000 fibers for each replication to determine fiber quality depending upon pre-determined parameters. As little as 0.5 mg of fiber samples can be measured accurately (Wartelle et al., 1995). Recently it was established that a 10,000 fiber analysis with a single replication is no different than testing a 3,000 fiber sample with three replications on AFIS. This change in protocol saves time and money (Hequet et al., 2006). AFIS works on the principle of individualizing fibers and cleaning them before they are presented to an electro optical sensor. High velocity air flow causes fibers to move past the optical sensor. These fibers tend to generate electrical signals. The interruption of the moving light beam impinging on the electro optical sensor produces two types of signals of interest (Bragg and Shofner, 1993). One signal results from the light beam that is being blocked by the fiber in proportion to its mean optical diameter and in direct relation to its time of flight in the sampling volume. The other

signal is the result of the light scattered by the same fiber at 40^{o} from the beam direction. Data from the attenuated signal is used to measure the individual length and diameter of the fibers. The data from this 40^{o} scattering signal yield fineness and maturity measurements. Some underestimation of fiber length can arise due to crimp present in the individualized fibers (Hinohosa and Thibodeaux, 1994).

CHAPTER III

MATERIALS AND METHODS

Experimental Material

Box Mapping Study

Four genotypes, Acala 1517-99, Fibermax 832, Half and Half and Texas Marker-1 (TM-1) were selected for this study. These were selected based on growing habits, fiber quality, rate of crop maturity and adaptation to Texas.

Acala 1517-99 is a cultivar with acceptable yields and high-quality fiber. The cultivar has an indeterminate growing habit and dense foliage. Plant height under normal cultivation is generally 105cm and resistant to Verticillium wilt and to a lesser extent, bacterial blight. It was derived from a cross between B742/E1141 and developed at the New Mexico Agricultural Experimental Station (Cantrell et al., 2000). Fibermax 832 was developed in Australia by the Commonwealth Scientific and Industrial Research Organization (CSIRO) in Australia and marketed by Bayer CropScience. It is a cultivar with an okra leaf, acceptable fiber yield, and high-quality fiber (Constable, 2001). Half and Half was developed in 1936 in Georgia. Known for its short staple and round bolls, this cultivar also has higher fiber micronaire values (Brown, 1936). Texas Marker-1 (TM-1) is a standard reference for American upland cotton. TM-1 was selected in 1947 from a commercial variety ‘Deltapine 14’ which was originally released in 1941 (Kohel et al., 1970). It has green foliage, broad leaves, cream pollen, a non-cluster fruiting habit

and white lint. This genotype has been widely used in research programs, isoline development, genetic and physical mapping, and QTL analysis (Kohel et al., 2002).

Boll Sampling Study

FiberMax 832 and Deltapine 491 are commercial upland cultivars with excellent fiber quality. FiberMax 832 is an okra leaf type plant which is known for high fiber quality and acceptable yields. Deltapine 491 is a commercial variety which has normal leaves and has high yields with excellent fiber quality (Table 2).

Diallel Study

Genotypes were selected for this study specifically on the basis of fiber maturity and micronaire. They included Acala 1517-99, Deltapine 90, Fibermax 832, Half and Half and Tamcot HQ-95. Fibermax 832 and Deltapine 90 are commercial cultivars with fine fibers and good fiber maturity (Table 2).

Potential parents were grown in the greenhouse in fall 2008 and in the field during summer 2009. Seed cotton was harvested from the plants, then ginned and fiber samples sent to the Texas Tech University's Fiber and Biopolymer Research Institute (FBRI) in Lubbock, TX, for fiber testing with AFIS and HVI. A 50-boll sample was randomly picked from plots of each genotype with three replications for fiber testing. Based on the data from HVI and AFIS testing, five parents, Acala 1517-99, Deltapine 90, Fibermax 832, Half and Half and Tamcot HQ-95,were selected to intermate in a partial diallel during the summer of 2009 and 2010 in the field. Ten crosses were made in all combinations for the partial diallel mating system employed (Acala 1517-99 / Fibermax 832, Acala 1517-99/ Deltapine 90, Acala 1517-99/ Half and Half, Acala 1517-

99/ Tamcot HQ-95, Fibermax 832/ Deltapine 90, Fibermax 832/ Tamcot HQ-95, Fibermax 832/ Half and Half, Deltapine 90/ Half and Half, Deltapine 90/ Tamcot HQ-95 and Tamcot HQ-95/ Half and Half). Seed from the crosses were used for growing F_1 plants. During the summer of 2010, F_1 plants generated F_2 seed for heritability estimation. BC_1F_1 seed was generated in the summer of 2011. Parents, F_1's and F_2's were grown in a randomized complete block design in the field at College Station, Texas, in 2011. Grab samples were harvested from this test, ginned on a laboratory ten saw gin and fiber testing was done using HVI and AFIS. This test was repeated in summer 2012 in the field at the same location with an inclusion of BC_1F_1 for diallel analysis and heritability estimates.

Genotypes used as parents for this test were specifically chosen and hence were not randomly generated populations. Results of this study apply only to the specific parents and generations used.

Table 2: Pedigree and traits of parental genotypes

GENOTYPE	DESCRIPTION
Acala 1517-99	Acala 1517-99 is a high quality cultivar released from the New Mexico Agricultural Experiment Station in 1999. (Cantrell et al., 2000). This cultivar originated from a single-plant selection from experimental B2541. B2541 was derived from the cross between B742/E1141. The pedigree of B742 is Acala 9136/250. Acala 9136 has significant introgression from G. *barbadense* (Cantrell, et al., 2000)
Deltapine 90	Mississippi Obsolete Variety Collection - G. hirsutum characterized by high quality cotton fibers, short plants and acceptable yields (PI 529529).
Fibermax 832	Fibermax 832 is an okra-leaf type with a reputation for high fiber quality and yield. This cultivar was developed by Commonwealth Scientific and Industrial Research Organization (CSIRO) in Australia and marketed by Bayer CropScience (Constable, 2001).
Half and Half	Half and Half belongs to the round-boll, short-staple group of varieties. It was developed by selection from Cook by H. H. in Georgia. It received the name 'Half and Half' because it was marketed as producing seed cotton that was half lint and half seed, which was not completely accurate. The first selection was made in 1906 and the cultivar was released in 1936 (Brown, 1936).
Tamcot HQ-95	Tamcot HQ-95 was developed in the Texas Agricultural Experimental Station by Thaxton and El-Zik (1990). This is a high quality cultivar. The pedigree of this genotype was from a cross between Tamcot CD3H X MAR-CABU'CS-2-1-83 and designated MAR-CABUCD3H-1-86. Tamcot CD3H originated from cross Tamcot SP37H X CDPS-1-77. CABU'CS-2-1-83 originated from cross CAMD-21-S-78 X BCUS-8-76 (El-Zik and Thaxton, 1990).
Deltapine 491	Deltapine 491 is a commercial variety with high quality fiber and high yield potential. Identification and registration: PI 618609 PVPO.

Experimental Design

Box Mapping Study

All genotypes were grown in field trials in 2009, 2010 and 2011 at the Texas AgriLife Research farm at College Station, Texas, and at the Texas AgriLife Research & Extension Center at Lubbock, Texas, in 2010 and 2011. All genotypes were grown in two-row plots (12 m x 1.0 m) with three replications each year. The soil type at College Station was Westwood silt loam, a fine-silty, mixed thermic Fluventic Ustochrept, intergraded with Ships clay which is a fine, mixed, thermic Udic Chromustert. Soil in Lubbock was Acuff loam a fine-loamy, mixed, superactive, thermic Aridic Paleustolls type.

The experiment was arranged in a randomized complete block design. Seed cotton was harvested from all the plants and was partitioned by fruiting branch. Seed cotton was hand-harvested from the first fruiting position on each sympodial branch. Approximately thirteen samples were harvested from each genotype. Seed cotton was ginned on a ten-saw laboratory scale gin, and sent to the Fiber and Biopolymer Research Institute (FBRI) for fiber testing with AFIS. For AFIS testing, one non-replicated sample was used with 10,000 fibers per sample. Fiber testing was done at the FBRI at Lubbock, Texas. For sample preparation, a 500mg tuft of fibers was drawn into a 25 cm length sliver and 10,000 fibers were measured from that sample. Conditioning and testing were carried out under constant climate controlled conditions. The standard temperature for textile testing is 20 ± 2°C and 65 ± 2% relative humidity. Prior to testing, samples were arranged in single layers and allowed to equilibrate for 48 h under standard atmospheric

conditions. In order to minimize experimental error, the same technician ran all the samples. The machine was calibrated every morning for efficiency and stability of fiber testing.

The genotypes used for this test were specifically chosen and hence are not a randomly generated sample. The results from this study apply only to the specific cultivars used.

Boll Sampling Study

The genotypes were grown in the field in 2009, 2010 and 2011 at the Texas AgriLife Research farm at College Station, Texas. Both genotypes were grown in four-row plots (12 m x 1.0 m) with four replications during all years tested. The soil type at College Station was the same as the box mapping study. The experiment was set up as a randomized complete block design. The seed cotton sampling protocol included ten methods. Seed cotton was harvested, ginned on a ten-saw laboratory scale gin, and sent to the FBRI for fiber testing with HVI and AFIS. Sampling techniques included a grab sample machine-picked from an entire row within the plot. Three random handfuls of seed cotton were taken from a harvest sack from each plot. This sample was considered as the representative of true fiber quality of the plot. The other sampling techniques included three sets of 15, 25 and 50 hand-picked boll samples. The first set of 15, 25 and 50 boll samples were picked only from the bottom half of the plant, the second set of 15, 25, 50 boll samples were picked only from the top half of the plant and the last set of 15, 25 and 50 boll samples were picked randomly from all parts of the plant(s) within the

row. The first set was designated as ‘high quality (HQ)’, the second set designated as ‘low quality (LQ)’ and the last set designated as named ‘random (RND)’.

HVI testing was performed with a single, non-replicated measure for micronaire and two replications for fiber length and strength. AFIS testing was performed with the same procedure used to test the box mapping samples.

The genotypes used for this test were specifically chosen and hence are not a randomly generated source of variation. Results of this study apply only to FiberMax 832 and Deltapine 491.

Diallel Study

In 2011, parents and the filial progeny were grown at the Texas AgriLife Research Farm located near College Station in a randomized complete block design with four replications. In 2011 Parents, F_1's and F_2's were grown in single row plots. This study was hand planted and thinned to contain 20 plants per row. Each row size was 7.62 m x 1.0 m and thinned in order to minimize intra-plant competition. Soil type was a Westwood silt loam, a fine-silty, mixed thermic Fluventic Ustochrept, intergraded with Ships clay which is a fine, mixed, thermic Udic Chromustert.

For fiber testing and analysis, all rows were machine harvested using a mechanical cotton picker harvester. A grab sample was ascertained by taking three random handfuls of seed cotton from the harvest sack. Fibers were ginned on a laboratory saw gin. HVI testing was performed with one sample for micronaire and two replications for fiber length and strength. For AFIS testing, one sample replication was used with 10,000 fibers for the test. Fiber testing was performed at the FBRI in Lubbock,

Texas, with sample preparation and conditions maintained as per the protocols mentioned in the box mapping and boll sampling studies described earlier.

Statistical Analysis

Box Mapping Study

The trial design was a split-plot design where the factorial arrangement of treatment (genotypes) was the main plot and the thirteen sympodial branches (sympodial) were the split-plot factor for each year. For this analysis it was assumed that sympodial branches are independent from each. Replications (rep), rep x factorial treatments (genotypes), rep x sympodial (branch) were considered random effects. Years, years x factorial treatments (genotypes), years x sympodial (branch) were also considered random effects. Factorial effects, genotypes and sympodial (branches) were considered as fixed effects. For mean separation, the Waller-Duncan method was used. For the purpose of mean separation testing, replications (rep) and years were considered random effects. Fiber data for the samples were analyzed and ANOVA with means, standard deviation and mean separations (Waller-Duncan method) calculated using the PROC GLM SAS 9.3 (SAS Institute, 2012).

Boll Sampling Study

The trail design was a split-plot design where the factorial arrangement of treatment (genotypes) was the main plot and the ten sampling techniques (sample) were the split-plot factor for each year. Replications (rep), rep x factorial treatments (genotypes), and rep x samples were considered random effects. Years, years x factorial

treatments, and years x sample were also considered random effects. Factorial effects, genotypes and sampling techniques were considered as fixed effects. For mean separation, the Waller-Duncan method was used. For the purpose of mean separation testing, replications (rep) and years were considered random effects. Fiber data for the samples were analyzed and ANOVA with means, standard deviation and mean separations (Waller-Duncan method) calculated using the PROC GLM SAS 9.3 (SAS Institute, 2012).

Diallel Study

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 F1.s but not reciprocal F1.s are included [p (p+1)/2 combinations= 15 combinations (5 parents)]. Multiple programs can be used for diallel analysis. This testing was done using diallel analysis utilizing Diallel-SAS05 as described by Zhang et al. (2005).

Heritability estimates were calculated from the data in the diallel. Variances for additive and dominance effects were calculated from the variance from GCA and SCA respectively. Formulas were used from Singh and Chaudhry (1985) and, Hallauer and Miranda (1981). Narrow-sense heritability, h^2 = Va/Vp Vp= Va + Vd + Ve (Vp= Variance of phenotype, Va= additive variance, Vd= dominance variance, Ve= error variance).

CHAPTER IV

BOX MAPPING STUDY

Results and Discussion

AFIS testing indicated genotype x year interaction for all traits with the exception of neps and nepsize (Table A.1). Hence length (w), length (n) parameters and fiber fineness, MR, IFC and trash were analyzed separately each year. Fiber nepsize had no effect from genotype or sympodial branch indicating that this trait had no variability within the plants in College Station. Fiber neps had a highly significant effect from sympodial branches within the plant. Neps had no interaction from the genotype (Table A.3). Fiber neps were highest at the thirteenth branch followed by branch eleven and twelve (Table 3). Plants had the fewest neps from sympodial branches one through ten. Regression data showed there was a strong relationship between increasing neps from branch one through thirteen (Figure B.1). There was a weak relationship between sympodial branches and nepsize (Figure B.2).

In 2009, fiber fineness, IFC and MR showed no interaction from genotypes. Fineness and MR did not have an effect from sympodial branch either, suggesting there was no variability for these two traits within the plant (Table 4). While there were no significant differences among means, regression data suggests there is a strong relationship between fiber fineness and sympodial branch (Figure B.3). Fibers tend to get finer from the first branch to the thirteenth. MR also displays a trend of decreasing value from branch one through thirteen (Figure B.4). IFC had a significant sympodial

branch effect. IFC was highest in cotton produced from the thirteenth branch. The lowest proportion of immature fibers was in samples collected from branches one through five. Although average MR data showed no significant differences among sympodial branches, the percentage of immature fibers significantly increased from bolls harvested in the top half of the plant. Regression showed a moderate relationship between sympodial branch and IFC (Figure B.5). Because immature fibers are associated with neps, the high frequency of IFC is a possible explanation for the high incidence of neps.

Fiber length (w), UQL (w), SFC (w), length (n), SFC (n) and trash had a highly significant interaction between genotype x sympodial branch. All genotypes had a significant/highly significant interaction between sympodial branches within the plant for all these traits (Table A.5). Fiber data from Acala 1517-99 showed fiber length (w) was highest at branch three. The shortest length was observed from cotton produced on branches six, seven, nine and thirteen. Longer fibers were seen from branches one through five, branches eight, eleven and twelve. Predictably, UQL (w) was highest at branch three and lowest at branches six through eleven and branch thirteen. SFC (w) was highest at branch six which was significantly different (lower) from branches one, three, five and twelve. Fiber length (n) was highest at branches three and twelve and lowest at six and thirteen. SFC (n) was highest at branch six and significantly lower at branch twelve. Trash content, which includes(dust and trash combined, was significantly lower at branches eight and eleven compared to six and two (Table 5). Regression showed a weak to moderate relationship between sympodial branch and length (w) and sfc(w) respectively (Figure B.6 and Figure B.7). There was a weak relationship between

sympodial branch and length (n) and SFC (n) while a stronger relationship was observed between sympodial branch and UQL (w) (Figures B.8-B.10). Trash seemed to consistently decrease from the first sympodial branch to the thirteenth (Figure B.11).

Fiber analyses from FiberMax 832 in 2009 showed a general trend where the upper sympodial branches of the plants had significantly poor fiber quality compared to the lower ones (Table 6). Length (w) was highest at branch one and significantly lower at branches eleven and twelve. Branch thirteen produced the shortest fiber length (w). This was also the situation in regards to UQL (w) and SFC (w). Length (n) was highest at branch one and significantly lower at branches eleven and thirteen. High SFC (n) was observed at branch thirteen. Trash content was high in the lower branches and improved starting branch nine. Regression showed a strong relationship of decreasing quality of length parameters from the bottom branches to the top (Figures B.12-B.16). Trash decreased from the bottom of the plant to the top (Figure B.17).

TM-1 had fiber quality that was distinctly poor at the upper region of the plant. Fiber length (w) was significantly higher from branches one through five and lower at branches eight through thirteen (Table 7). This same trend was observed for SFC (w), UQL (w) and length (n) as well. Additionally fiber length from branches six and seven was better than from branches eight through ten. Branches eleven through thirteen produced the shortest fiber. SFC (n) was highest from branches ten through thirteen when compared to branches one through four. Trash content was significantly higher from the first, third and fifth branches compared to branches ten, eleven and twelve. Regressions showed a strong relationship between sympodial branch and length

parameters (Figures B.18-B.22). There was a weak relationship between trash and sympodial branches (Figure B.23).

Half and Half had shorter fiber length (w) from branches nine, ten, twelve and thirteen in comparison to branches three and six. SFC (w) was highest at branches nine, ten, twelve and thirteen. Fiber length (n) at the top two branches was the shortest relative to the rest of the plant. In general, for this genotype the mid zone of the plant had better fiber quality compared to the rest of the plant. Fiber from branch three was significantly better than fiber from the upper region bolls (Table 8). There was a strong relationship between length parameters and sympodial branch (Figures B.24-B.28).

In 2010 there was no interaction from genotype for SFC (w), SFC (n), fineness, IFC and MR. However all five traits had a highly significant variation within the sympodial branches (Table A.6). Fiber length (w), UQL (w), length (n) and trash had a genotype effect. Acala 1517-99, FiberMax 832 and TM-1 had a highly significant sympodial branch effect. Half and Half had no interaction from sympodial branches any of the four fiber traits (Table A.7).

Means showed that for all genotypes SFC (w) and SFC (n) was significantly higher at branch thirteen relative to the rest of the plant. Additionally, branches nine through twelve had higher amount of short fibers relative to the bottom half of the plant. Fibers were finer from the thirteenth branch relative to the rest of the plant. Fiber fineness remained unchanged between branches one and ten. IFC showed a trend of increasing proportion of immature fibers as the progression went from branch one through thirteen. IFC was lower in cotton from the first six branches and significantly

higher from branches ten through thirteen. Fiber MR was significantly lower starting branch eight and declining further at eleven, twelve and thirteen relative to the first five sympodial branches. Regression analysis showed a strong relationship between sympodial branch and fineness, MR, SFC (w), SFC (n), IFC (Figures B.30-B.34).

Acala 1517-99 had high fiber length from branch one relative to branches eight through thirteen and three. In general fiber length (w), length (n) and UQL (w) was higher from the first nine branches relative to the rest of the plant with the exception of branch three. Trash content remained unchanged within the plant. Regression data showed a stronger relationship between sympodial branch and length parameters in 2010 for Acala1517-99 as compared to 2009 analysis (Figures B.35-B.37). Fiber analysis of FiberMax 832 indicated length (w), length (n) and UQL (w) were all significantly better from branches one through five relative to the rest of the plant. Trash content was significantly lower from branches nine through thirteen relative to branches one through four. Consistent with 2009, regressions showed a strong relationship between sympodial branch and length parameters (Figures B.39-B.41). Relationship between trash content and sympodial branches was also strong (Figure B.42). Means from TM-1 data showed fiber length (w), length (n) and UQL (w) were significantly higher at branches one through seven relative to the rest of the plant. For all three traits, branch thirteen was the poorest quality relative to the rest of the plant. There was a moderate relationship between length (w) and UQL (w) with sympodial branch while a stronger relationship between length (n) and sympodial branch was seen (Figures B.43-B.45). Trash content remained unchanged within the plant. Fiber samples were harvested from twelve

sympodial branches for Half and Half in 2010. This genotype was relatively stable for fiber length throughout the plant with the exception of branches ten and eleven. Branch twelve however, had the best fiber quality in terms of length (w) and UQL (w). Fiber length (n) and trash content showed no variability within the plant (Tables 9-13) . All four traits had a weak relationship with sympodial branch (Figures B.47-B.50).

In 2011 there was no genotype effect for fiber length (w), UQL (w), SFC (w), length (n), SFC (n), trash, IFC and MR. Fiber fineness had a genotype interaction. There was a sympodial branch interaction for fiber SFC (n), trash content, IFC and MR. Fiber fineness had a sympodial branch effect for all four genotypes. Means showed fiber length (w) and UQL (w) were constant within the plant. However regressions showed a moderate relationship between sympodial branch and both traits (Figure B.51 and Figure B.53). SFC (w) means separated into two groups but had no significant differences within the plant. However, regression analysis showed a strong relationship indicating a trend for increasing SFC (w) from sympodial branch one through twelve (Figure B.52). Length (n) remained constant within the plant while regression suggested a strong relationship between sympodial branch and length (n) (Figure B.54). SFC (n) was lowest in branches one through eight and significantly higher at the upper branches (10-12). Trash content did not change within the plant. IFC was significantly higher in branches seven through twelve relative to the rest of the plant with the greatest IFC deriving from the twelfth branch. MR declined from branches seven through twelve compared to branches one through five. Regression analysis showed a strong relationship between sympodial branch and IFC, MR and SFC (n) (Figures B.55-B.57). Fiber fineness

declined from branch seven through twelve relative to the rest of the plant in Acala 1517-99. FiberMax 832 also demonstrated a similar pattern with fibers trending finer starting at branch six and upwards. TM-1 had coarser fibers at the bottom of the plant compared to the top. Fibers became significantly finer starting at the eighth branch. Half and Half had extremely coarse fibers from branch one through eight. This was not surprising because this genotype is known for coarse fibers. Branches nine and twelve were significantly finer than the rest of the plant (Table 14 and Table 15). Regression showed a strong relationship between sympodial branch and fineness for Acala 1517-99, FiberMax 832 and TM-1 while Half and Half displayed a moderate relationship (Figures B.58-B.61).

Table 3: Fiber nepsize and neps (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2009 and 2010 in College Station, Texas. §

Sympodial Branch	Nepsize (µm)	Neps (count)
1	689.690 a	130.600 c
2	698.290 a	126.790 c
3	682.112 a	132.110 c
4	678.630 a	130.830 c
5	692.290 a	141.400 c
6	676.000 a	149.090 c
7	678.740 a	147.260 c
8	682.740 a	152.970 c
9	679.000 a	167.440 c
10	682.830 a	165.600 c
11	672.820. a	235.240 b
12	687.250 a	225.630 b
13	692.720 a	379.940 a

§ Means with the same letter are not significantly different

Table 4: Fiber fineness, MR and IFC (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2009 at College Station, Texas.§

Sympodial Branch	Fineness (mg/kg)	MR (units)	IFC (%)
1	175.636 a	0.912 a	5.663 b
2	177.200 a	0.908 a	5.760 b
3	178.273 a	0.923 a	5.363 b
4	174.909 a	0.910 a	5.772 b
5	174.364 a	0.907 a	5.872 b
6	174.091 a	0.902 a	6.081 ab
7	173.273 a	0.900 a	6.272 ab
8	174.909 a	0.910 a	5.827 b
9	172.800 a	0.902 a	6.080 ab
10	174.364 a	0.910 a	5.881 b
11	171.818 a	0.901 a	6.163 ab
12	169.500 a	0.904 a	6.050 ab
13	164.200 a	0.867 a	7.490 a

§ Means with the same letter are not significantly different

Table 5: Fiber length (w), UQL (w), SFC (w), length (n), SFC (n) and trash (AFIS) for Acala 1517-99 in 2009 at College Station, Texas.§

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	SFC (w) (%)	Length (n) (mm)	SFC (n) (%)	Trash (count)
1	27.559 ab	32.893 abc	5.750 b	22.225 ab	21.500 ab	1370 ab
2	27.178 abc	32.893 abc	7.350 ab	20.955 abc	26.850 ab	1381 a
3	27.940 a	33.274 a	5.650 b	22.733 a	20.600 ab	935 abc
4	27.178 abc	32.893 abc	7.100 ab	21.209 abc	25.550 ab	1240 abc
5	27.686 ab	33.020 ab	5.550 b	22.479 ab	20.812 ab	1187 abc
6	25.019 cd	30.734 e	9.750 a	19.304 bc	29.801 a	1384 a
7	25.654 cd	30.861 e	8.000 ab	20.193 abc	25.701 ab	699 abc
8	26.162 abcd	31.369 cde	6.950 ab	20.955 abc	23.412 ab	470 c
9	25.654 cd	31.115 de	7.950 ab	20.320 abc	25.211 ab	596 bc
10	26.035 bcd	31.496 bcde	7.900 ab	20.574 abc	25.750 ab	664 abc
11	26.416 abcd	31.369 cde	6.812 ab	21.082 abc	23.802 ab	572 c
12	27.559 ab	32.512 abcd	5.401 b	22.733 a	19.601 b	657 abc
13	25.527 cd	30.861 e	8.400 ab	19.939 bc	27.320 ab	645 abc

§ Means with the same letter are not significantly different

Table 6: Fiber length (w), UQL (w), SFC (w), length (n), SFC (n) and trash (AFIS) for FiberMax 832 in 2009 at College Station, Texas.§

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	SFC (w) (%)	Length (n) (mm)	SFC (n) (%)	Trash (count)
1	28.363 a	33.189 a	4.667 b	23.537 a	18.233 b	995 ab
2	27.178 ab	32.512 ab	6.120 b	21.844 ab	23.101 ab	14230 a
3	27.686 ab	32.681 ab	5.000 b	22.860 ab	19.167 b	938 ab
4	27.770 ab	32.596 ab	5.033 b	22.86 ab	18.967 b	909 ab
5	27.262 ab	32.596 ab	6.101 b	22.182 ab	21.433 b	667 bc
6	27.347 ab	32.596 ab	5.501 b	22.521 ab	20.067 b	733 bc
7	27.008 ab	32.258 ab	6.367 ab	21.759 ab	22.700 ab	516 bc
8	27.008 ab	32.004 ab	5.300 b	22.182 ab	19.933 b	761 bc
9	26.924 ab	32.131 ab	6.100 b	21.717 ab	22.300 ab	294 c
10	27.008 ab	31.496 b	4.500 b	22.606 ab	17.610 b	301 c
11	26.246 b	31.326 b	6.600 ab	21.166 bc	23.201 ab	369 c
12	26.416 b	31.326 b	6.067 b	21.505 ab	21.133 b	364 c
13	24.553 c	29.802 c	9.067 a	19.134 bc	28.833 a	301 c

§ Means with the same letter are not significantly different.

Table 7: Fiber length (w), UQL (w), SFC (w), length (n), SFC (n) and trash (AFIS) for TM-1 in 2009 at College Station, Texas. §

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	SFC (w) (%)	Length (n) (mm)	SFC (n) (%)	Trash (count)
1	27.516 a	32.004 a	4.710 d	23.114 a	17.533 c	1534 a
2	26.924 abc	31.834 a	5.400 cd	22.436 ab	18.867 c	819 bcd
3	27.178 ab	32.004 a	5.567 cd	22.606 ab	19.767 c	1504 a
4	26.839 abc	31.919 a	5.667 cd	22.436 ab	19.333 c	1231 abc
5	26.670 bc	31.750 ab	6.433 bcd	21.674 abc	22.033 abc	1379 ab
6	26.246 cd	31.242 ab	6.333 bcd	21.590 bc	21.333 bc	978 abcd
7	25.823 de	30.988 bc	7.033 abcd	20.743 cd	24.067 abc	799 bcd
8	25.400 ef	30.226 cd	6.933 abcd	20.743 cd	22.867 abc	1014 abcd
9	25.484 def	30.310 cd	7.000 abcd	20.658 cd	23.310 abc	901 bcd
10	24.723 fg	29.718 de	8.467 ab	19.727 de	26.700 ab	792 cd
11	24.469 gh	29.379 ef	8.933 a	19.304 de	28.100 a	579 d
12	24.807 fg	29.379 ef	7.200 abc	20.066 de	23.933 abc	526 d
13	23.749 h	28.702 f	9.150 a	18.796 e	28.100 a	1243 abc

§ Means with the same letter are not significantly different

Table 8: Fiber length (w), UQL (w), SFC (w), length (n), SFC (n) and trash (AFIS) for Half and Half in 2009 at College Station§ Texas.

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	SFC (w) (%)	Length (n) (mm)	SFC (n) (%)	Trash (count)
1	18.118 abcd	20.320 abcd	11.867 cde	15.578 abcd	24.700 cde	3351 a
2	18.203 abcd	20.574 abc	11.033 cde	16.002 abc	22.800 cde	2173 cd
3	18.881 a	21.251 a	8.533 e	16.764 a	18.567 e	2110 cde
4	18.372 abc	20.912 abc	11.000 cde	16.002 abc	23.167 cde	2209 cd
5	17.949 abcd	20.320 abcd	11.767 cde	15.748 abcd	23.900 cde	2487 abc
6	18.711 ab	21.082 ab	9.767 de	16.340 ab	21.201 de	2526 abc
7	18.034 abcd	20.404 abcd	12.167 cde	15.409 bcde	26.167 bcd	3132 ab
8	17.780 bcde	20.320 abcd	14.000 bc	15.155 bcde	28.433 abc	1677 cde
9	17.610 cde	19.642 dc	12.500 cd	15.578 abcd	23.767 cde	2239 bcd
10	17.356 cde	19.727 bcd	14.100 bc	15.070 cde	27.733 abc	1472 de
11	18.034 abcd	20.489 abcd	13.133 bcd	15.663 abcd	26.167 bcd	1328 de
12	16.764 e	19.177 d	18.000 a	14.351 e	32.650 a	1217 e
13	17.272 de	19.812 bcd	16.633 ab	14.562 de	32.133 ab	1515 de

§ Means with the same letters are not significantly different

Table 9: SFC (w), SFC (n), fineness and MR (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2010 at College Station, Texas.§

Sympodial Branch	SFC (w) (%)	SFC (n) (%)	Fineness (mg/kg)	IFC (%)	MR (units)
1	5.508 f	16.825 g	171.083 a	5.466 e	0.932 abc
2	5.617 f	16.942 g	176.000 a	5.208 e	0.944 a
3	6.375 def	18.550 fg	171.500 a	5.650 de	0.930 abc
4	5.975 ef	17.625 fg	173.583 a	5.533 e	0.935 ab
5	6.033 ef	17.758 fg	174.500 a	5.416 e	0.942 a
6	7.117 cdef	20.767 ef	169.750 a	5.925 de	0.923 abcd
7	7.091 cdef	20.773 ef	167.091 ab	5.881 de	0.925 abc
8	8.291 bcde	22.609 de	166.545 ab	6.289 cd	0.912 cd
9	8.508 bcd	23.425 cde	167.667 a	6.310 cd	0.918 bcd
10	9.167 bc	24.517 bcd	163.333 abc	6.800 bc	0.903 de
11	10.036 ab	27.291 b	154.727 bcd	7.236 b	0.885 e
12	9.340 bc	26.610 bc	152.000 cd	7.230 b	0.889 e
13	12.350 a	32.163 a	142.750 d	8.512 a	0.855 f

§ Means with the same letters are not significantly different

Table 10: Length (w), UQL (w), length (n) and trash (AFIS) for Acala 1517-99 in 2010 at College Station, Texas.

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	Length (n) (mm)	Trash (count)
1	28.194 a	33.020 a	23.791 a	822.700 a
2	27.855 ab	32.850 a	23.452 ab	748.000 a
3	25.992 de	30.903 bcd	21.505 de	460.000 a
4	27.601 abc	32.596 a	23.283 abc	660.700 a
5	27.516 abc	32.173 abc	23.368 ab	631.300 a
6	26.585 cde	31.834 abc	22.182 abcd	373.300 a
7	27.008 abcd	31.919 abc	22.775 abcd	370.700 a
8	26.924 bcd	32.004 abc	22.225 abcd	252.000 a
9	26.754 bcd	32.004 abc	22.013 bcde	305.300 a
10	26.754 bcd	32.258 ab	21.674 cde	442.000 a
11	26.416 cde	32.004 abc	21.166 de	465.300 a
12	25.484 e	30.818 cd	20.404 ef	522.700 a
13	24.257 f	29.845 d	19.050 f	323.000 a

§ Means with the same letters are not significantly different

Table 11: Length (w), UQL (w), length (n) and trash (AFIS) for FiberMax 832 in 2010 at College Station, Texas.

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	Length (n) (mm)	Trash (count)
1	28.024 a	33.189 ab	23.791 a	460.700 ab
2	26.585 bcd	31.665 cde	22.182 cd	477.300 ab
3	27.686 ab	32.935 abc	23.537 ab	553.300 ab
4	28.278 a	33.782 a	23.960 a	734.700 a
5	27.347 abc	32.850 abc	22.521 bc	362.000 ab
6	26.331 cde	31.834 bcd	21.336 def	543.300 ab
7	25.823 def	31.072 def	21.505 cde	380.700 ab
8	25.230 efg	30.734 defg	20.404 efg	457.300 ab
9	24.722 fgh	29.972 fgh	20.066 gh	314.700 b
10	24.892 fgh	30.310 efgh	20.235 fg	250.700 b
11	24.130 gh	29.633 gh	19.304 gh	307.300 b
12	23.791 h	29.040 hi	18.965 h	246.700 b
13	22.436 i	28.024 i	17.272 i	308.700 b

§ Means with the same letters are not significantly different

Table 12: Length (w), UQL (w), length (n) and trash (AFIS) for TM-1 in 2010 at College Station§ Texas.

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	Length (n) (mm)	Trash (count)
1	25.569 ab	29.633 bcd	22.182 ab	765.300 a
2	25.230 abc	29.125 cd	22.013 abc	661.300 a
3	26.077 a	30.310 abc	22.436 a	413.300 a
4	26.331 a	30.734 ab	22.521 a	520.700 a
5	26.331 a	30.734 ab	22.690 a	376.700 a
6	26.500 a	31.157 a	22.267 a	895.300 a
7	25.908 a	30.903 a	21.336 abcd	807.300 a
8	24.214 bc	28.786 de	20.066 cde	758.700 a
9	24.045 c	28.786 de	19.727 def	510.000 a
10	24.130 bc	28.448 de	20.150 bcde	528.000 a
11	24.214 bc	29.464 cd	19.050 ef	520.000 a
12	24.045 c	29.125 cd	19.304 def	542.700 a
13	22.521 d	27.770 e	17.695 f	891.300 a

§ Means with the same letter are not significantly different.

Table 13: Length (w), UQL (w), length (n) and trash (AFIS) for Half and Half in 2010 at College Station, Texas. §

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	Length (n) (mm)	Trash (count)
1	19.727 ab	22.606 ab	17.441 a	722.700 a
2	19.304 abc	21.928 abc	17.356 a	652.700 a
3	18.965 abc	21.759 abc	16.848 a	684.700 a
4	18.880 abc	21.674 abc	16.764 a	501.300 a
5	18.880 abc	21.759 abc	16.848 a	636.700 a
6	19.050 abc	22.182 abc	16.848 a	801.300 a
7	18.415 abc	21.336 bc	16.002 a	587.000 a
8	18.711 abc	21.590 abc	16.510 a	553.300 a
9	19.134 abc	22.182 abc	16.848 a	609.300 a
10	17.695 bc	20.743 bc	15.070 a	479.300 a
11	17.272 c	20.066 c	14.986 a	533.000 a
12	20.320 a	23.876 a	17.018 a	758.000 a

§ Means with the same letters are not significantly different

Table 14: Fiber length (w), UQL (w), SFC (w), length (n), SFC (n), trash, IFC and MR (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2011 at College Station, Texas.

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	SFC (w) (%)	Length (n) (mm)	SFC (n) (%)	Trash (total) (count)	IFC (%)	MR (units)
1	23.812 a	27.707 a	5.750 ab	20.976 a	15.225 c	642.500 a	4.250 f	0.978 a
2	24.214 a	28.046 a	5.158 ab	21.357 a	14.275 c	646.700 a	4.125 f	0.975 ab
3	23.727 a	27.580 a	5.867 ab	20.764 a	15.783 bc	494.000 ab	4.450 ef	0.9675 abc
4	23.854 a	27.601 a	5.658 ab	21.103 a	14.633 c	375.300 ab	4.241 f	0.967 abc
5	23.854 a	27.707 a	5.933 ab	20.933 a	15.383 c	420.200 ab	4.566 def	0.959 abcd
6	24.130 a	28.088 a	6.125 ab	21.082 a	16.017 bc	432.000 ab	4.800 cdef	0.950 bcde
7	24.362 a	28.426 a	5.850 ab	21.272 a	15.692 bc	437.300 ab	5.125 bcde	0.941 cdef
8	24.405 a	28.469 a	5.433 ab	21.314 a	15.050 c	421.700 ab	5.116 bcde	0.937 def
9	24.130 a	28.215 a	6.367 ab	20.891 a	17.008 abc	347.500 ab	5.583 abc	0.932 efg
10	23.939 a	27.961 a	6.367 ab	20.828 a	16.592 abc	386.500 ab	5.375 abcd	0.924 efg
11	23.029 a	26.987 a	7.833 ab	19.833 a	19.342 ab	361.500 ab	5.808 ab	0.918 fg
12	22.415 a	26.458 a	8.142 a	19.198 a	20.167 a	399.500 ab	6.033 a	0.910 g

§ Means with the same letters are not significantly different

Table 15: Fiber fineness (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2011 at College Station, Texas. §

	Fineness (mg/kg) 2011			
Sympodial Branch	**Acala 1517-99**	**FiberMax 832**	**TM-1**	**Half and Half**
1	171.333 a	175.000 ab	195.667 a	207.00 abc
2	169.333 ab	178.333 a	195.333 a	208.667 ab
3	161.667 bc	177.000 ab	188.333 abc	213.333 a
4	161.000 bc	176.667 ab	190.333 ab	210.333 ab
5	158.000 c	176.000 ab	184.333 bc	205.333 abc
6	155.333 c	169.000 abc	182.000 bcd	199.667 bc
7	145.000 d	167.000 bcd	181.000 cd	204.667 abc
8	145.333 d	161.667 cde	174.333 ed	204.333 abc
9	142.667 d	162.667 cde	180.333 cd	186.333 d
10	141.667 d	157.333 ed	174.667 ed	200.667 bc
11	140.667 d	156.00 ef	167.667 e	196.000 cd
12	145.667 d	146.667 f	168.667 e	186.667 d

§ Means with the same letters are not significantly different

In general, fiber quality was better in the bottom half of the plant compared to the top half. It was frequently observed that the middle zone of the plants, sympodial branches three to six, had excellent fiber quality relative to the rest of the plant. Trash content had no specific trend among the sympodial branches. It would be logical to assume lower position bolls might have high trash content because of its proximity to the

soil surface and the greater amount of time bolls were open in comparison to upper position bolls.

The nature of fiber quality variability within the plant has implications throughout the cotton industry. For the cotton plant breeder, this highlights the importance of using appropriate boll sampling techniques for estimation of fiber quality. Results from related studies suggest that variability in fiber quality is heritable. Efforts to minimize this variability can be effective if a genetic component is involved.

Many fiber traits had more variability in 2009 and 2010 compared to when they were measured in 2011. In 2009 Half and Half had a highly significant sympodial branch effect for fiber length (n) and length (w). However in 2010 both fiber length traits had no significant difference between sympodial branches. Acala 1517-99, FiberMax 832 and TM-1 had highly significant sympodial branch effects for fiber length (n) and UQL (w) in 2010, but in 2011 there were no significant effects for sympodial branches. There is strong evidence that growing environment plays a significant role in fiber quality variability.

In order to determine a genetic component for fiber quality variability within the plant, length (n) was used as a model trait. It appeared that the difference between the longest and shortest fibers within a plant over a three year period, varied more so in some genotypes than others. To test this hypothesis, the difference between highest and lowest performers for each genotype in all three years was tabulated and the percentage of decrease in fiber length (n) was calculated relative to the longest fibers in the plant. There were no interactions among genotype and years; however, a significant genotype

effect was seen. Acala 1517-99 and Half and Half tended to align together, and FiberMax 832 and TM-1 were clustered together. Half and Half was significantly different from the rest of the genotypes in terms of the percentage of relative variability of fiber length (n) within the plant (Table 16). These results suggest a genetic component associated with fiber quality variability within the plants. If growing environment was the only contributing factor, all genotypes which were tested would have had the same degree of variability. Clearly, Half and Half and Acala 1517-99 have a lesser degree of fiber length (n) variability within the plant. In order to increase the efficiency of a breeding program that may be targeting a reduction of within-plant fiber variability, bolls should be sampled from the bottom five sympodial branches and then compare those fiber quality values against that of fiber derived from the upper five sympodial branches. These boll samples of at least 50 bolls/sample may be harvested randomly in different plants across the row(s) under study. Calculating the percentage of difference in fiber trait of interest and running a mean separation could assist the cotton plant breeder in making better decisions for selection.

Table 16: Percentage of difference in fiber length (n) among the longest and shortest fibers within the plant across Acala 1517-99, FiberMax 832, TM-1 and Half and Half in College Station, Texas in 2009, 2010 and 2011. §

Genotype	**Percent difference**
Acala 1517-99	18.920 ab
FiberMax 832	22.502 a
Half and Half	15.439 b
TM-1	22.706 a

§ Means with the same letters are not significantly different

Uniform fiber quality in cotton is of great importance to the spinner and weaver. This trait is probably one of the greatest disadvantages that cotton has against man-made fibers. One of the reasons for variable fibers in a bale is the presence of short fibers. Short fiber content is described as the fibers which are less than 12.7mm long (ASTM, 2004). This is usually a product of fiber processing. Weak, immature fibers tend to break easily compared to strong, mature fibers. The importance of short fiber content in determining fiber-processing success, yarn properties, and fabric performance has led the textile and spinning sector of the US cotton industry to give top priority to minimizing this fraction no matter what the cause (Rogers, 1997).

Fiber neps are entangled, small knots of fibers (typically immature) or associated with seed coat and motes (Verschraege, 1989). Neps result in compromised dye-uptake and result in barrè in the finished textile product. Barrè is defined as, unintentional, repetitive visual pattern of continuous bars or stripes usually parallel to the filling of woven fabric or to the courses of circular knit fabric (Textile Technology, 2012).

Mechanical neps are a result of fiber processing and biological neps arise from bract tissue, seed coat and motes (Hebert et al., 1988). These two traits are inter-twined with each other in terms of fiber quality. For that matter, almost all fiber quality traits are a result of mingled associations between each other. In general, high quality fiber will process better at gin and harvest tools (processing) which will reduce over short fiber content and nep formation. Fiber length, strength, maturity and fineness are important in nep formation (Verschaege, 1989). Cotton fiber maturity plays a significant role in the harvesting, ginning, and spinning processes and is as an important factor influencing the tendency of nep formation and short fibers (Herbert et al., 1988). Herbert et al., (1986) deduced that fine cottons tend to nep more than coarser ones independent of fiber maturity. Mature, stronger fibers contribute to its ability to withstand mechanical stress during harvesting and ginning (Behery, 1993).

Analysis of fiber quality variability within the plants reveals that short fibers increase in the upper half region of the plants significantly compared to the middle to lower bolls. This also applies to fiber neps and immature fibers (IFC). In order to minimize the impact of these detrimental traits to the textile industry, more attention needs to be paid by the cotton plant breeders to minimize variability within the plant.

Fiber length distributions for sympodial branches in were unique for each genotype. In 2009, Acala 1517-99 had the longest fiber from branch one and shortest fiber from branch thirteen. Length (n) distribution revealed that the proportion and size of shorter fibers was slightly greater from the thirteenth branch. It is to be noted though that average length (n) of Acala 1517-99 cotton fibers from these two branches were not

significantly different from each other. A similar pattern was seen with FiberMax 832. Fiber length (n) from sympodial branch one and thirteen were significantly different from each other. Interestingly, even at the first sympodial branches, short fibers were quite high relative to the length (n) distribution in Half and Half. The overall fiber length (n) for Half and Half is short in comparison to modern Upland cultivars. However, the distribution clearly shows that the first sympodial branch produces better quality cotton with a lower SFC compared to the thirteenth branch. TM-1 distribution also shows a distinct shift in mean length (n) and a lower proportion of short fibers in the first sympodial branch (Figure 1).

In 2010, fiber length (n) and length (w) statistics showed sympodial effect in Acala 1517-99, FiberMax 832 and TM-1. Half and Half had no significant difference between sympodial branches across the plant (Table A.7). Length (n) distribution indicates a higher proportion of short fibers from sympodial branch thirteen compared to branch one. However the percentage of short fibers around the range of 0-4 mm was actually higher from the first sympodial branch. FiberMax 832 had fibers from sympodial branch three that were clearly better than fibers from branch thirteen. TM-1 showed a length distribution with a bell shaped curve (desirable) from the high quality sample while the low quality sample was skewed towards shorter fibers. Average means for length (n) at branch one and thirteen were 22.182mm and 17.695mm respectively. Average length (n) in Half and Half was not significantly different across sympodial branches however, the length distribution shows a slight shift in means between the two branches. Proportion of short fibers in both branches seems to be lower (Figure 2).

In 2011 the length (n) distribution of Acala 1517-99 shows a drastic difference between fiber from the first and twelfth sympodial branches. Fiber length drops significantly at the upper branches in this year. A similar pattern is seen for Half and Half. Fiber from FiberMax 832 was not different between the 1st and 12th branch; however, there was a trend of declining quality among the sympodial branches. Lastly, TM-1 had a higher mean length and higher proportion of longer fibers at the first sympodial branch compared to the twelfth. Short fibers also seemed to increase in the twelfth position bolls (Figure 3). In general a trend of decline in fiber quality was associated in the upper sympodial branches of the plants in 2011. While a trend was seen, significant differences were not observed in length in some genotypes. This differential pattern of fiber quality variability within genotypes is suggestive of a genetic influence of variability in cotton fiber quality within the plants.

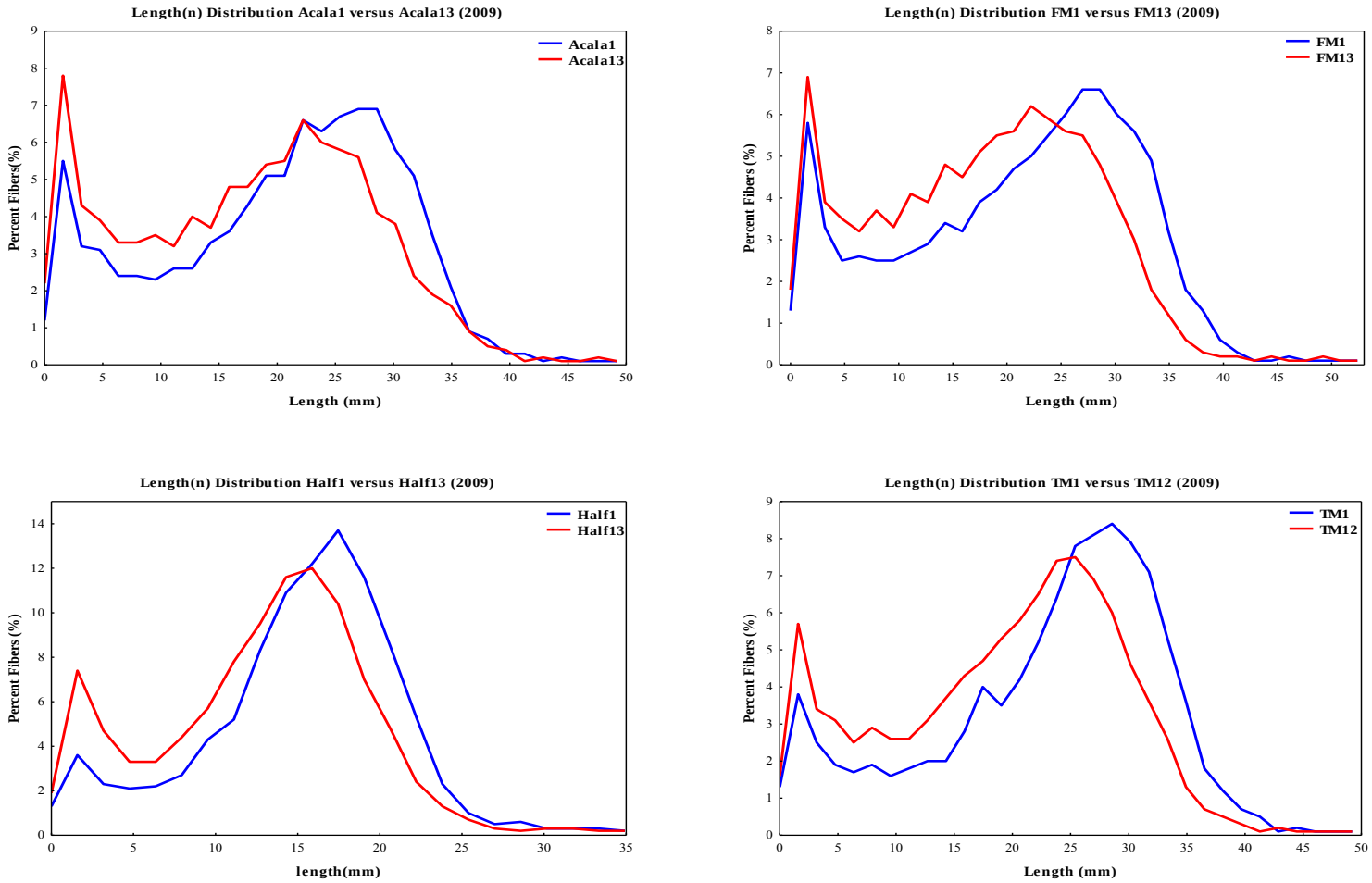

Figure 1: Fiber length (n) distribution of Acala 1517-99 at sympodial branch 1 (Acala1) and 13 (Acala13), FiberMax 832 at sympodial branch 1 (FM1) and 13 (FM13), Half and Half at sympodial branch 1 (Half1) and 13 (Half13) and TM-1 at sympodial branch 1 (TM1) and 13 (TM13) in 2009 at College Station, Texas.

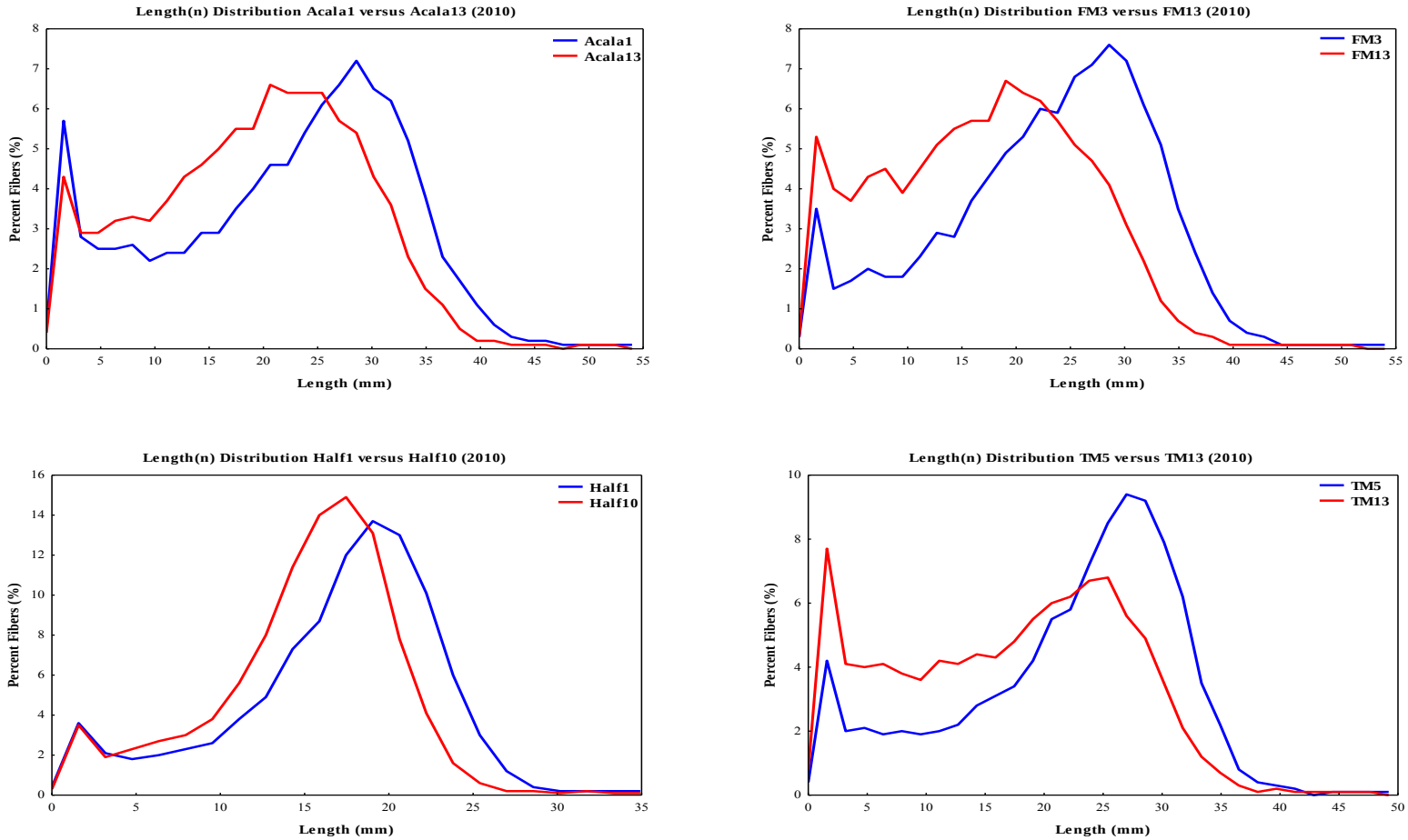

Figure 2: Fiber length (n) distribution of Acala 1517-99 at sympodial branch 1 (Acala1) and 13 (Acala13), FiberMax 832 at sympodial branch 3 (FM3) and 13 (FM13), Half and Half at sympodial branch 1 (Half1) and 10 (Half10) and TM-1 at sympodial branch 5 (TM5) 13 (TM13) in 2010 at College Station, Texas and 13 (TM13) in 2010 at College Station, Texas.

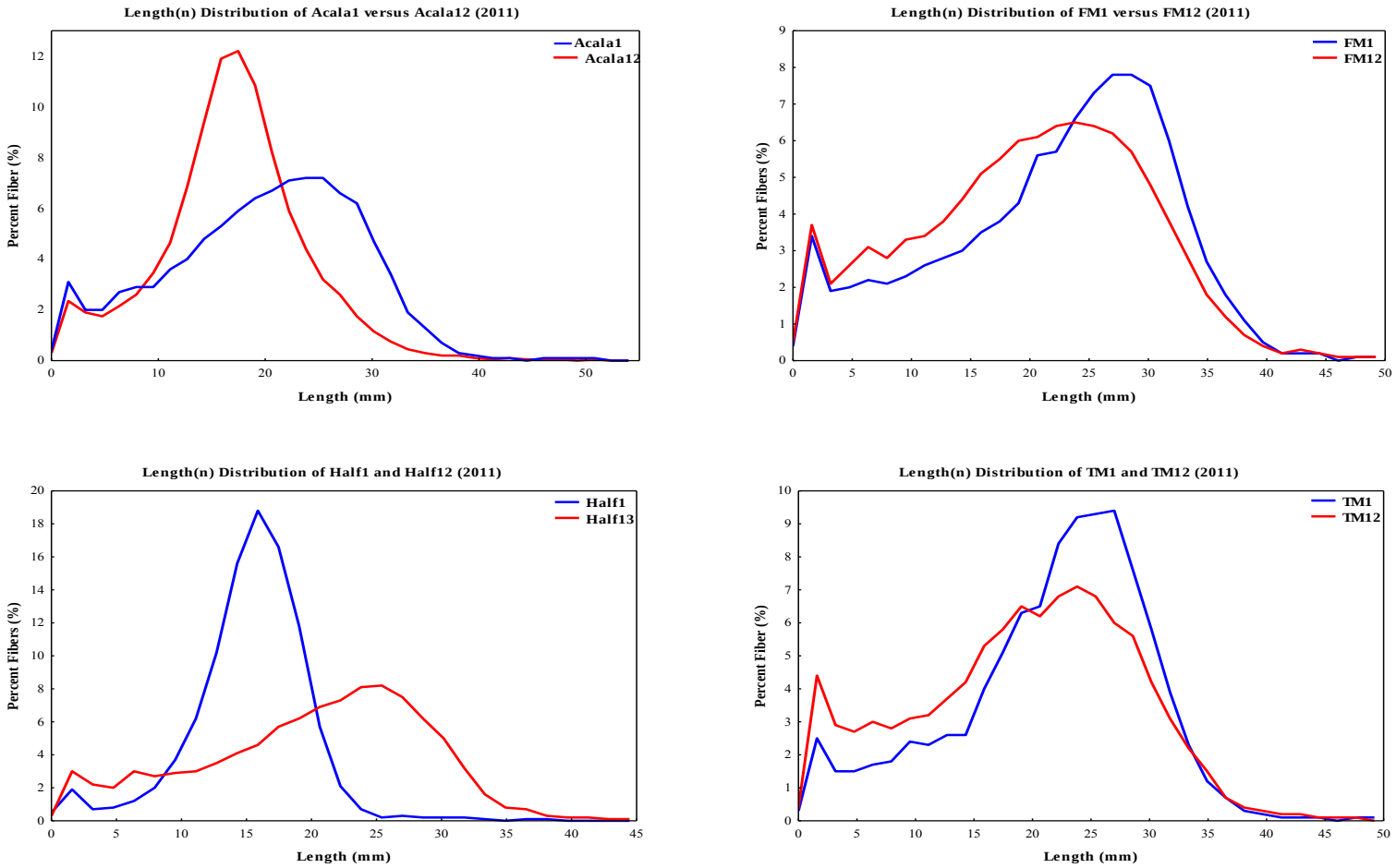

Figure 3: Fiber length (n) distribution of Acala 1517-99 at sympodial branch 1 (Acala1) and 12 (Acala12), FiberMax 832 at sympodial branch 1 (FM1) and 12 (FM12), Half and Half at sympodial branch 1 (Half1) and 13 (Half13) and TM-1 at sympodial branch 1 (TM1) and 12 (TM12) in 2011 at College Station, Texas.

Besides genotype and processing effects at harvest and gin level, producer practices (i.e. running faster gins) to gain pricing advantages by supplying cleaner cotton to spinners also result in higher short fiber content and neps in bales. Lint cleaning improves value from cleaner cotton, but impacts the spinning performance of fibers. Short fibers are detrimental to the efficiency of the textile industry (Backe E, 1986; Bargeron, 1986). High short fiber content is generally associated with inferior yarn processing ability and yarn quality because it increases waste during fiber processing, produces weaker, less uniform and more hairy yarn, and results in poorer quality fabric (Cai et al., 2010). Typically short fibers are allowed to float between the drafting rollers where they either bunch up or thin out causing thick and/or thin imperfections in the yarn with accompanying diminished strength (Behery, 1993). This indirect impact of short fibers and neps are not currently regulated as fiber quality requirements for pricing.

Field trials for estimating fiber quality variability were performed at Lubbock, Texas, in 2010 and 2011. There was a genotype x year effect for length (w), UQL (w), SFC (w), length (n), SFC (n) and MR. Neps, nepsize, trash and fineness remained unaffected across years, genotypes and sympodial branches (Table 17). However a moderate to strong relationship was seen between sympodial branch and these traits except nepsize from regression analysis (Figures B.62-B.65). IFC had a genotype x sympodial (branch) interaction and was analyzed separately for each genotype. ANOVA showed a significant sympodial branch effect for Acala 1517-99 and FiberMax 832. Half and Half and TM-1 remained unaffected in IFC content throughout the plant. Sympodial branch thirteen in Acala 1517-99 produced a significantly higher amount of immature

fibers compared to branches five, six, eight, ten, eleven and twelve. However, branches one through four were not significantly different from branch thirteen in terms of IFC. FiberMax 832 had the lowest percentage of immature fibers in branches one through six and thirteen relative to the rest of the plant. Regression showed a weak relationship between sympodial branch and IFC in Acala1517-99, Half and Half and TM-1 while a moderate relationship was seen with FiberMax 832 (Table 18).

In 2010 SFC (w), SFC (n) and MR did not have a genotype x sympodial branch or sympodial branch effect (Table 19). Length (w), UQL (w) and length (n) had a significant genotype x sympodial branch interaction (Table A.14). Consequently traits were analyzed separately for all four genotypes. ANOVA showed a highly significant sympodial branch effect for all three traits in FiberMax 832 and significant in Half and Half. Acala 1517-99 and TM-1 remained unchanged across sympodial branches (Table A.15 and Table 22). Length parameters had a weak relationship with sympodial branch in Acala 1517-99 (Figures B.69-B.71) (Table 20). Fiber length (w) and length (n) from FiberMax 832 dropped significantly at sympodial branches ten, eleven and twelve relative to the rest of the plant (Table 21). UQL (w) was also significantly lower at branches ten through twelve. Regression analysis showed a strong relationship among sympodial branch and length parameters Fiber length (w) was significantly lower in sympodial branches one and two compared to the rest of the plant in Half and Half. This was also the case with fiber length (n), which was significantly lower at branches two and nine relative to the rest of the plant. Higher lengths were observed in fibers from the

upper half of the plants in comparison to fiber from the lower sympodial branches in Half and Half (Table 23).

In 2011, UQL (w) and SFC (n) had a significant genotype x sympodial branch effect. All genotypes, with the exception of TM-1, had no sympodial branch effect (Table A.16). Length (w), SFC (w), length (n) and MR were unaffected by genotype and sympodial branch (Tables 24-26). The highest amount of short fibers were ascertained from sympodial branch twelve and the lowest amounts of short fibers produced in branches six, nine, ten and eleven.

In general a non-predictable trend was observed in the Lubbock location as compared to the College Station location for the trials conducted in this study. While we were able to establish a genetic component associated with intra-plant variability in College Station, the data obtained from Lubbock suggests that drastic environmental effects can affect fiber quality and the trends of variability observed. Half and Half showed similar intra-plant fiber quality trends in 2011 at both locations.

Table 17: Fiber nepsize, neps, trash and fineness (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2010 and 2011 at Lubbock, Texas. §

Sympodial Branch	Nepsize (units)	Neps (per gram)	Trash (count)	Fineness (mg/kg)
1	690.910 a	110.180 a	526.730 a	177.273 a
2	670.640 a	104.090 a	521.180 a	178.682 a
3	716.500 a	112.550 a	498.730 a	178.091 a
4	679.950 a	114.910 a	425.450 a	177.227 a
5	710.500 a	107.910 a	446.910 a	176.682 a
6	701.680 a	99.550 a	429.270 a	177.318 a
7	698.730 a	116.730 a	421.550 a	177.045 a
8	673.910 a	103.270 a	495.270 a	177.864 a
9	676.000 a	118.910 a	359.450 a	176.727 a
10	684.230 a	179.730 a	382.550 a	173.591 a
11	707.820 a	165.000 a	339.450 a	172.682 a
12	685.450 a	139.500 a	473.000 a	177.150 a
13	672.710 a	140.570 a	367.430 a	176.714 a

§ Means with the same letter are not significantly different

Table 18: Fiber IFC (AFIS) in 2010 and 2011 at Lubbock, Texas.§

	IFC (%)			
Sympodial Branch	**Acala 1517-99**	**FiberMax 832**	**TM-1**	**Half and Half**
1	5.416 abc	4.616 b	4.760 a	5.020 a
2	5.450 abc	4.783 b	4.640 a	4.940 a
3	5.766 ab	4.466 b	4.640 a	4.960 a
4	5.316 abc	4.766 b	4.940 a	4.820 a
5	5.200 bc	4.600 b	5.320 a	4.800 a
6	5.016 bc	4.450 b	4.560 a	5.440 a
7	5.316 abc	5.133 ab	4.860 a	4.960 a
8	4.816 bc	4.750 b	5.240 a	5.180 a
9	5.533 abc	4.916 ab	4.680 a	5.240 a
10	4.933 bc	6.900 a	4.520 a	5.160 a
11	4.850 bc	6.800 a	5.720 a	5.120 a
12	4.533 c	6.016 ab	4.850 a	5.075 a
13	6.400 a	4.700 b	4.800 a	5.150 a

§ Means with the same letter are not significantly different

Table 19: Fiber SFC (w), SFC (n) and MR (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2010 at Lubbock, Texas. §

Sympodial Branch	**SFC (w) (%)**	**SFC (n) (%)**	**MR (units)**
1	5.340 a	15.950 a	0.943 a
2	5.650 a	16.390 a	0.942 a
3	5.290 a	15.880 a	0.947 a
4	4.670 a	14.360 a	0.949 a
5	5.550 a	16.270 a	0.935 a
6	4.830 a	14.530 a	0.946 a
7	5.610 a	16.87 a	0.940 a
8	5.840 a	17.450 a	0.942 a
9	6.190 a	17.850 a	0.934 a
10	6.500 a	18.370 a	0.919 a
11	7.830 a	21.250 a	0.909 a
12	6.022 a	17.144 a	0.936 a
13	5.971 a	17.343 a	0.928 a

§ Means with the same letter are not significantly different

Table 20: Fiber length (w), UQL (w) and length (n) (AFIS) for Acala 1517-99 in 2010 at Lubbock, Texas.

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	Length (n) (mm)
1	27.347 a	32.258 a	23.452 a
2	26.924 a	31.580 a	23.114 a
3	27.008 a	31.919 a	22.775 a
4	28.024 a	32.850 a	24.384 a
5	28.109 a	32.850 a	24.214 a
6	28.024 a	32.681 a	24.553 a
7	27.940 a	32.935 a	23.452 a
8	27.855 a	32.596 a	23.791 a
9	27.178 a	32.258 a	23.198 a
10	27.432 a	32.342 a	23.622 a
11	28.617 a	33.612 a	24.553 a
12	28.363 a	33.020 a	24.722 a
13	26.543 a	31.877 a	21.971 a

§ Means with the same letter are not significantly different

Table 21: Fiber length (w), UQL (w) and length (n) (AFIS) for FiberMax 832 in 2010 at Lubbock, Texas.

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	Length (n) (mm)
1	27.432 a	32.512 a	23.368 a
2	27.262 a	32.342 ab	23.114 a
3	27.432 a	32.3425 ab	23.537 a
4	27.686 a	32.596 a	23.791 a
5	27.178 a	32.596 a	22.944 a
6	27.601 a	32.681 a	23.622 a
7	26.416 ab	31.580 ab	22.267 ab
8	26.754 a	31.834 ab	22.775 a
9	26.416 ab	31.580 ab	22.182 ab
10	24.468 bcd	30.056 bc	19.981 bc
11	22.944 d	28.448 c	18.203 c
12	23.791 cd	28.786 c	19.558 bc
13	25.781 abc	30.353 abc	22.098 ab

§ Means with the same letter are not significantly different

Table 22: Fiber length (w), UQL (w) and length (n) (AFIS) for TM-1 in 2010 at Lubbock, Texas. §

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	Length (n) (mm)
1	26.289 a	30.480 a	22.987 a
2	26.924 a	30.988 a	23.876 a
3	26.289 a	30.353 a	23.368 a
4	26.289 a	30.607 a	22.987 a
5	25.527 a	30.353 a	22.098 a
6	26.797 a	31.242 a	23.241 a
7	26.289 a	30.734 a	22.606 a
8	25.527 a	30.099 a	21.717 a
9	25.654 a	30.226 a	22.098 a
10	27.051 a	31.242 a	23.622 a
11	25.019 a	29.972 a	20.828 a
12	26.416 a	30.480 a	23.368 a
13	25.400 a	29.718 a	21.844 a

§ Means with the same letter are not significantly different

Table 23: Fiber length (w), UQL (w) and length (n) (AFIS) for Half and Half in 2010 at Lubbock, Texas.§

Sympodial Branch	Length (w) (mm)	UQL (w) (mm)	Length (n) (mm)
1	18.923 b	21.717 bc	17.272 abcd
2	18.542 b	21.082 c	16.637 cd
3	19.304 ab	22.098 abc	17.526 abcd
4	19.558 ab	22.098 abc	18.034 abc
5	19.558 ab	22.479 abc	17.526 abcd
6	19.685 ab	22.479 abc	17.653 abcd
7	19.939 ab	22.733 abc	18.034 abc
8	19.177 ab	22.098 abc	17.145 bcd
9	19.177 ab	21.971 abc	17.018 cd
10	20.701 a	23.622 a	18.542 a
11	19.939 ab	22.606 abc	17.907 abcd
12	20.066 ab	22.987 ab	18.161 abc
13	20.574 a	23.622 a	18.415 ab

§ Means with the same letter are not significantly different

Table 24: Fiber length (w), SFC (w), length (n) and MR (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2011 at Lubbock, Texas.§

Sympodial Branch	Length (w) (mm)	SFC (w) (%)	Length (n) (mm)	MR (units)
1	25.061 a	5.458 a	21.568 a	0.954 a
2	25.484 a	5.366 a	21.992 a	0.956 a
3	25.082 a	5.550 a	21.611 a	0.948 a
4	24.997 a	5.658 a	21.632 a	0.948 a
5	25.548 a	5.283 a	22.098 a	0.958 a
6	25.569 a	5.583 a	22.203 a	0.955 a
7	25.019 a	6.125 a	21.547 a	0.950 a
8	25.611 a	5.433 a	22.098 a	0.957 a
9	25.463 a	5.450 a	21.907 a	0.955 a
10	25.548 a	5.691 a	21.949 a	0.949 a
11	25.188 a	6.008 a	21.526 a	0.949 a
12	25.746 a	6.072 a	21.867 a	0.951 a

§ Means with the same letter are not significantly different

Table 25: Fiber UQL (w) (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2011 at Lubbock, Texas§.

	UQL (w) (mm)			
Sympodial Branch	**Acala 1517-99**	**FiberMax 832**	**TM-1**	**Half and Half**
1	30.564 a	31.072 a	29.125 a	27.347 a
2	30.903 a	32.088 a	29.802 a	27.686 a
3	30.818 a	31.496 a	29.887 a	25.400 a
4	30.818 a	30.818 a	29.464 a	26.924 a
5	30.818 a	31.580 a	30.310 a	27.601 a
6	31.072 a	31.496 a	30.056 a	27.601 a
7	30.395 a	30.903 a	30.395 a	26.585 a
8	31.496 a	31.750 a	30.649 a	27.516 a
9	32.004 a	31.326 a	30.310 a	26.754 a
10	31.834 a	31.072 a	30.988 a	27.855 a
11	31.072 a	30.903 a	31.157 a	25.992 a
12	32.427 a	32.088 a	30.988 a	24.892 a

§ Means with the same letter are not significantly different

Table 26: Fiber SFC (n) (AFIS) across genotypes (Acala 1517-99, FiberMax 832, TM-1 and Half and Half) in 2011 at Lubbock, Texas.§

	SFC (n) (%)			
Sympodial Branch	**Acala 1517-99**	**FiberMax 832**	**TM-1**	**Half and Half**
1	16.867 a	13.000 a	17.633 ab	16.733 a
2	16.900 a	14.600 a	15.300 abc	17.267 a
3	18.200 a	12.467 a	17.100 abc	17.167 a
4	15.667 a	15.867 a	15.000 abc	18.633 a
5	17.633 a	12.833 a	14.600 abc	18.233 a
6	17.167 a	13.033 a	12.300 c	21.133 a
7	18.200 a	15.667 a	13.633 abc	20.533 a
8	14.833 a	14.300 a	15.467 abc	18.767 a
9	16.767 a	16.033 a	13.467 bc	18.267 a
10	16.400 a	18.833 a	13.300 bc	17.933 a
11	16.333 a	21.033 a	13.300 bc	19.000 a
12	13.500 a	22.067 a	18.433 a	18.200 a

§ Means with the same letter are not significantly different

Data from trials conducted in Lubbock indicate that overall IFC was affected by sympodial branch in both years for FiberMax 832. In 2010, FiberMax 832 had significant variability within plants for fiber length (w), length (n) and UQL (w). Half and Half had a sympodial branch effect in 2010 indicating overall fiber length (w), length (n) and UQL (w) improved in the upper branches relative to the lower five sympodial branches. In 2011, TM-1 had a sympodial branch effect for SFC (n) where branch six produced the lowest proportion of short fibers in comparison to other branches. All other traits across genotypes and years remained stable and showed no indication of within-plant variability for fiber quality. Data from 2010 was similar to that generated at College Station trials especially data related to FiberMax 832.

Length (n) distributions were plotted for both years. In 2010, Acala 1517-99 and FiberMax 832 had a significantly greater amount of short fibers in the samples collected from sympodial branch thirteen compared to branch one. Half and Half remained stable at all branches. The distribution of short fibers from TM-1 indicates the proportion of short fibers is higher in the eleventh sympodial branch compared to the first (Figure 4). In 2011, length (n) distribution of FiberMax 832 showed a higher amount of short fibers in the upper branch compared to branch one. This is consistent with the average values observed (Figure 5).

The average length (w) range in 2010 was 27.347 - 26.543 mm (Acala 1517-99) , 27.432-22.944 mm (FiberMax 832), 26.289-25.400 mm (TM-1) and 20.701-18.973 mm (Half and Half). For commercial upland cultivars, four classes for length have been 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). Acala 1517-99, FiberMax 832 and TM-1 fibers were within the medium-long range for premiums in the lower half sympodial branches of the plants. Fiber from Acala 1517-99 stayed within that range throughout the plants; however, fiber from FiberMax 832 and TM-1 digressed into the medium fiber length from the upper half sympodial branches of the plants. Fiber from Half and Half stayed within the short fiber length category throughout the plant.

The average length (w) range in 2011 was 25.993-26.247 mm (Acala 1517-99) , 27.347- 25.823 mm (FiberMax 832), 26.755-24.807 mm (TM-1) and 23.114-21.336 mm (Half and Half). Fiber length variability was observed among genotypes, but a different pattern was observed in 2011 than in 2010. Acala 1517-99 demonstrated a trend of increasing fiber length (w) from sympodial branches one to twelve. Variability within the plants was less pronounced compared to trials in 2010 at Lubbock and College Station, Texas. This may have been a result of extreme weather conditions that occurred in 2011 in Lubbock. Lubbock was abnormally hot and dry in the 2011 growing season. High day and night temperatures were noted through the first three months in the growing season. Even with intensive irrigation schedules, it was difficult to maintain adequate soil moisture.

Growing degree days were calculated in Lubbock during the 2011 growing season. Between the period of the first square set until initial peak bloom, abnormally high GDD were noted. Temperatures returned to normal in the last 50 days of the season relative to the rest of the growing season (Table 27).

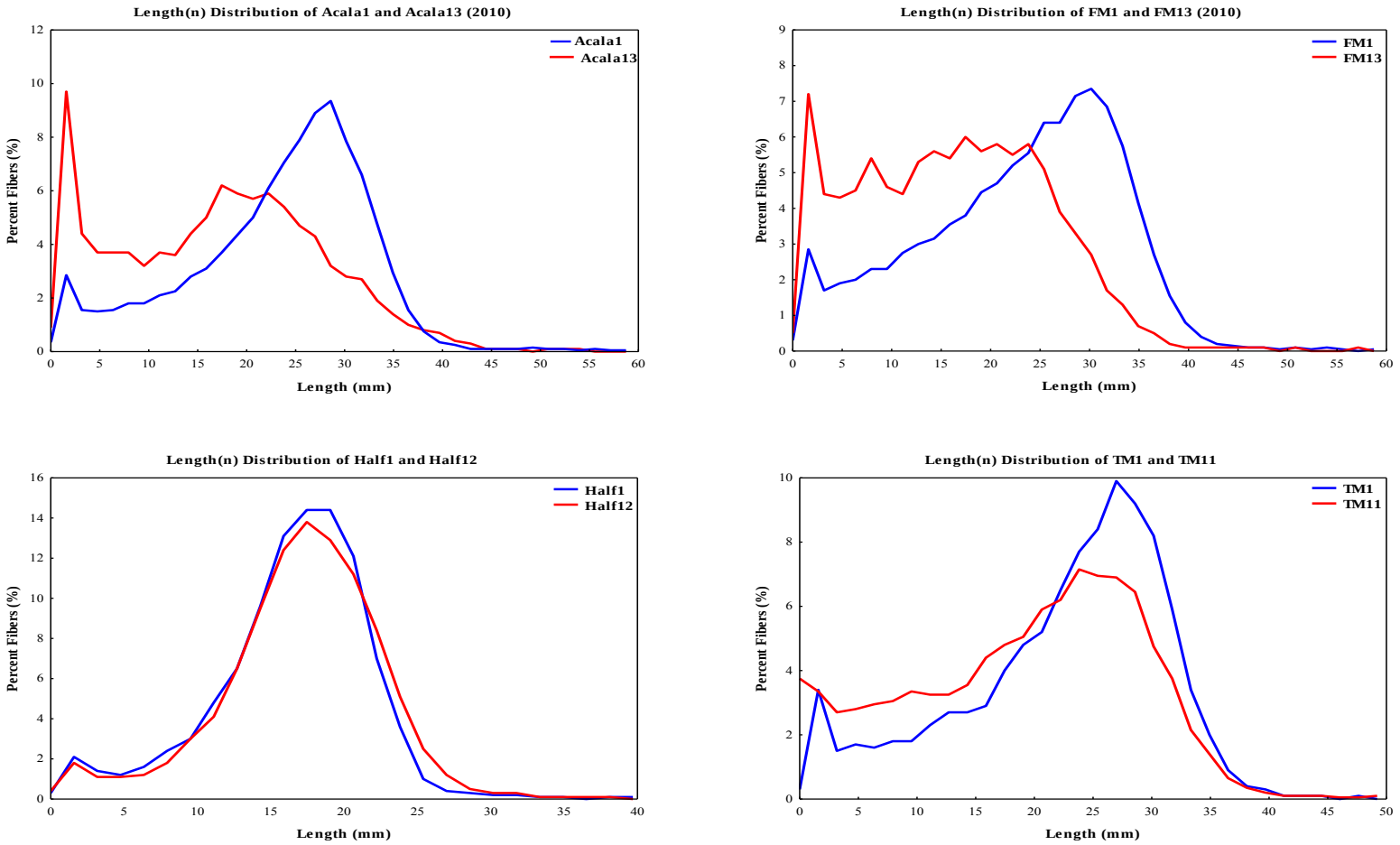

Figure 4: Fiber length (n) distribution of Acala 1517-99 at sympodial branch 1 (Acala1) and 13 (Acala13), FiberMax 832 at sympodial branch 1 (FM1) and 13 (FM13), Half and Half at sympodial branch 1 (Half1) and 12 (Half12) and TM-1 at sympodial branch 1 (TM1) and 11 (TM11) in 2010 at Lubbock, Texas.

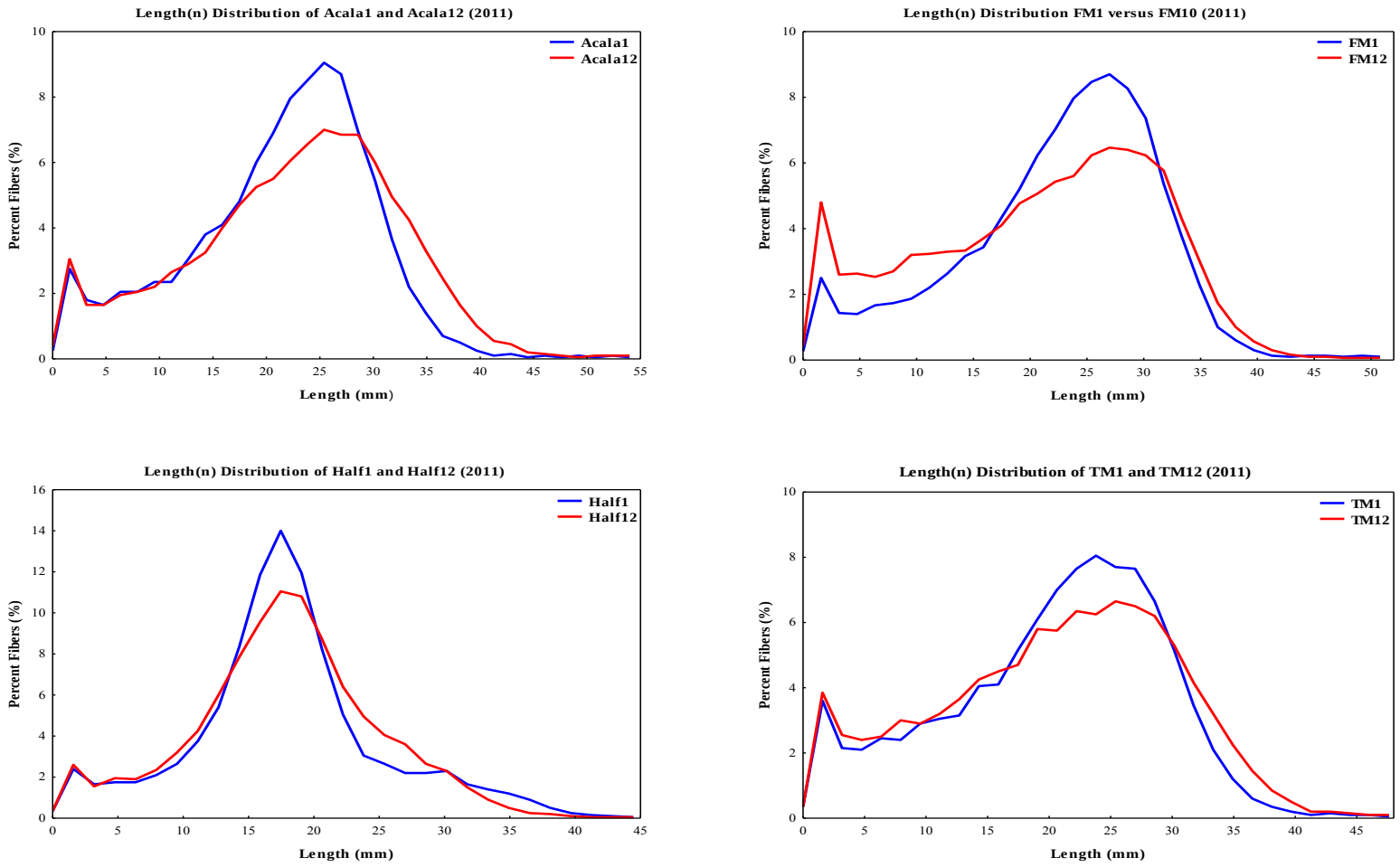

Figure 5: Fiber length (n) distribution of Acala 1517-99 at sympodial branch 1 (Acala1) and 13 (Acala13), FiberMax 832 at sympodial branch 1 (FM1) and 13 (FM13), Half and Half at sympodial branch 1 (Half1) and 12 (Half12) and TM-1 at sympodial branch 1 (TM1) and 11 (TM11) in 2011 at Lubbock, Texas.

Table 27: Growing degree days (GDD) in 2010 and 2011 at Lubbock, Texas.

Event	DPA	Recommended GDD (Ritche et al., 2004)	2010	2011
Emergence (stand establishment)	7	45-130	54	45
Appearance of first square	41	440-530	721	780
Appearance of first flowers	62	780-900	1089	1362
Peak blooming	90	1350-1500	1665	2138
First open boll	120	1650-1850	2453	2932
Defoliation	155	1900-2600	2629	3117

The National Oceanic and Atmospheric Administration (NOAA) released data showing the first four months of 2011 in Lubbock were the 4th driest start to the year on record. This included the driest April on record, without any rainfall for the first time in the 100 years. Until June 1, only 27.94 mm of rain had fallen. It was not until early-mid September that the weather had cooled and some rainfall was received (NOAA, 2012). It was observed that plant height was significantly lower in Lubbock (2011) compared to in college station. Plant height was approximately 610mm tall. Distance between nodes was also reduced from normal lengths as a likely result of environmental stress.

Cotton plant height and branch formations can be influenced by growing environment inclusive of high temperatures (Hanson et al., 1956; Reddy et al.,1990). Fiber quality also is significantly affected by growing conditions. It has been shown that optimal temperatures for cotton fiber length was around 19 to 20 °C depending on the

genotype (Gipson and Joham,1968; Gipson and Ray, 1970). Fiber length is influenced by the elongation phase during fiber development. Studies have shown early-stage fiber elongation is highly temperature dependent; late fiber elongation may be temperature independent (Gipson and Joham, 1969; Xie et al., 1993). HVI UHML was negatively correlated with the difference between maximum and minimum temperature (Hanson et al., 1956). Studies exclusive to the High Plains region have shown that temperatures at night of approximately 15 °C, compared to 25 °C caused a four to five days delay in fiber elongation (Gipson and Joham, 1968). Variations in fiber length and the elongation period also were associated with relative heat-unit accumulations. Regression analyses showed that genotypes that produced longer fibers were more responsive to heat-unit accumulation levels than were genotypes that produced shorter fibers (Quisenberry and Kohel, 1975). The rates of secondary wall deposition in both upland and pima genotypes were closely correlated with heat-unit accumulation (Johnson et al., 1997; Bradow et al., 1996). An early study of the effects of suboptimal temperatures on fiber development used micronaire fineness to quantify the effects of heat-unit deficits (Hessler et al., 1959). The rate of increase in fiber micronaire has been correlated with heat unit accumulations (Johnson et al., 1997).

In terms of water requirements, Grimes and Yamada (1982) showed fiber length was not affected unless the water deficit was great enough to lower the yield to 700 kg/ha when water deficit occurred later in the flowering period, fiber length was decreased (Marani and Amirav, 1971; Hearn, 1976). Severe water deficits during the fiber elongation stage have been known to reduce fiber length (Hearn, 1994).

Given the extreme weather conditions that the plants were subjected to in 2011 at Lubbock fiber data may have been adversely affected. Despite the stress, significant within-plant variability was observed in fiber quality for some genotypes and fiber length based traits.

Conclusions

Results from trials at College Station and Lubbock suggest that cotton fiber quality variability exists within a plant. This observation was made even in high stress conditions (e.g. Lubbock, 2011) from excess heat and reduced moisture. The trend in College Station was consistent across genotypes and years suggesting that fiber quality declines from the bottom sympodial branches towards the top. This was also seen in Lubbock, Texas, in 2010. Stressful conditions in 2011 at Lubbock reversed that trend; however, this was an exceptional year. In general, better fiber quality exists in the lower half of the plants with the drawback that it frequently contains higher trash content compared to the upper half. Fiber quality remains of prime importance to the spinner for efficient, high quality textile processing. Variability in cotton bales coming from physical attributes have been shown to affect the finished-product quality and manufacturing efficiency (Bradow et at;,1996). Moore (1996) concluded for efficiency of blending, spinning, dyeing process to be optimized, textile mills require effective description and measurement of fiber quality traits.

It was also seen with the College Station length (n) data that the degree of variability in fiber quality changes among genotypes. Half and Half, which has the

coarsest fiber, and Acala 1517-99, which has the finest fiber, displayed a lower degree of variability in fiber length (n) as compared to FiberMax 832 and TM-1.

Results of these studies can help the cotton plant breeder to develop and practice adequate boll sampling protocols in research programs so as to make the correct estimate of inherent fiber quality. This will enable scientists and researchers to make well-informed and unbiased decisions during the selection process. Secondly, efforts can be directed into reducing the within-plant variability in cotton fiber quality utilizing various breeding tools and technologies available to the cotton plant breeders.

CHAPTER V

BOLL SAMPLING STUDY

Results and Discussion

HVI testing showed no year or genotype effect for fiber micronaire, length uniformity ratio and elongation. There was a genotype x year interaction for fiber length and strength and hence these traits were analyzed separately. In 2009, an interaction between genotype and sample was observed. In 2010 and 2011, there was no genotype x sample for any trait. There were highly significant differences ($P \leq 0.01$) among sampling techniques for all traits in both genotypes across all years with the exception of fiber elongation. This analysis verifies our initial hypothesis that within-plant fiber variability impacts final fiber quality assessment of plots when boll samples are sampled (Tables A18-A20)

Data from HVI suggest that for all traits, with the exception of fiber elongation, fiber quality was estimated with a high degree of accuracy when 25 or more bolls were randomly picked. For fiber micronaire measurements 15 RND, 25 RND, 50 RND and 25 HQ were all good estimators. Fiber length uniformity ratio was well estimated by 15 RND, 25 RND and 50 RND while fiber elongation was best estimated by all but 25 LQ sample picked. The 25LQ technique underestimated fiber elongation. Fiber length was closely estimated by all random (RND) and high quality (HQ) samples picked for both genotypes in 2009 and 2011; however, in 2010 all random samples and only 15HQ and 25HQ were representative of true fiber length. Based on these means, with the exception

of fiber elongation, it was concluded that HVI fiber measurements were best estimated with randomized boll samples. Because 15 and 25 boll samples, when picked from LQ and HQ areas in the plants, were not representative of inherent fiber quality. Only 50 RND samples is recommended for HVI boll sampling. Fiber strength was estimated best with random boll samples as well as high quality boll samples in 2009 and 2010. However in 2011, accurate estimates came from all random and 15 and 50 low quality (LQ) samples (Tables 28- 31).

Table 28: Fiber micronaire, UI and elongation (HVI) for FiberMax 832 and Deltapine 491 in 2009, 2010 and 2010 in College Station, Texas.§

Sample	Micronaire (units)	UI (%)	Elongation (%)
15HQ	4.629 a	83.462 a	5.450 ab
25HQ	4.494 ab	83.392 a	5.429 ab
50HQ	4.546 a	83.605 a	5.470 ab
15LQ	3.854 d	80.333 c	5.358 ab
25LQ	3.715 d	80.112 c	5.258 b
50LQ	3.691 d	80.442 c	5.345 ab
15RND	4.255 c	82.325 b	5.537 ab
25RND	4.310 c	82.350 b	5.466 ab
50RND	4.274 c	82.375 b	5.495 ab
ALLBOLLS	4.3425 bc	82.121 b	5.55 a

§ Means with the same letter are not significantly different

Table 29: Fiber length (HVI) for the year 2009 in College Station, Texas.§

	Length (mm)	
Sample	**FiberMax 832**	**Deltapine 491**
15HQ	29.294 abc	27.940 a
25HQ	29.845 a	28.511 a
50HQ	29.654 ab	28.638 a
15LQ	28.194 d	24.638 c
25LQ	27.686 de	25.908 b
50LQ	27.178 e	26.606 b
15RND	29.210 abc	27.813 a
25RND	29.146 bc	27.876 a
50RND	28.893 c	28.003 a
ALLBOLLS	29.337 abc	28.003 a

§ Means with the same letter are not significantly different

Table 30: Fiber length (HVI) for FiberMax 832 and Deltapine 491 in 2010 and 2011 in College Station, Texas. §

Sample	Length 2010 (mm)	Length2011 (mm)
15HQ	30.543 abc	29.877 a
25HQ	30.638 ab	29.686 ab
50HQ	30.924 a	29.908 a
15LQ	27.781 e	27.686 d
25LQ	27.527 e	27.845 d
50LQ	27.844 e	28.257 cd
15RND	29.591 d	28.988 bc
25RND	29.845 cd	29.242 ab
50RND	29.591 d	29.051 b
ALLBOLLS	30.099 bcd	29.242 ab

§ Means with the same letter are not significantly different

Table 31: Fiber strength (HVI) for FiberMax 832 and Deltapine 491 in 2009, 2010 and 2011 in College Station, Texas.§

Sample	Strength (kN m kg-1) (2009)	Strength (kN m kg-1) (2010)	Strength (kN m kg-1) (2011)
15HQ	285.800 a	309.656 a	324.370 a
25HQ	294.210 a	299.604 ab	323.510 a
50HQ	298.130 a	306.224 ab	325.101 a
15LQ	235.980 b	274.719 c	286.730 de
25LQ	243.950 b	272.880 c	283.180 e
50LQ	247.870 b	270.060 c	286.850 de
15RND	282.440 a	292.739 b	305.370 abcd
25RND	287.590 a	297.152 ab	308.310 abc
50RND	280.730 a	296.662 ab	302.060 cde
ALLBOLLS	284.400 a	299.236 ab	303.530 bcd

§ Means with the same letter are not significantly different

Analysis using AFIS indicated no effect from year for all traits with the exception of fiber length (w). This trait also was affected by genotype in 2009. All other fiber traits had no effect from genotype in all three years. Interestingly both measuring systems, HVI and AFIS, revealed interactions from year and genotype for fiber length. Given that length (w) from AFIS and fiber length from HVI are both somewhat weight biased, this can be understandable. It is to be noted that there was no genotype and year effect for AFIS SFC (w). Also length (n) given by AFIS has no interaction from years and genotypes.

Data from AFIS suggested that for fiber neps, SFC (w), length (n), fineness, IFC and MR a random mix of boll samples was a good estimate of true fiber quality (Table 32). Any bias involved, such as selecting an over-abundance of bolls from the top or bottom region of the plants clearly underestimates or overestimates fiber quality respectively. In regards to nep size, it is to be noted that the 'all bolls' sample coming from the picker harvest was determined by following samples: 15HQ, 50HQ, 15LQ, 25LQ, 50LQ and 15RND. For this trait, 25RND and 50RND samples did not work.

Total trash content was difficult to evaluate because of the confounding effect of comparing machine harvested samples versus hand harvest. The machine harvester introduces considerably more trash into samples. Boll samples are cleaner and provide better quality seed in contrast to machine harvested samples. Trash content was not truly estimated by any boll sample in this test.

Fiber length (w) data was analyzed based on genotypes in 2009 because of genotype x sample interaction (Table 33 and Table 34). In 2009, fiber length (w) for FiberMax 832 was closely estimated by 15HQ, 25HQ, 15LQ, 15RND, 25RND and 50RND. It was interesting that this was one of the few tests where 15LQ was a good estimator of fiber quality. 15LQ being representative of the overall fiber length (w) is probably an odd occurrence which was not seen in other years. This is unlikely to be repeatable on a consistent basis because if the top bolls from the plants truly had good fiber quality, then the 25LQ and 50LQ sample would have represented no significant difference from the random or high quality samples. Deltapine 491 in 2009 showed 15HQ, 25HQ, 50HQ, 15RND, 25RND and 50RND provided consistent results. A likely

reason that some HQ samples work in this test is because FiberMax 832 and Deltapine 491 are recognized as producing high quality fibers and often used as checks when testing against experimental lines. It is possible that the lower region bolls from the plants are able to compensate for the poor quality bolls in the upper half region of the plants given the right growing environment.

Fiber length (w) data in 2010 revealed that 15RND, 25RND and 50RND were good estimators; however, in 2011 length (w) was closely estimated by 15RND, 25RND, 50RND, 15LQ, 25LQ and 50LQ. 15HQ, 25HQ and 50HQ ended up overestimating fiber length (w). In 2011, overall fiber length (w) from a grab sample was probably impacted negatively by the bolls growing in the upper half of the plants. A likely cause is the extreme heat in that year. In 2011, it was seen that 3,416 heat units (growing degree days) were accumulated over the entire growing season from planting to harvest. This was much higher than the recommended GDD required for normal growth for cotton plants (Table 27).

Table 32: Fiber nepsize, neps, SFC (w), length (n), SFC (n), trash (total), IFC, fineness, MR (AFIS) across genotypes (FiberMax 832 and Deltapine 491) in 2009, 2010 and 2010 in College Station, Texas.§

Sample	Nep size (µm)	Neps (gm^{-1})	SFC (w) (%)	Length (n) (mm)	SFC (n) (%)	Total trash (count)	Fineness (mg/kg)	IFC (%)	MR (units)
15HQ	707 abcd	108.261 c	4.900 c	22.834 a	16.526 c	400 b	174.826 a	4.617 c	0.965 a
25HQ	683 d	106.416 c	4.746 c	23.038 a	16.137 c	437 b	173.083 a	4.541 c	0.967 a
50HQ	714 abc	115.417 c	4.967 c	22.809 a	16.708 c	494 b	173.125 a	4.763 c	0.963 a
15LQ	710 abcd	331.750 a	9.612 a	19.284 c	26.054 a	605 b	155.291 c	6.804 a	0.900 c
25LQ	706 abcd	334.000 a	9.717 a	19.202 c	26.592 a	472 b	153.916 c	7.058 a	0.893 c
50LQ	716 ab	302.417 a	9.617 a	19.304 c	26.767 a	483 b	152.666 c	7.096 a	0.891 c
15RND	702 abcd	171.250 bc	6.417 b	21.463 b	20.121 b	488 b	165.292 b	5.504 b	0.939 b
25RND	691 bcd	159.833 bc	6.516 b	21.361 b	20.450 b	379 b	166.375 b	5.504 b	0.942 b
50RND	684 cd	156.833 bc	6.442 b	21.387 b	20.183 b	472 b	165.458 b	5.412 b	0.937 b
ALLBOLLS	729 a	193.412 b	7.125 b	21.031 b	22.137 b	1712 a	164.500 b	5.796 b	0.932 b

§ Means with the same letter are not significantly different

Table 33: Fiber length (w) (AFIS) for the year 2009 in College Station, Texas.§

	Length (w) (mm)	
Sample	**FiberMax 832**	**Deltapine 491**
15HQ	26.754 abc	25.336 abc
25HQ	27.051 ab	25.781 a
50HQ	27.432 a	25.463 ab
15LQ	25.844 c	21.336 d
25LQ	24.066 d	21.907 d
50LQ	23.495 d	22.288 d
15RND	25.844 c	24.574 bc
25RND	26.035 c	24.447 c
50RND	26.416 bc	24.447 c
ALLBOLLS	26.162 bc	24.892 abc

§ Means with the same letter are not significantly different

Table 34: Fiber length (w) (AFIS) for FiberMax 832 and Deltapine 491 in 2010 and 2011 in College Station, Texas.

Sample	Length (w) (mm) 2010	Length (w) (mm) 2011
15HQ	27.019 a	27.527 a
25HQ	27.495 a	27.305 a
50HQ	26.924 a	27.336 a
15LQ	22.765 d	24.892 d
25LQ	23.051 cd	25.273 d
50LQ	23.685 c	25.431 cd
15RND	25.559 b	26.479 b
25RND	25.971 b	26.130 bc
50RND	25.685 b	26.130 bc
ALLBOLLS	25.971 b	25.590 cd

§ Means with the same letter are not significantly different

Fiber length distributions were plotted from AFIS data for length (w) and length (n). A comparison was made across years between the two length measurements. For this comparison, only the 50 HQ, 50LQ and 50RND samples were used.

Length distributions clearly show that length (w) underestimates SFC. Differences between the shape of the distribution of the 50LQ and 50HQ samples, indicate length (n) is a better predictor of the amount of short fibers the sample actually contains (Figure 6). The RND sample also has a higher SFC content indicating that the top half of the plant, which carries the poorest fiber quality cotton bolls, negatively

impacts overall length properties in the field. In that context, if the average SFC (w) versus SFC (n), SFC (w) underestimates the percent of short fibers by three to four times as compared to the SFC (n).

Cotton plant breeders need to consider SFC and amount of neps in cotton because of the increasing problems caused by these traits at the spinning level. As of today, cotton production decisions are influenced more so by government loan programs and cotton merchants than by the end-users of the commodity. Therefore prices are not directly driven by yarn quality. However, based on the spinning requirements, this may change and the value of cotton may be determined by the true spinning value of cotton (ICAC, 2004). Eventually the textile industry will develop a rapid and reliable method to include neps and SFC measurements in the HVI module and cotton producers must be ready to adjust to these new parameters.

Length (w) from AFIS measurements have often been used by researchers to estimate fiber length with the assumption that it relates well with weight based measurements used commercially. However, it is important to look at length parameters given by number from AFIS in order to rapidly and efficiently improve length characteristics. Fiber length (w) provided by AFIS is biased in the sense that the machine assumes linear density to be equal across all the fibers. It is well established that immature fibers have difference in linear density compared to mature ones. Given that paradigm, length (w) tends to underestimate SFC. This is because longer fibers weigh more than shorter fibers. Secondly fiber length (w) is not a direct length measurement. AFIS calculates length (w) from the length (n) and average fineness. Hence, this is not a

reliable measurement (Mananghar et al., 2012 and Kelly, 2006). Fiber length measurement for a cotton plant breeder should come from the length by number when using AFIS because the objective is to improve cotton by using the most effective and precise tools as opposed to a producers or sellers whose main goal is to market cotton. Given that the AFIS also renders a certain degree of stress on the fibers during measurement of length (n), it mimics the processing effect to some extent making the measurement a more realistic one (Krifa, 2006). Rodgers (1997) described the importance of SFC in determining ultimate yarn quality and performance at the textile level which has led the post-harvest sector of the US cotton industry to make SFC minimization its top priority. SFC is a result processing effect when dealing with higher quality cultivars. Cotton fiber strength is associated with SFC in an indirect manner. This is because weaker fibers tend to break easily during harvesting and ginning because of a compromised ability to withstand the mechanical stress. This is reflected by the measurement of fiber strength given by HVI and measurements of SFC (n) and SFC (w) given by AFIS. Lower fiber quality boll samples were weaker and also resulted in higher SFC in the tested samples.

HVI length is also a weight biased measurement where the machine assumes linear density to be the same across all the fibers tested given by the micronaire testing module. The same logic applies to this measurement in the sense that fineness changes among fibers depending on the maturity. This assumption is validated by the pattern of length measurement from HVI and length (w) from AFIS which behave in an identical fashion in this study (Table 35).

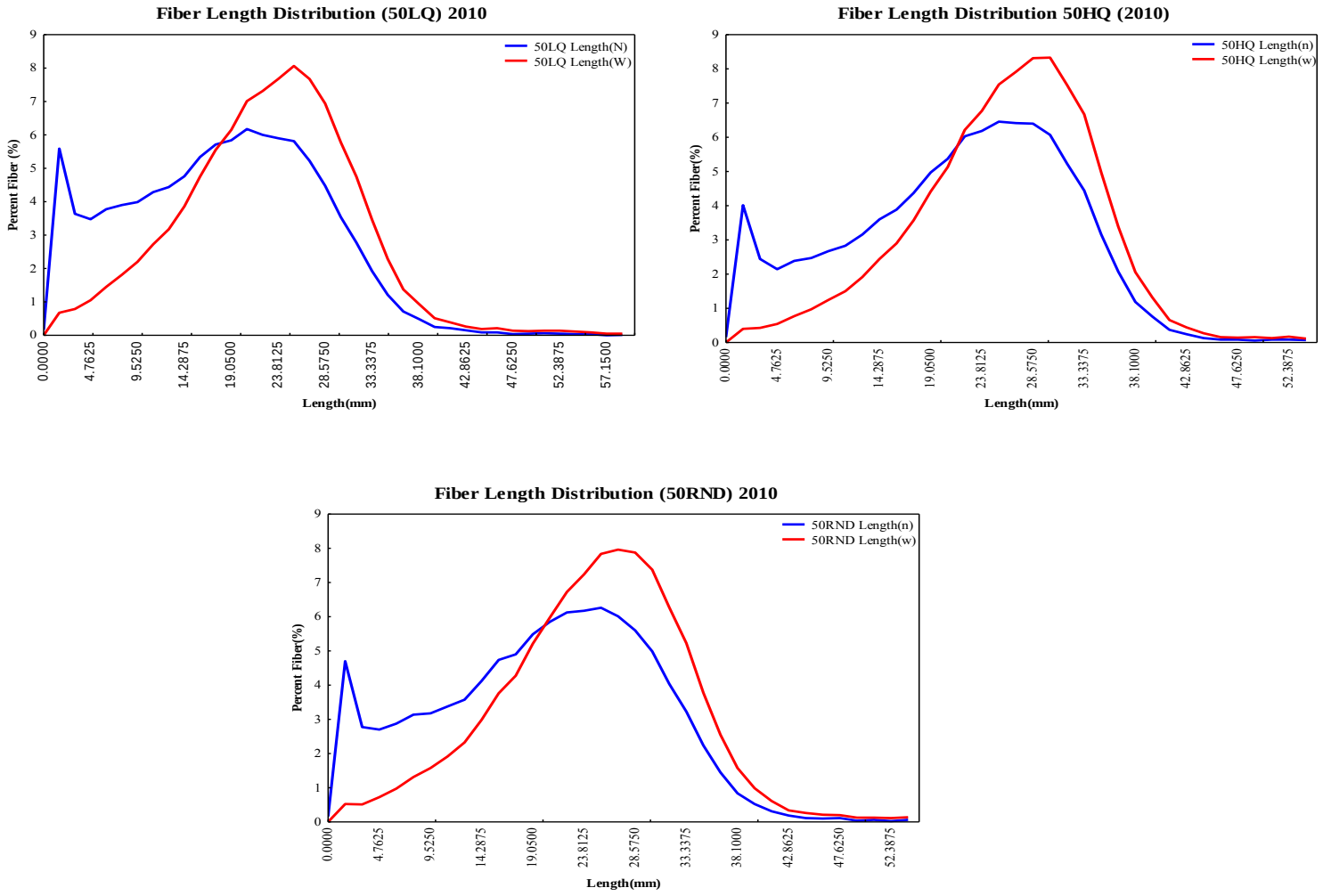

Figure 6: Fiber length distributions for length (w) and length (n) as given by AFIS for FiberMax 832 and Deltapine 491 in 2010 for 50LQ, 50HQ and 50RND boll samples at College Station, Texas.

Table 35: Fiber length (n) and fiber length (w) (AFIS) across genotypes (FiberMax 832 and Deltapine 491) in 2010 in College Station, Texas.§

Sample	Length (n) (mm)	Length (w) (mm)
15HQ	22.542 a	27.019 a
25HQ	23.018 a	27.495 a
50HQ	22.383 a	26.924 a
15LQ	18.097 c	22.764 cd
25LQ	18.288 c	23.051 cd
50LQ	18.827 c	23.685 c
15RND	20.986 b	25.558 b
25RND	21.336 b	25.972 b
50RND	20.923 b	25.685 b
ALLBOLLS	20.732 b	25.972 b

§ Means with the same letter are not significantly different

Fiber traits such as total trash content, which is the sum of trash and dust, and nep size are affected by environmental factors. Neps are not present in unopened cotton bolls in the field. The formation of neps and its sizes are a result of processing cotton from field to textile. When a cotton boll opens, fibers will dry, convolute and collapse leading to nep formation (Bradow and Davidonis, 2010). Immature fibers tend to be weaker and lead to higher amount of neps being formed during processing.

Fiber elongation on the other hand may have a stronger genetic component. Fiber elongation data ascertained from HVI showed that with the exception of 25LQ

elongation was estimated by bolls picked by any other sampling technique employed. This could mean that elongation was less affected by environment because it stayed relatively stable throughout the plant. Based on the data obtained from this test, it can be predicted that breeding for traits such as trash and neps size might be challenging. Secondly, both traits may be associated with machine harvesting indicating a strong environmental influence. It is difficult to understand the reason for 25LQ underestimating fiber elongation which is not reflected by 50LQ especially given that this trait was stable across years and genotypes.

Fiber lint percent is an important yield component. There was a significant genotype by year interaction hence all years were separately analyzed (Table A.25). There was also a significant genotype x sample effect in 2009. Means from 2009, 2010 and 2011 indicate fiber lint percent varied considerably among years. During the course of this study, none of the boll sampling techniques were representative of true lint percent. In 2010, only the 15HQ method estimated lint percent accurately. All other methods underestimated lint percent and failed to provide reliable and consistent results. In 2011, all boll samples, regardless of position and bias, accurately estimated lint percent. Thus in 2011 we had no sampling effect. In 2009, we had a genotype by sample interaction and therefore reported FiberMax 832 and Deltapine 491 separately. It was interesting to see that Deltapine 491 had a sampling effect but FiberMax 832 did not. All random and high quality samples closely estimated lint percent for Deltapine 491 in 2009. It is difficult to predict what sampling technique could provide the best estimate of

fiber lint percent since it is highly environmentally regulated. It might be best to use a machine harvest sample to evaluate this trait (Table 36 and Table 37).

Table 36: Fiber lint percent for FiberMax 832 and Deltapine 491 in 2009 in College Station, Texas.§

	Lint Percent (2009)	
Sample	**FiberMax 832**	**Deltapine 491**
15HQ	38.504 a	40.429 ab
25HQ	37.683 a	40.089 ab
50HQ	37.546 a	40.742 ab
15LQ	39.026 a	38.325 bc
25LQ	38.389 a	31.361 d
50LQ	35.304 a	36.740 c
15RND	38.238 a	41.828 a
25RND	37.559 a	39.361 abc
50RND	36.673 a	41.996 a
ALLBOLLS	37.099 a	41.312 a

§ Means with the same letter are not significantly different

Table 37: Fiber lint percent for FiberMax 832 and Deltapine 491 in 2010 and 2011 in College Station, Texas.§

Sample	Lint Percent (2010)	Lint Percent (2011)
15HQ	37.291 ab	36.601 a
25HQ	35.849 bc	37.364 a
50HQ	34.440 bcde	37.369 a
15LQ	33.432 cde	36.608 a
25LQ	31.726 e	38.359 a
50LQ	34.573 bcde	38.754 a
15RND	32.370 ed	38.368 a
25RND	35.834 bc	38.133 a
50RND	35.658 bcd	38.742 a
ALLBOLLS	39.372 a	36.118 a

§ Means with the same letter are not significantly different

This study suggest within-plant variability in cotton fiber quality affects fiber quality evaluation because of the methods cotton plant breeders use to ascertain seed cotton estimates from plots. Having the most accurate information for decision making is important for cotton plant breeders to maximize genetic gain for fiber quality and yield. In order to effectively make decisions, the best boll sampling techniques should be used. Based on this study, it was determined that a randomized mix of bolls sampled within the row gave the best estimate of fiber characteristics. However, when sampling small numbers of bolls such as 15 and 25 boll samples, caution should be exercised because

inadvertently picking biased bolls may easily skew data. It is routine practice to collect hundreds and sometimes thousands of boll samples per day in cotton breeding programs. Many people may have a tendency to pick bolls that 'look good' regardless of the position in the plant and therefore induce bias into the evaluation process. Even a few extra bolls picked from the upper half of the plants may skew the overall fiber quality of the sample when dealing with 25 or 15 boll samples. When picking 50 bolls, a certain amount of human error can be diluted to the point where an accurate estimate of fiber quality can be made. Protocols for boll sampling need to be established which is inclusive of fibers that represent the 'true' fiber quality in the plot/field. When dealing with traits such as trash content, it is best to use samples from a machine harvester and take a grab sample.

Conclusions

Boll sampling techniques employed for fiber testing and evaluation need to be established for efficient estimation of fiber quality. Randomly harvesting boll samples with high number of bolls (50RND) works well to accurately determine cotton fiber quality. Cotton plant breeders can make educated decisions for selection purposes in their program when a reliable estimate of fiber quality is available to them. If AFIS testing is available and economically feasible, a breeder should examine the different length and maturity parameters. When dealing with fiber length, it is best to consider fiber length by number given by the AFIS because of the precision in estimating overall mean and SFC of the samples tested. For measuring yield characteristics and trash

content measurements, the best approach may be to ascertain a grab sample coming from a full row/plot harvest using a mechanical cotton harvester.

CHAPTER VI

DIALLEL FOR FIBER MATURITY AND STANDARD FINENESS

Results and Discussion

There was significant difference between entries (parents and F_1s) in the test for all the fiber traits evaluated (Table A26 and Table A27). Fiber traits associated with fiber maturity, such as micronaire, length, uniformity index and strength given by HVI were evaluated. Fiber neps, length (n), SFC (n), fineness, maturity ratio, IFC given by AFIS were included in this analysis. Standard fineness (Hs) was calculated from the AFIS data (AFIS fineness/maturity ratio) (Hequet et al., 2006) was also included in the study. GCA effects were observed for all HVI and AFIS traits and SCA effects were observed for all traits with the exception of fiber micronaire given by HVI and fiber fineness and standard fineness given by AFIS.

HVI data showed Half and Half had the highest micronaire compared to Acala1517-99 which had the lowest. Parents were significantly different from each other with respect to fiber micronaire. The optimum range for cotton micronaire is between 3.8 and 4.6 (international standard) and 3.5-4.9 (U.S. standard). In that regard, Deltapine 90, FiberMax 832 and Tamcot HQ-95 were in the optimal micronaire range. Half and Half, had higher micronaire than other cultivar parents and Acala1517-99 had lower fiber micronaire than other cultivar parents thereby falling in the discounted pricing for cotton.

Acala1517-99, FiberMax 832 and Half and Half had significant GCA estimates for fiber micronaire. Half and Half had the highest significant GCA effect for improving HVI micronaire followed by Acala1517-99. FiberMax 832 had a negative GCA effect for fiber micronaire ($P \leq 0.05$). The cross between the best two general combiners, Half and Half and Acala1517-99, exhibited negative, although non-significant, SCA effects for fiber micronaire. GCA sum of squares accounted for 90% of total treatment mean squares for fiber micronaire indicating that additive gene effects were more important than non-additive gene effects. Since miconaire is a measurement of air permeability, which is an indicator of fineness-maturity complex; it is not an accurate measure of fiber maturity. Hence fiber maturity ratio given by AFIS was considered as a true maturity measurement for this study. To understand the fineness and maturity component combined together, fiber standard fineness was used for this study.

Means showed fiber maturity was significantly different between parents. Acala1517-99 was the least mature compared to FiberMax 832 which had the highest fiber maturity. Parents were also significantly different from each other in terms of fiber standard fineness with Tamcot HQ-95 being the finest and Half and Half being the coarsest. This indicated the rationale for selecting parents for this study was appropriate.

Deltapine 90 and Tamcot HQ-95 had significant ($P \leq 0.01$) GCA effects in terms of fiber maturity ratio. Deltapine 90 had a negative and Tamcot HQ-95 had a positive GCA effect. The cross between Acala 1517-99 and Tamcot HQ-95 had a highly significant positive SCA effect (0.093 units) followed by the cross between Deltapine 90 and Half and Half (0.014 units). GCA sum of squares accounted for 19% of the total

sum of squares for fiber maturity ratio. GCA mean squares accounted for 38% of the total treatment mean squares indicating that the trait was influenced by non-additive gene effects more than additive gene effects.

AFIS gives the immature fiber content (IFC) characterized by fibers having a maturity ratio of less than 0.25. Analysis revealed Deltapine 90 had a highly significant GCA effect (0.205 %) (not desirable) and Half and Half had a significant negative GCA effect (-0.194 %) (desirable). The cross between Acala1517-99 and Tamcot HQ-95 had a negative SCA effect ($P \leq 0.01$) of -2.720 % (desirable). All other SCA effects were non-significant. It is interesting to see that the same combination had a positive ($P \leq 0.01$) maturity ratio SCA effect (0.093 %). Means showed Acala1517-99 had the highest proportion of immature fibers (6.500%), TamcotHQ-95 (5.700%) and the lowest was Half and Half (4.825%). The cross between Acala1517-99 and TamcotHQ-95 had an IFC value of 5.025% which was significant lower than both parents.

Standard fineness (Hs) had a highly significant GCA effect and no significant SCA effects. Acala1517-99 (-5.856 mg/km), FiberMax 832 (-4.831 mg/km), Half and Half (12.628 mg/km) had significant ($P \leq 0.01$) GCA effects and Tamcot HQ-95 had (-1.698 mg/km) GCA effect ($P \leq 0.05$). GCA accounted for approximately 96% of the treatment sum of squares and 98% of treatment mean squares, suggesting additive gene effects were relatively more important than the non-additive gene effects for this trait. Half and Half had coarse fiber with the highest standard fineness value (205.513 mg/km) and FiberMax 832 had the finest fibers with the lowest standard fineness value (168.387mg/km).

Fiber length was measured using both, AFIS and HVI. AFIS length (n) was considered for the analysis while HVI has weight-biased length measurements which were taken into account. There were highly significant GCA and SCA effects observed for length measurements from both testing instruments. AFIS length (n) showed that Acala1517-99, FiberMax 832 and Tamcot HQ-95 had highly significant GCA effects (positive) and Half and Half had a highly significant negative GCA effect (not desirable). Acala1517-99 was the best combiner for length (n) (1.081 mm). The cross between Acala1517-99 and Tamcot HQ-95 was the best performer with SCA estimate of 5.767 mm. This cross also had the highest SCA effects for maturity ratio and for lowering immature fiber content. Deltapine 90 (non-significant) had a negative GCA effect. However, the cross between Deltapine 90 and Tamcot HQ-95 both having negative GCA effects, had a highly significant positive SCA effect (1.472 mm). The crosses of Deltapine 90/ Tamcot HQ-95, FiberMax 832/Tamcot HQ-95, and Half and Half/Tamcot HQ-95 had negative SCA effects ($P \leq 0.01$). Means showed FiberMax 832 had the longest fibers followed by Tamcot HQ-95, Acala1517-99, Deltapine 90 and Half and Half. The crosses between Acala1517-99 and Deltapine 90 and, Acala1517-99 and FiberMax832 yielded the longest fibers.

Fiber length given by HVI showed all five parents had highly significant GCA effects with Acala1517-99 having a GCA estimate of 3.712 mm(highest) and Half and Half having a GCA estimate of -3.175 mm (lowest, not desirable). The cross of Acala1517-99/Tamcot HQ-95 had the highest SCA effect of 4.470 mm. Means for parents and crosses showed results similar to AFIS length (n) data with the exception

that in general, length was overestimated. AFIS length (n) was more sensitive to SCA effects as compared to HVI length.

Short fiber content(n) given by AFIS showed Acala1517-99 and Deltapine 90 had highly significant GCA effects. Acala 1517-99 had a GCA estimate of -1.222 % (desirable) and Deltapine 90 had a GCA estimate of 1.499 % (not desirable). The cross between Acala 1517-99 and Tamcot HQ-95 had a highly significant SCA effect of -12.441 % (desirable). The cross between Deltapine 90 and Tamcot HQ-95 had an SCA effect of 2.993% (not desirable). Means showed Acala 1517-99 had the highest SFC (21%) among all parents and FiberMax832 had the lowest SFC (15%). Going by HVI length measurements, Acala 1517-99 would be earning a premium for its high fiber length. However short fiber content of 21.325% is detrimental to the textile industry. The cross between Acala 1517-99 and Half and Half had a highly significant SCA effect (-1.881%) and means indicated this was also the entry with the lowest amount of short fibers (13.025%). HVI uniformity index showed FiberMax 832 had the highest UI among parents (83.150%) and Half and Half had the lowest (75.050%). Acala 1517-99 had acceptable uniformity (US standards) (80.800%).

Fiber strength data showed Acala 1517-99, FiberMax 832, Tamcot HQ-95 and Half and Half had highly significant GCA effects. Half and Half had a GCA effect -3.068 kN m kg-1 (not desirable). Acala 1517-99 had the highest GCA effect 2.140 kN m kg-1 (desirable). Fibermax 832 and Tamcot HQ-95 also had positive GCA effects. The cross between Acala 1517-99 and Tamcot HQ-95 had the highest SCA effect of 11.826 kN m kg-1. The cross between Acala 1517-99 and FiberMax 832 yielded an SCA effect

of 0.830 kN m kg-1 and that of Acala1517-99 and Deltapine 90 was 1.223 kN m kg-1. Half and Half and Deltapine 90 had both negative GCA estimates (Deltapine 90, non-significant) but the cross between these parents had a positive SCA effect of 1.707 kN m kg-1 ($P \leq 0.01$).

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). Means showed FiberMax 832 had the highest fiber strength among parents and Half and Half had the lowest strength. The cross between Acala 1517-99 and FiberMax 832 yielded the strongest fibers among all entries. Acala 1517-99/Tamcot HQ-95 had fiber strength 311.127 kN m kg-1. The cross between the two weakest parents, Half and Half and Tamcot HQ-95, was also the weakest entry among all progeny (258.169 kN m kg-1). Acala 1517-99 had average fiber strength of 276.802 kN m kg-1 (average) which probably explains why we see a high proportion of short fibers in that entry with weaker fibers that break easily. However, average length and UI values from HVI data are acceptable for this entry and do not discount for the short fiber content present.

The cross between Deltapine 90 and Tamcot HQ-95 had 20.550% of short fiber content. HVI data shows this entry had 298.623 kN m kg-1 fiber strength and length of 28.765mm. UI was reported to be 82.050% which is acceptable by US and international standards. This sample would in fact, gain premium pricing for fiber length and strength; however, it may not be the best fiber quality for spinners given its proportion of short fibers. Not only are short fibers a matter of concern, but fiber neps also pose problems

for spinners and weavers. Acala 1517-99 had the highest number of neps among parents (250 count gm^{-1}) and Half and Half (107 count gm^{-1}) had the lowest. Acala 1517-99 had a significant GCA effect 19.636 count gm^{-1} (not desirable) and Half and Half had a highly significant GCA effect -24.192 gm^{-1} (desirable). The cross between Acala 1517-99 and Tamcot HQ-95 had an SCA effect of -118.025 count gm^{-1} ($P \leq 0.01$). Deltapine 90/Tamcot HQ-95 had an SCA effect of 46.681 count gm^{-1} ($P \leq 0.05$) while all other SCA effects were non-significant. It is to be noted that means for all entries had acceptably low amounts of fiber neps (Table 40 and Table 41).

Finally, fiber elongation was evaluated for combining abilities. All parents with the exception of Tamcot HQ-95 had highly significant GCA effects. Half and Half (0.365 %) and Acala 1517-99 (0.135 %) had positive GCA effects while Deltapine 90 (-0.233 %) and FiberMax 832 (-0.197 %) had negative GCA effects. The two best general combiners also had a positive SCA effect (0.278 %) when crossed (Acala1517-99/Half and Half). The cross between FiberMax 832 and Half and Half yielded the highest SCA estimate of 0.311 % (Table 38 and Table 39).

Table 38: GCA and SCA estimates for fiber micronaire, length, uniformity index (UI), strength and elongation (HVI) for five parents (Acala 1517-99, Deltapine 90, FiberMax 832, Half and Half and Tamcot HQ-95) and ten (F1) progeny.

	GCA				
Entry	**Micronaire**	**Length**	**UI**	**Strength**	**Elongation**
Acala 1517-99	0.155**	1.371**	1.761**	20.987**	0.135**
Deltapine 90	-0.044	0.457**	-0.262	-1.873	-0.233**
FiberMax 832	-0.108*	0.889**	0.502**	6.404**	-0.197**
Half and Half	0.248**	-3.175**	-2.883**	-30.088**	0.356**
Tamcot HQ-95	0.059	0.431**	0.882**	4.561*	-0.061

Table 38: Continued

	SCA				
Entry	**Micronaire**	**Length**	**UI**	**Strength**	**Elongation**
Acala 1517-99/Deltapine 90	0.089	0.228	0.528	11.993**	0.117
Acala 1517-99/FiberMax 832	0.078	0.304	-0.161	8.139*	-0.017
Acala 1517-99/Half and Half	-0.003	-0.228	1.074**	-5.364	0.278**
Acala 1517-99/Tamcot HQ-95	0.785**	4.470**	8.149**	116.271**	0.121
Deltapine 90/FiberMax 832	-0.057	0.508	0.137	2.559	-0.151*
Deltapine 90/Half and Half	-0.014	2.133**	0.473	16.741**	-0.154*
Deltapine 90/Tamcot HQ-95	-0.125	0.101	-0.643	-4.422	-0.136
FiberMax 832/ Half and Half	0.151	-0.635	1.334**	-10.150**	0.311**
FiberMax 832/ Tamcot HQ-95	-0.085	-0.203	-1.457	-12.690**	-0.171*
Half and Half/ Tamcot HQ-95	-0.067	-1.447**	-0.372	-16.642**	0.000

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

Table 39: Fiber micronaire, length, uniformity index (UI), strength and elongation (HVI) for five parents and ten (F1) progeny. §

Entry	Micronaire (units)	Length (mm)	UI (%)	Strength (kN m kg1)	Elongation(%)
Acala 1517-99	3.700 g	28.1305 de	80.800 f	276.802 ef	6.100 c
Deltapine 90	4.450 cdef	27.242 e	81.300 def	283.177 e	5.775 d
FiberMax 832	4.225 f	29.591 abc	83.150 ab	319.217 b	5.700 de
Half and Half	4.950 a	21.463 h	75.050 h	247.871 h	6.575 b
Tamcot HQ-95	4.350 ef	27.178 e	81.000 ef	268.221 fg	6.050 c
Acala 1517-99/Deltapine 90	4.375 def	29.845 ab	84.100 a	331.476 a	6.100 c
Acala 1517-99/FiberMax 832	4.300 ef	30.353 a	84.175 a	335.889 a	6.000 c
Acala 1517-99/Half and Half	4.575 bcde	25.717 f	82.025 cde	285.874 e	6.850 a
Acala 1517-99/Tamcot HQ-95	4.225 f	29.274 bc	83.275 ab	311.127 bc	5.775 d
Deltapine 90/FiberMax 832	4.275 ef	29.654 abc	82.450 bc	307.449 cd	5.500 e
Deltapine 90/Half and Half	4.675 abcd	27.178 e	79.400 g	285.138 e	6.050 c
Deltapine 90/Tamcot HQ-95	4.375 def	28.765 cd	82.050 cd	298.623 d	5.650 de
FiberMax 832/Half and Half	4.775 ab	24.828 f	81.025 def	266.505 fg	6.550 b
FiberMax 832/Tamcot HQ-95	4.350 ef	28.892 bcd	82.000 cde	298.623 d	5.650 de
Half and Half/Tamcot HQ-95	4.725 abc	23.558 g	79.700 g	258.169 gh	6.375 b

§ Means with the same letter are not significantly different

Table 40: GCA and SCA estimates for fiber neps, length (n), Short Fiber Content (SFC) (n), fineness (H), standard fineness (Hs), Immature Fiber Content (IFC) and Maturity Ratio (MR) (AFIS) for five parents (Acala 1517-99, Deltapine 90, FiberMax 832, Half and Half and Tamcot HQ-95) and ten (F_1) progeny.

	GCA						
Entry	**Neps**	**Length (n)**	**SFC (n)**	**H**	**Hs**	**IFC**	**MR**
Acala 1517-99	19.636*	1.081**	-1.222**	-5.327**	-5.856**	0.063	0.002
Deltapine 90	10.337	-0.081	1.499**	-1.638**	-0.242	0.205**	-0.008**
FiberMax 832	10.837	0.564**	-0.053	-4.746**	-4.831**	0.062	-0.001
Half and Half	-24.019**	-1.931**	-0.075	12.111**	12.628**	-0.194*	0.001
Tamcot HQ-95	-16.792	0.365**	-0.147	-0.398	-1.698*	-0.136	0.007**

Table 40: Continued

	SCA						
Entry	**Neps**	**Length (n)**	**SFC (n)**	**H**	**Hs**	**IFC**	**MR**
Acala 1517-99/Deltapine 90	-27.246	0.619*	-1.456*	1.721	0.279	-0.171	0.008
Acala 1517-99/FiberMax 832	4.253	0.038	0.647	2.077	1.101	-0.028	0.006
Acala 1517-99/Half and Half	2.111	0.247	-1.881**	-1.779	-0.961	0.028	-0.004
Acala 1517-99/Tamcot HQ-95	-118.025**	5.767**	-12.441**	11.662	-4.352	-2.720**	0.093**
Deltapine 90/FiberMax 832	3.052	-0.069	0.999	-2.611	-1.512	0.105	-0.006
Deltapine 90/Half and Half	-19.591	1.472**	-1.828*	-0.717	-3.563	-0.312	0.014**
Deltapine 90/Tamcot HQ-95	46.681*	-0.886**	2.993**	-4.457	-2.471	0.353	-0.012*
FiberMax 832/Half and Half	-6.591	0.131	-1.901*	-0.753	1.213	-0.269	0.007
FiberMax 832/Tamcot HQ-95	13.182	-0.578*	1.547	2.639	1.091	0.296	-0.009
Half and Half/Tamcot HQ-95	-3.461	-0.623**	-0.331	-0.6	0.789	-0.021	0.004

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

Table 41: Fiber neps, length (n), Short Fiber Content (n), Fineness (H), Standard Fineness(Hs), Immature Fiber Content (IFC) and Maturity Ratio(MR) (AFIS) for five parents and ten progeny.§

ENTRY	Neps (count per gm)	Length (n) (mm)	SFC (n) (%)	H (mg/km)	Hs (mg/km)	IFC (%)	MR (units)
Acala 1517-99	250 a	20.257 c	21.325 a	154 g	169 ij	6.500 a	0.910 f
Deltapine 90	160 bc	20.701 c	18.850 bc	171 de	182 de	5.350 bc	0.940 de
FiberMax 832	156 bcd	22.796 a	15.450 de	161 f	168 j	5.000 cde	0.958 abc
Half and Half	107 cd	16.955 e	19.025 bc	194 a	205 a	4.825 cde	0.947 bcde
Tamcot HQ-95	138 bcd	20.320 c	20.025 ab	166 ef	178 ef	5.700 b	0.935 e
Acala 1517-99/Deltapine 90	144 bcd	23.050 a	15.025 ef	166 ef	173 ghi	5.025 cde	0.960 ab
Acala 1517-99/FiberMax 832	176 b	23.114 a	15.575 de	163 f	169 hij	5.025 cde	0.965 a
Acala 1517-99/Half and Half	139 bcd	20.828 c	13.025 f	176 cd	184 cd	4.825 cde	0.955 abcd
Acala 1517-99/Tamcot HQ-95	165 bc	21.971 b	17.525 cd	163 f	171 ghij	5.025 cde	0.957 abc
Deltapine 90/FiberMax 832	165 bc	21.844 b	18.650 bc	162 f	172 ghij	5.300 bc	0.943 cde
Deltapine 90/Tamcot HQ-95	181 b	20.828 c	20.550 ab	165 f	174 fg	5.350 bc	0.945 bcde

Table 41: Continued

ENTRY	Neps (count per gm)	Length (n) (mm)	SFC (n) (%)	H (mg/km)	Hs (mg/km)	IFC (%)	MR (units)
FiberMax 832/Half and Half	121 bcd	20.193 c	14.1750 ef	181 bc	188 bc	4.525 e	0.965 a
FiberMax 832/Tamcot HQ-95	148 bcd	21.781 b	17.550 cd	165 ef	173 gh	5.150 cd	0.955 abcd
Half and Half/Deltapine 90	108 cd	20.891 c	15.800 ef	181 bc	187 bc	4.625 de	0.965 a
Half and Half/Tamcot HQ-95	97 d	19.241 d	15.650 de	185 b	190 b	4.575 e	0.970 a

§ Means with the same letter are not significantly different

Table 42: Narrow-sense heritability (h^2) of fiber traits from HVI and AFIS calculated from diallel analysis of five parents and ten progeny (F1).

HVI	Heritability
Length	0.82
Micronaire	0.71
Strength	0.56
Uniformity Index	0.68
Elongation	0.67

AFIS	Heritability
Neps	0.51
Length (n)	0.66
SFC (n)	0.00
IFC	0.01
Fineness	0.91
Standard Fineness	0.95
Maturity Ratio	0.00

In order to have success in a cotton breeding program it is important to understand gene action and importance of gene effects for the traits under consideration. GCA estimates additive genetic effects. The GCA effects reflect performance of parental lines in combination with all other lines evaluated. Therefore, parents with the highest GCA effects should logically, have the most significant influence on improving a trait.

Traditionally sum of squares have been considered as a measure to estimate variance coming from additive gene effects (Becelaere and Miller, 2004; Braden, 2005; Gardner and Eberhart, 1966). Sum of squares relative to treatment sum of squares give an indication of the proportion of additive gene effects for the particular trait. Mean squares take into account the degrees of freedom of the parameters (sources of variation) thereby standardizing the variance to some extent. When running ANOVA, it is assumed that there is no bias in the experiment, leaving only variance to be accounted for. In any experiment, a researcher would try to optimize the balance between variance and bias. This is possible only when mean squares are taken into consideration not sum of squares. In the diallel presented here, SCA has a higher number of degrees of freedom (df = 9) compared to GCA (df = 4). Therefore, from a statistical point of view, it would make more sense to compare mean squares for inferring the additive gene effects.

In the diallel study conducted here, it was observed that fiber maturity had strong influence of non-additive gene effects. There is approximately 38% variation coming from additive gene effects keeping mean squares in account. This makes improvement from selections challenging for a cotton plant breeder. However, standard fineness, which is estimated as a ratio of AFIS fineness and fiber maturity, had high GCA values. Mean squares accounted for 98.5% variation coming from GCA indicative of the strong additive component associated with this trait. Secondly, narrow-sense heritability data showed that standard fineness was highly heritable (Table 42).

Standard fineness has potential to be a useful tool for cotton plant breeders for improving fiber quality in the future. Standard fineness takes into account fiber maturity

along with fiber fineness, which truly represents fiber diameter (Hequet et al., 2006). The absolute fiber maturity ratio has lower potential and impact for improvement because the trait has relatively low additive genetic effects and lowly heritable; however, problems associated with fiber maturity/immaturity have been well documented (Hosseinali et al., 2012; Hequet and Abidi, 2007; Hequet et al., 2006). Immature fibers result in neps, increased short fiber content from fiber breakage, reduction in mean length thereby reducing uniformity and reduced dye uptake. One approach to improve fiber maturity would be to optimize fiber standard fineness which reduces the volume of the fiber for a given length, thereby making cellulose deposition optimum during fiber development.

The relationship of standard fineness was compared with other important fiber traits such as fiber length, strength, UI and micronaire (HVI) and fiber length (n), SFC (n), IFC and neps. The relationship between HVI length and standard fineness was quite strong with an R square value of 0.55. There was a relationship between UI and standard fineness (R square = 0.637). In general, length parameters (HVI) improved with finer fibers. Coarse fibers were associated with lower lengths. Fiber strength and standard fineness also had a relationship (R square = 0.38) indicative of finer fibers being stronger (Figures 7- 9).

AFIS length (n) had a relationship with standard fineness (R squared = 0.23), but was less so in relation to HVI length (figure 7 and Figure 8). There was a strong relationship between standard fineness and fiber neps (R squared = 0.59) (Figure 12). AFIS data demonstrated finer fibers had a tendency to be longer, with higher immature

fiber content and high amount of neps (Figure 10 and Figure 11). HVI data showed finer fibers were associated with longer, stronger and uniform fibers whereas AFIS can expose problems that arise from the presence of fine fibers which are related to neps, short fibers, and immature fibers. Optimizing fiber standard fineness might enable a cotton plant breeder to achieve a balance between long, strong fibers and reducing the short, immature fibers. Short fiber content had a stronger relationship with fiber maturity ratio compared to standard fineness (Figure 13 and Figure 14). Regression analysis showed immature fibers were associated with high proportions of SFC (n).

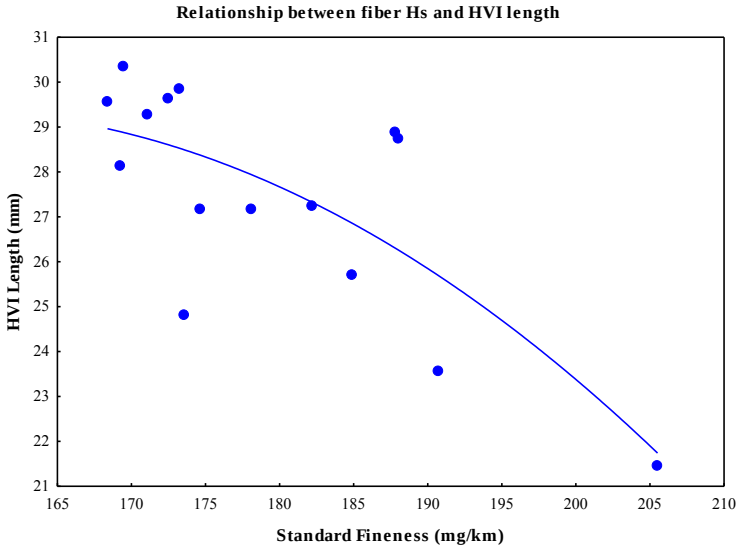

Figure 7: Relationship between standard fineness (mg/kg) (AFIS) and length (HVI). HVI length = -0.0033x2 + 1.0225x - 50.915. R squared = 0.5594.

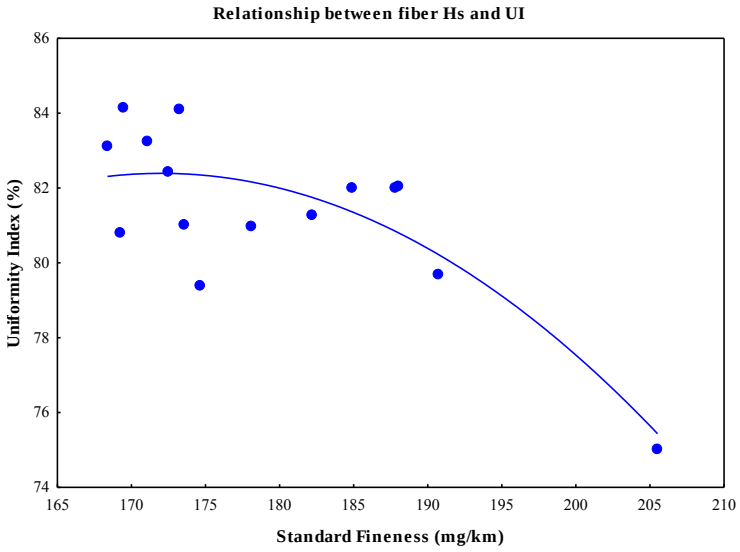

Figure 8: Relationship between standard fineness (mg/kg) (AFIS) and UI (HVI). UI = -0.0062x2 + 2.1331x - 101.07. R squared = 0.6376.

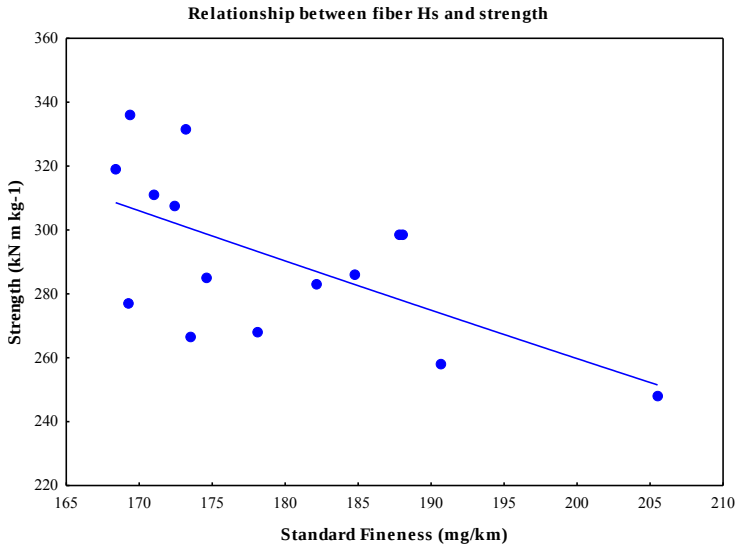

Figure 9: Relationship between fiber standard fineness (mg/km) (AFIS) and strength (kN m kg-1) (HVI). Strength = 0.0013x2 - 2.0398x +613.92. R squared = 0.3796.

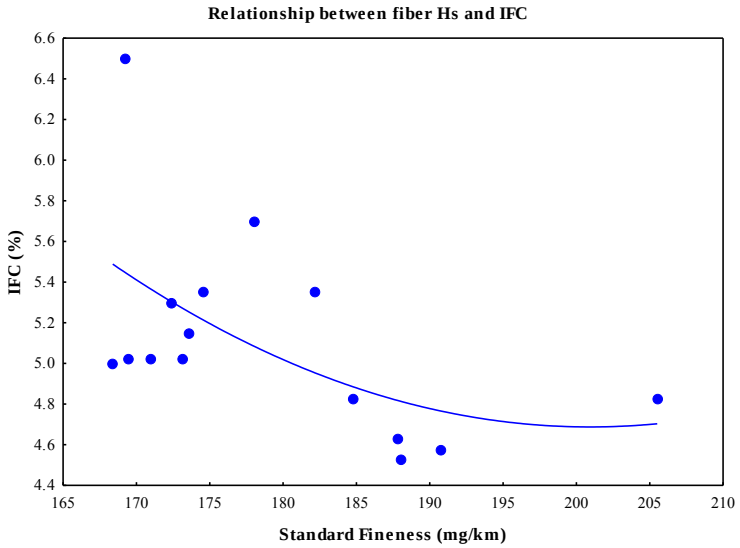

Figure 10: Relationship between standard fineness (mg/kg) (AFIS) and immature fiber content (%) (AFIS). Immature fiber content= 0.0008x2 - 0.3037x + 35.203. R squared = 0.3020.

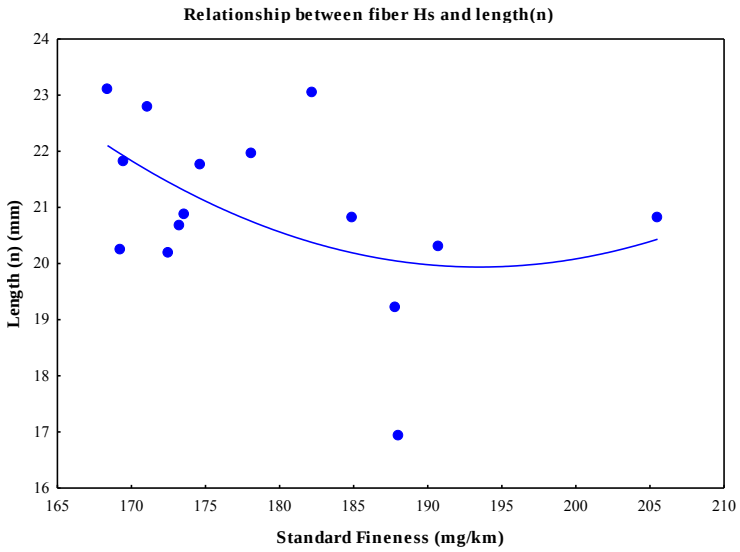

Figure 11: Relationship between standard fineness (mg/kg) (AFIS) and length (n) (%) (AFIS). Length (n) = 0.0034x2 - 1.328x + 148.43. R squared = 0.2314.

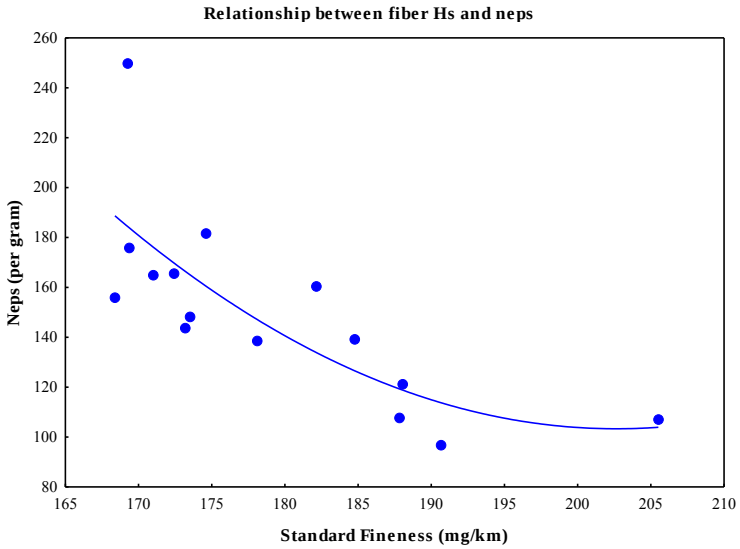

Figure 12: Relationship between standard fineness (mg/kg) (AFIS) and neps (gm-1) (AFIS). Neps = 0.0728x2 - 29.486x + 3090.8. R squared = 0.5889.

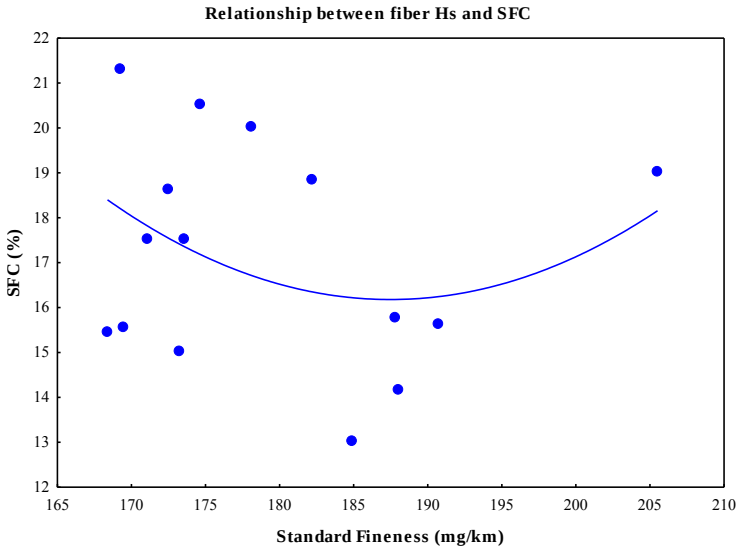

Figure 13: Relationship between standard fineness (mg/kg) (AFIS) and SFC (n) (%) (AFIS). SFC (n) = 0.0061x2 - 2.2817x +230.08. R squared = 0.1139.

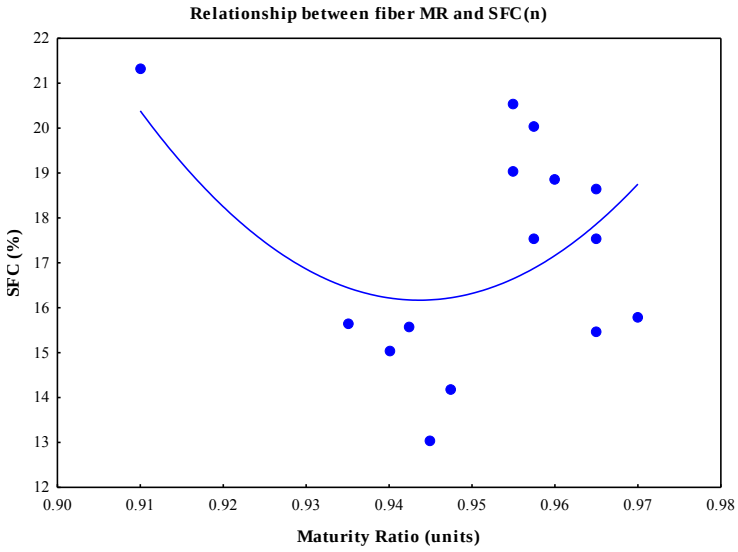

Figure 14: Relationship between fiber maturity ratio (units) (AFIS) and SFC (n) (%) (AFIS). SFC (n) = 3722.8x2 - 7026x + 3331.2. R squared = 0.2242.

Data from the diallel study suggest fiber length is highly heritable (HVI= 0.82 and AFIS length (n) = 0.66). There were high GCA values associated for all length based traits with the exception of short fiber content(n). Of the total F_1 mean squares 45% were attributable to GCA component for SFC (n).

Acala 1517-99 and Tamcot HQ-95 combined well to produce a significant positive SCA effect for HVI measured length (4.470 mm), strength (11.856 kN m kg-1), uniformity index (8.149) and micronaire (0.785 units). The combination also had significant positive SCA effect for AFIS measured length (n) (5.767 mm), fineness (11.662 mg/km) and maturity ratio (0.093 units). It had significant negative effects (desirable) for AFIS measurements of SFC (n) (-12.441 %), neps (-118.025 count gm^{-1}), IFC (-2.720%) and standard fineness (-4.352 mg/km). SCA values account for dominant

gene action effects. It is the deviation of hybrid performance from that expected from the GCA effects of each parent. SCA effects can identify the best hybrid combination, but they can also identify complementary alleles for trait performance (Kearsey and Pooni, 1996). A cotton plant breeder would be interested in lines with good mean performance and significant GCA effects which also have significant (and desirable) SCA effects. Acala 1517-99 was for the most part an excellent general combiner for all fiber traits with the exception of fiber neps. Tamcot HQ-95 was a good general combiner for some traits having non- significant, non-desirable GCA effects. This combination can be beneficial to the cotton plant breeder for improvement. Fiber length (n) (AFIS) and length (HVI) for the Acala 1517-99/Tamcot HQ-95exceeded the mean fiber length (n) of both parents. Fiber UI and strength of Acala 1517-99/Tamcot HQ-95 were significantly higher than values of both parents while SFC (n) and IFC were significantly less than the parents. HVI detected a positive fiber micronaire SCA effect while AFIS detected no SCA effects for any entry for fineness or standard fineness. However, Acala 1517-99/Tamcot HQ-95 had a significant maturity ratio SCA effect.

AFIS fiber length (n) SCA effects were more sensitive compared to the length measurements from HVI. AFIS additionally identified SCA effects for the entries Acala 1517-99/Deltapine 90 (0.619 mm), Deltapine 90/Tamcot HQ-95(-0.886 mm) and FiberMax 832/Tamcot HQ-95 (-0.578 mm). It was interesting to note that the cross between Deltapine 90 and Tamcot HQ-95 had an SCA value of -0.886 mm (AFIS) length (n) while HVI showed a positive SCA effect of 0.101 mm. While most GCA

effects were overestimated by HVI length measurements compared to AFIS length (n) measurements, SCA effects were underestimated by HVI measurements.

Choice of instrument for fiber testing, which can maximize accuracy and genetic gain to make improvements, will enable a breeder to make correct decisions on parental choices and to make selections in a breeding program. Increasing fiber maturity by optimizing standard fineness in well adapted cotton cultivars in Texas may prove to be beneficial especially to address problems associated with fiber maturity. This study shows significant variation in fiber standard fineness among four parents and significant variation in fiber maturity among two parents within the diallel that can be utilized for improvement in the cotton industry.

CHAPTER VII

SUMMARY AND CONCLUSIONS

Fiber quality variability was investigated across sympodial branches within a plant for four diverse genotypes in two locations. It was revealed that fiber quality deteriorates towards the upper half sympodial branches of the plants. Most fiber traits have excellent fiber quality at the bottom half of the plant relative to the top. However trash content increases at the bottom sympodial branches and is significantly lower in the upper branches. Results suggest that while variability of fiber quality persists within a plant across genotypes, the degree of variability is genotype specific. Some genotypes decline in quality quicker compared to others. Breeding efforts may be employed to reduce the degree of fiber quality variability by slowing the decline as much as possible. One method would involve sampling bolls from the first five sympodial branches and comparing against bolls from the top five sympodial branches.

FiberMax 832 displayed the best fiber quality among all four genotypes. However, it was also the genotype with consistent variability within the plant across years. Acala 1517-99 had the finest fiber while Half and Half had the coarsest fiber among all genotypes tested. Both these genotypes displayed lower degree of variability within the plants for all three years in College Station, Texas. A potential cause of this variability is the source-sink relationship. Sources are the plant parts where net fixation of carbon dioxide occurs and sinks are sites where photosythate energy is stored/used. Given the boll load at the bottom of the plant, the upper bolls on the sympodial branches

remain under-assimilated. Sung (1978) showed that leaves in the upper canopy of the plants allocated the greatest portion of assimilate to the vegetation below the treated leaf while the leaves in the lower canopy directed 50% of assimilate lower than the treated leaf. Subtending leaves direct photosynthate towards the attached boll. The basis of source-sink depends on the genetics of the plants, which has scope for improvement.

Because of within-plant variability in cotton fiber quality, boll sampling techniques were evaluated to ascertain techniques to accurately measure fiber quality. Ten sampling techniques for boll samples were evaluated. Random and biased picked samples were used in number of 15, 25 and 50 bolls. Results showed randomly harvested boll samples with high number of bolls (50 bolls) worked well to accurately determine cotton fiber quality. Cotton plant breeders can make educated, unbiased decisions for selection purposes in their program when a reliable estimate of fiber quality is available to them. If AFIS testing is available and economically feasible, a breeder should examine the different length and maturity parameters. When dealing with fiber length, it is best to consider fiber length by number measurement given by the AFIS because of the precision in estimating overall mean and SFC of the samples tested. Fiber lint percent, measurement was unpredictable across years. Trash content was highest in machine picked samples. Therefore to measure yield characteristics and trash content measurements, the best approach may be to ascertain a grab sample coming from a full row/plot harvest using a mechanical cotton harvester.

Diallel analysis showed standard fineness calculated from AFIS output has potential to be a useful tool for cotton plant breeders for improving fiber quality in the

future. Standard fineness takes into account fiber maturity along with fiber fineness, which truly represents fiber diameter (Hequet et al., 2006). The absolute fiber maturity ratio has lower potential and impact for improvement because the trait has relatively low additive genetic effects and is lowly heritable. HVI offers micronaire measurements which is a complex of fineness and maturity. Comparison was made between HVI micronaire and AFIS fineness and maturity measurements for this diallel study. According to HVI data, Acala 1517-99 and Half and Half had positive GCA estimates to increase micronaire while FiberMax 832 had a negative GCA estimates to decrease micronaire. Deltapine 90 and Tamcot HQ-95 remained non-significant. AFIS standard fineness data showed Acala 1517-99, Tamcot HQ-95 and FiberMax 832 had negative GCA effects (desirable) while Half and Half had positive GCA effects. Based on that comparison alone, it can be concluded that HVI micronaire is not sensitive to detecting fineness/maturity traits compared to AFIS. Increasing micronaire is not generally considered as an 'improvement' for cotton plant breeders unless dealing with highly immature fibers. Based on HVI data, one might underestimate the usefulness of Acala 1517-99 in a breeding program. Secondly, Tamcot HQ-95 was not significant for GCA when estimated with HVI. However, AFIS detected significant GCA estimates for fiber standard fineness and maturity ratio. In that context, the cross between Acala 1517-99 and Tamcot HQ-95 was the best performer in the diallel conducted. Deltapine 90 showed a positive GCA estimate for HVI length and elongation. While that information might lead a breeder to believe it was a useful combiner, AFIS revealed that Deltapine

90 also had positive GCA effects for SFC (n) and IFC (not desirable) and negative GCA estimates for fiber maturity ratio.

Overall the diallel conducted here showed Acala 1517-99, FiberMax 832 and Tamcot HQ-95 to be the best combiners for improving standard fineness while Half and Half was the best general combiner for increasing standard fineness.

Standard fineness also relates well with other pertinent fiber traits. Improving fiber quality can be addressed with a new perspective by employing AFIS standard fineness as a trait for parental selection.

REFERENCES

Abbott, A.M., G.J. Higgerson, R.L. Long, S.R. Lucas, G.R.S. Naylor, C.R. Tischler and M.M. Purmalis. 2010. An instrument for determining the average fiber linear density (fineness) of cotton lint samples. Textile Research Journal, 80 (9): 822-833.

Acquaah, G.2007. Principles of Plant Genetics and Breeding, Wiley, New York.

Al-Rawi, K.M., and R.J. Kohel. 1969. Diallel analyses of yield and other agronomic characters in Gossypium hirsutum L. Crop Science 9:779–78.

Allard, R. W.1999. Principles of Plant Breeding. Wiley, New York.

American Society for Testing and Materials (ASTM). 1994. Standard test methods for length and length distribution of cotton fibers (array method) (D 1440-90). p. 377-382. *In* Annual Book of ASTM Standards. Vol. 07.01. ASTM, Philadelphia, PA.

Anthony, W.S. 1999. Postharvest management of fiber quality. p. 293-337. *In* A.S. Basra (ed.) Cotton fibers, developmental biology, quality improvement, and textile processing. Food Products Press, New York.

Auld, D.L., Efrem Bechere, M.D. Ethridge, W.D. Becker, E. Hequet and R.G. Cantrell. 2000. Registration of TTU 202-1107B and TTU 271-2155C mutant germplasm lines of upland cotton with improved fiber quality. Crop Science, 40:1835-1836.

Backe E. 1986. Effect of short fiber content in cotton on plant performance and quality. Textile Research Journal, 56(2) 112–115.

Basra, A. 1999.Cotton Fibers: Developmental Biology, Quality Improvement, and Textile Processing. Binghamton, NY: Food Products Press.

Basra, A. S. and C. P.Malik. 1984. Development of the Cotton Fiber. International Review of Cytology, 89:65-113.

Becelaere G and J. Miller. 2004. Methods of inoculation of sunflower heads with Sclerotinia sclerotiorum. Crop Science 44: 1542-1545.

Bednarz C., R. Nichols, and S. Brown. 2006. Plant density modifies within-canopy cotton fiber quality. Crop Science, 46: 950–956.

Bednarz, C., C.Bridges, and S.Brown. 2000. Analysis of cotton yield stability across population densities. Agronomy Journal 92:128-135.

Behery, H. 1993. Short fiber content and uniformity index in cotton. International Cotton Advisory Committee Rev. Article 4, CABI International, Wallingford, UK.

Berger, G., S. Hague, C.W.Smith. 2012. Diallel analysis of fiber traits for extra-long staple cotton progeny. Crop Science Vol. 52:2 683-689.

Blenda, A., J. Scheffler, B. Scheffler, M. Palmer, M. Lacape, J. Yu, C. Jesudurai, S. Jung, S. Muthukumar, P. Yellambalase, S. Ficklin, M. Staton, R. Eshelman, M. Ulloa, S. Sahas, B. Burr, S. Liu, T. Zhang, D. Fang, A. Pepper, S. Kumpatla, J. Jacobs, J. Tomkins, R. Cantrell and D. Main. 2006. CMD: A cotton microsatellite database resource for *Gossypium* genomics. BMC Genomics 7.

Bowman, D.T. 2000. Attributes of public and private cotton breeding programs. J. Cotton Sci. 4:130-135 [Online]. Available at http://www.jcotsci.org/2000/issue02/article09.pdf

Bowman, D.T., O.L. May, and D.S. Calhoun. 1997. Coefficients of parentage for 260 cotton cultivars released between 1970 and 1990. U.S. Government Printing Office, Washington, DC.

Boyd, M.L., B.J.Phillips, and J.A. Wrather. 2004. Cotton pests scouting and management.Missouri State Extension. Available online: http://ipm.missouri.edu/ipm_pubs/ipm1025.pdf

Braden, C. 2005. Inheritance of cotton fiber length and distribution. Ph.D. dissertation, Texas A&M University, College Station, Texas.

Bradow, J. and G. Davidonis. 2000. Quantitation of fiber quality and the cotton production-processing interface: A physiologist.s perspective. Journal of Cotton Science 4: 34-64.

Bradow, J. and G. Davidonis, 2010. Effects of Environment on Fiber Quality. Physiology of Cotton. Chapter 21: 229-245.

Bradow, J.M., G.F. Sassenrath-Cole, O. Hinojosa, and L.H. Wartelle. 1996. Cotton fiber physical and physiological maturity variation in response to genotype and environment. p. 1251–1254. Proceedings of the Beltwide Cotton Conferences, Nashville, TN. 9–12 Jan. 1996. *In* Bradow J. and G. Davidonis.2000. Quantitation of Fiber Quality and the Cotton Production-Processing Interface: A Physiologist's Perspective. Journal of Cotton Science, 4:34-64.

Bragg, C., and Shofner, F. 1993. A rapid, direct measurement of short fiber content. Textile Research Journal, 63:171-176.

Bridge, R.R., and W.R. Meredith, Jr. 1983. Comparative performance of obsolete and current cotton cultivars. Crop Science 23:949–952.

Brown, H. B. 1936. Cotton varieties recognized as standard commercial varieties. Journal of American Society of Agronomy 28(1):69.

Brown, J., and Peter D. S. Caligari. 2008. An Introduction to Plant Breeding.Blackwell Publications.

Brubaker, C. L., F. M. Bourland and J. F. Wendel.1999a. The origin and domestication of cotton. *In* "Cotton: Origin, History, Technology and Production" (C. W. Smith and J. T. Cothren, Eds.), pp. 3–31. Wiley, New York.

Brubaker, C. L., A. H. Paterson, and J. F. Wendel. 1999b. Comparative genetic mapping of allotetraploid cotton and its diploid progenitors. Genome 42, 184 –203. *In* "Cotton: Origin, History, Technology and Production" (C. W. Smith and J. T. Cothren, Eds.), pp. 3–31. Wiley, New York.

Cai, Y, X. Cui. J. Rodgers, D. Thibodeaux, V. Martin, M. Watson and S. Pang. 2010. An investigation on different parameters used for characterizing short cotton fibers. Textile Research Journal, 81 (3) 239–246.

Cantrell, R.G., C.L. Roberts, and C. Waddell. 2000. Registration of 'Acala 1517-99' cotton. Crop Science 40:1200-1201.

Constable, G.A., P.E. Ried, and N.J. Thomson. 2001. Approaches utilized in breeding and development of cotton cultivars in Australia. p. 1-16. *In* J.N. Jenkins and S. Saha (ed.) Genetic improvement of cotton: Emerging technologies. Science Publ. Inc., Enfield, NH.

Cotton Incorporated. 2012. US and Global Market Fundamentals. Available online: http://www.cottoninc.com/corporate/Market Data/MonthlyEconomicLetter/.

Clouvel P et al. Variability of Cotton Fiber Quality. *In*: 2nd world cotton research conference – new frontiers in cotton. *In* Krifa, M. Fiber length distribution variability in cotton bale classification: Interactions among length, maturity and fineness. Textile Research Journal, March 7, 2012.

Cranmer, L.M. 2004. A better understanding of the number of fibers per seed in cotton. Master's Thesis, Texas Tech University, Lubbock, TX.

Davidonis, G., Johnson, A., Landivar, J., Fernandez, J. 2004. Cotton fiber quality is related to boll location and planting date. Agronomy Journal, 96: 42-27.

Davidonis G, A. Johnson, J. Landivar and K.Hood. 1999. The cotton fiber property variability continuum from motes through seeds. Textile Research Journal, 69(10): 754–759.

Davidonis, G., Landivar, J., Fernandez, C. 2003. Growth environment alters fiber properties, motes, neps and white speck frequency. Textile Research Journal, 73:960-964.

El Mogahzy, Y. and Chewning, C. 2001. Cotton fiber to yarn manufacturing technology.

El-Zik, K.M. and P. M.Thaxton.1990. Registration of "TAMCOT HQ 95" cotton. Crop Science, 30:1359-1360.

Elms, M., C. Green and P. Johnson.2001. Variability of Cotton Yield and Quality. Communications in Soil Science and Plant Analyses, 32: 351–368.

Ethridge, D. and Simonton, J. 2004. Renewed focus on neps. Textile Topics, 2004-2: 2-7.

Falconer, D.S., and T.F.C. Mackay. 1996. Introduction to quantitative genetics. 4th ed. Longman Group Limited, Harlow, Essex, U.K.

Faulkner, B. 2008. Comparison of picker and stripper harvesters on irrigated cotton on the High Plains of Texas. Ph.D. Dissertation, Texas A&M University, College Station, TX.

Fehr, W.R. 1993. Principles of cultivar development. Vol. 1. Theory and technique. Macmillan Publishing, New York.

Fry, K. E. and Butler, G. O. 1982. Heat-unit calculations in cotton crop and insect models. A comparison of Algorithmic. Proc. Beltwide Cotton Prod. Res. Conference 54-55.

Garcia, A.A.F., L.L. Benchimol, A.M.M. Barbosa, I.O. Geraldi, C.L. Souza and A.P. de Souza. 2004. Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines. Genetics and Molecular Biology. 27:579-588.

Gardner, C. and S. Eberhart. 1966. Analysis and interpretation of the variety cross diallel and related populations. International Biometric Society. 22: 439-452.

Ghorashi, H.M., J.C. Baldwin, and M.A. Khan. 1994. AFIS advancement in neps and length measurements. p. 1433-1436. *In* D.J. Herber and D.A. Richter (ed.) Proc. Beltwide Cotton Conferences San Diego, CA. 5-8 Jan. 1994. National Cotton Council, Memphis, TN.

Gipson, J.R., and H.E. Joham. 1968. Influence of night temperature on growth and development of cotton (Gossypium hirsutum L.) II. Fiber properties. Agronomy Journal, 60:296–298.

Gipson, J.R., and H.E. Joham. 1969. Influence of night temperature on growth and development of cotton (Gossypium hirsutum L.) III. Fiber elongation. Crop Science, 9:127–129.

Gipson, J.R., and L.L. Ray. 1970. Temperature-variety interrelationships in cotton. I. Boll and fiber development. Cotton Growers Rev. 47:257–271.*In* Bradow J. and G. Davidonis.2000. Quantitation of Fiber Quality and the Cotton Production-Processing Interface: A Physiologist's Perspective. Journal of Cotton Science, 4:34-64.

Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. Australian Journal of Biological Science 9:463-493.

Grimes, D.W., and H. Yamada. 1982. Relation of cotton growth and yield to minimum leaf water potential. Crop Science, 22:134–139.

Hague, S, J.R. Gannaway, and R.K. Boman. 2008. Combining ability of upland cotton with traits associated with sticky fiber. Euphytica 164(1):75-79.

Haigler, C.H., B. Singh, G. Wang, D. Zhang. 2009. Genomics of cotton fiber secondary wall deposition and cellulose biogenesis. Plant Genetics and Genomics: Crops and Models 3:385-417.

Hanson, R.G., E.C. Ewing, and E.C. Ewing Jr. 1956. Effect of environmental factors on fiber properties and yield of Deltapine cottons. Agronomy Journal , 48:546–581.

Hayman, B.I. 1954. The theory and analysis of diallel crosses. Genetics 39: 789-809.

Hayman, B.I. 1960. The theory and analysis of diallel crosses III. Genetics 45: 155-172.

Hearn, A.B. 1976. Response of cotton to nitrogen and water in a tropical environment. III. Fiber quality. Journal of Agricultural Science (Camb.) 84:257–269. *In* Bradow J. and G. Davidonis.2000. Quantitation of Fiber Quality and the Cotton Production-Processing Interface: A Physiologist's Perspective. Journal of Cotton Science, 4:34-64.

Hearn, A.B. 1994. The principles of cotton water relations and their application in management. p. 66–92. *In* Bradow J. and G. Davidonis.2000. Quantitation of Fiber Quality and the Cotton Production-Processing Interface: A Physiologist's Perspective. Journal of Cotton Science, 4:34-64.

Hessler, L.E., H.C. Lane, and A.Y. Young. 1959. Cotton fiber development studies at suboptimum temperatures. Agronomy Journal, 51:125–128.

Hebert, D., D. Horton, P. Phipps, G. White, M. Roberts and H. Wilson.2009. Virginia cotton production guide. Available online: http://pubs.ext.vt.edu/424/424-300-09/424-300-09_pdf.pdf.

Hequet, E. and N.Abidi.2007.Importance of sample preparation in AFIS testing. Proc.Beltwide Cotton Conferences, New Orleans, Lousiana.1207.

Hequet, E. and N.Abidi.2010. Relationships between fiber length distributions and fiber maturity. Proc. of the Beltwide Cotton Conferences, New Orleans, Louisiana, 1430.

Hequet, E., B. Wyatt, N. Abidi, and D. Thibodeaux. 2006. Creation of a set of reference material for cotton fiber maturity measurements. Textile Research Journal, 76(7): 576-586.

Hequet, E. and Ethridge, D. 2000. Impacts on yarn quality of AFIS measurements of cotton fiber length distributions. Textile Topics Winter 2000:2-12.

Hinohosa, O., and D. Thibodeaux.1994. Applications of AFIS to measuring quality characteristics of cotton. Proc. Beltwide Cotton Conferences, San Diego, 1491.

Hsieh, Y-L., Hu, X-P. and Wang, A. 2000. Single fiber strength variations of developing cotton fibers-strength and structure of *G.hirsutum* and *G.Barbedense* Textile Research Journal 70(8): 682-690.

ICAC, 2004. Quality requirements on export markets for US cotton. Available online at http://www.icac.org/icac/cotton_info/speeches/estur/2004/quality_reqs_us_exp.pdf.

Jasdanwala, R.T., Y.D.Singh, and J.J. Chinoy. 1977. Auxin metabolism in developing cotton hairs. Journal of Experimental Botany. 28:1111-1116.

Jenkins J.N., J.C. McCarty, and W.L. Parrott. 1990. Fruiting efficiency in cotton: Boll size and boll set percentage. Crop Science 30:857-860.

Jensen N.F. 1988. Plant Breeding Methodology. Wiley, New York.

Johnson, R.M., G.F. Sassenrath-Cole, and J.M. Bradow. 1997. Prediction of cotton fiber maturity from environmental parameters. p. 1454–1455. Proceedings of the Beltwide Cotton Conferences, New Orleans, LA. 7–10 Jan. 1997.

Johnson, R., Downer, R., Bradow, J., Bauer, P., Sadler, E. 2002. Variability in cotton fiber yield, fiber quality, and soil properties in a southeastern coastal plain. Agronomy Journal 94:1305-1316.

Johnson R., J. Bradow, P. Bauer, and E.Sadler. 1999.Spatial variability of cotton fiber yield and quality in relation to soil variability. Proc. Of the Fourth International Conference on Precision Agriculture. Available online: http://ddr.nal.usda.gov/bitstream/10113/37420/1/IND44308590.pdf.

Jones M.A. and, R.Wells.1997. Dry matter allocation and fruiting patterns of cotton grown at two divergent plant populations. Crop Science 37:797-802.

Joy, K., C.W. Smith, E. Hequet, S. Hague, P.S. Thaxton, and C. Souder. 2010. Fiber properties and mini-spun yarn performance of extra-long staple upland cotton. J. Cotton Sci. 14:82–90.

Kearsey, M.J., and H.S. Pooni. 1996. The genetical analysis of quantitative traits. Chapman and Hall, London, U.K.

Kelly, C. 2008. Improving cotton (*Gossypium hirsutum* L.) for fiber and yarn quality. Ph.D. dissertation. Texas Tech University, Lubbock, Texas.

Kothari N., N. Abidi, E. Hequet. 2008. Multi-disciplinary approach to study cotton fiber quality variability within a plant. Proc. Beltwide Cotton Conferences, National Cotton Council, January 8-11, Nashville, TN.

Krifa, M. 2006. Fiber Length Distribution in Cotton Processing: Dominant Features and Interaction Effects. Textile Research Journal. Vol 76(5): 426–435.

Kerby, T.A. and, K.D., Hake. 1996. Monitoring cotton's growth. *In* Hake-Johnson, S., T.A. Kerby, and K.D. Hake (eds) Cotton Production Manual. University of California Division of Agriculture and Natural Resources, Publication No. 3352.

Kohel, R., D. Stelly, and J. Yu. 2002. Tests of six cotton mutants for association with aneuploids. The American Genetic Association 93: 130-132.

Kohel., R. and S. McMichael. 1990. Immature fiber mutant of upland cotton. Crop Science, 30:419-421.

Kohel, R., T. Richmond, and C. Lewis. 1970. Description of a Genetic Standard for *Gossypium hirsutum* L. Crop Science, 10:670-674.

Lacape, J.M., D. Dessauw, M. Rajab, J.L. Noyer and B. Hau. 2007. Microsatellite diversity in tetraploid Gossypium germplasm: Assembling a highly informative genotyping set of cotton SSRs. Molecular Breeding. 19:45-58.

Lacape, J.M., T.B. Nguyen, S. Thibivilliers, B. Bojinov, B. Courtois, R.G. Cantrell, B. Burr and B. Hau. 2003. A combined RFLP-SSR-AFLP map of tetraploid cotton based on a Gossypium hirsutum x Gossypium barbadense backcross population. Genome 46:612-626.

Lin, Z., Y. Wang, X. Zhang and J. Zhang. 2012. Functional markers for cellulose synthase and their comparison to SSRs in cotton. Plant Molecular Biology Reporter. Available online: http://www.springerlink.com/content/c24617712q801842/.

Liu, Y., D. Thibodeaux, and G. Gamble. 2011. Development of Fourier transform infrared spectroscopy in direct, non-destructive, and rapid determination of cotton fiber maturity. Textile Research Journal, 81 (15) 1559-1567.

Lord, E. 1981. The origin and assessment of cotton fiber maturity. Textile Research Division, International Institute for Cotton.

Lowery C.C., D. L. Auld, E. Bechere, R.J. Wright, E. Hequet, N. Abidi, C.W. Smith. 2007. Use of Chemical Mutagenesis in Improving Upland Cotton. World Cotton Research Conference-4, Sept. 10-14, 2007, Lubbock, TX, USA.

MacAlister III, D., Rogers, C. 2005. The effect of harvesting procedures on fiber and yarn quality on ultra-narrow-row cotton. Journal of Cotton Science 9:15-23.

Manandhar, R., Hequet, E., Abidi, N., Kelly, B. and Paudel, D., 2012. Within Sample Variability of Fiber Quality Measurements. Proc. Beltwide Cotton Conf. Orlando, FL 3-6Jan. 2012. National Cotton Council, Memphis, TN.

Mangialardi, G. J. 1987. Influence of Growth period of Neps in Cotton. Textile Research Journal, 57: 421-427.

Marani, A., and A. Amirav. 1971. Effects of soil moisture stress on two varieties of upland cotton in Israel. I. *In* Bradow J. and G. Davidonis.2000. Quantitation of Fiber Quality and the Cotton Production-Processing Interface: A Physiologist's Perspective. Journal of Cotton Science, 4:34-64.

Matic-Leigh, R. and D. Cauthen. 1994. Determining Cotton Fiber Maturity by Image Analysis. Textile Research Journal, 64: 534-544.

May, O.L., and G.M. Jividen. 1999. Genetic modification of cotton fiber properties as measured by single- and high- volume instruments. Crop Science. 39:328–333.

May, O.L., and R.A. Taylor. 1998. Breeding cotton with higher yarn tenacity. Textile Research Journal 68:302–307.

Meredith, W.R., Jr. 1992. Improving fiber strength through genetics and breeding. p. 289–302. In C.R. Benedict and G.M. Jividen (ed.) Cotton Fiber Cellulose: Structures, Functions, and Utilization Conference. 1992. Natl. Cotton Council, Memphis, TN.

Meredith, W.R., Jr. 1991. Contributions of introductions to cotton improvement. p.127-146. *In* H.L. Shands and L.E. Weisner (ed.) Use of plant introductions in cultivar improvement. Part 1. CSSA, Madison, WI.

Meredith, W.R., Jr. 2003. Thirty-six years of regional high quality variety test. p. 2561-2566. *In* P. Dugger and D. Richter (ed.) Proc. Beltwide Cotton Conference Nashville, TN. 7-11 Jan. 2003. Natl. Cotton Council, Memphis, TN.

Morton, W., Hearle, J.W.S. 1997. Textile Institute, Physical Properties of Textile Fibers.

Murray, J.C., and Verhalen, L.M.1970. Genetics of early yield and fiber properties in cotton (Gossypium hirsutum L.). Crop Science., 9: 752-799.

Myers, G. and F. Bordelon, 1995. Inheritance of yield components using variety trial data. *In* Proceedings of Beltwide Cotton Conferences, Memphis, TN.

Naithani, S.C., N.R. Rao, and Y.D. Singh. 1982. Physiological and biochemical changes associated with cotton fiber development. Physiologia Plantarum, 54:225-229.

Percy, R., J. Yu, D. Fang, R. Kohel, M.Ulloa, l. Hinze, J. Zhang, P.Chee, B. Scheffler and D.Jones. 2012 (in print). Development of a core set of SSR markers for the characterization of Gossypium germplasm. Euphytica.

Pearl, H.M., C. Nagai, P.H. Moore, D.L. Steiger, R.V. Osgood and R. Ming. 2004. Construction of a genetic map for arabica coffee. Theoretical and Applied Genetics. 108:829-835.

Pearson, N.L. 1949. Neps in cotton yarns as related to variety, location and season of growth. USDA Technical Bulletin. 878.

Percy, R. G., and, J. F. Wendel.1990. Allozyme evidence for the origin and diversification of Gossypium barbadense L. Theor. Appl. Genet. 79, 529 –542. *In* "Polyploidy and the Evolutionary History of Cotton" (J. F. Wendell and R. C. Cronn, Eds.), Advances in Agronomy 8:139–186.

Poehlman, J.M. 2006. Breeding Field Crops. 5th ed. Wiley-Blackwell Publishing.

Quisenberry, J.E., and R.J. Kohel. 1975. Growth and development of fiber and seed in upland cotton. Crop Science, 15:463–467.

Rana, M.K., V.P. Singh and K.V. Bhat. 2005. Assessment of genetic diversity in upland cotton (Gossypium hirsutum L.) breeding lines by using amplified fragment length polymorphism (AFLP) markers and morphological characteristics. Genetic Resources and Crop Evolution. 52:989-997.

Reddy, V.R., D.N. Baker, and H.F. Hodges. 1990. Temperature and mepiquat effects on cotton canopy architecture. Agronomy Journal, 82:190–195.

Robert, K., Price, J. and Cui, X. 2000. Cotton cleanability: Part II. Effect of simple random breakage on fiber length distribution. Textile Research Journal, 70:108-115.

Rodgers, C. 1997. Influence of ginning on spinning performance and yarn quality. *In* P. Dugger and D. Ritcher (ed.) Proc. Beltwide Cotton Conf. New Orleans, LA 6-10Jan. 1997. National Cotton Council, Memphis, TN.

Rodgers, J., C.Delhom, C. Fortier, and D. Thibodeaux. 2012. Rapid measurement of cotton fiber maturity and fineness by image analysis microscopy using the Cottonscope®. Textile Research Journal. 82 (3): 259-271.

Rungis, D., D. Llewellyn, E.S. Dennis and B.R. Lyon. 2005. Simple sequence repeat (SSR) markers reveal low levels of polymorphism between cotton (Gossypium hirsutum L.) cultivars. Australian Journal of Agricultural Research 56:301-307.

Ribaut, J. and D. Hoisington. 1998. Marker-assisted selection: New tools and strategies. Trends in Plant Science 3:236-239.

Saha, S., D. Agrawal, J. Jenkins, A.Zipf and, O.May. 1998. DNA fingerprinting in cotton using SSR primers from diverse plant species. Journal of Cotton Science. Available online: http://www.ars.usda.gov/research/publications/publications.htm?SEQ_NO_115=94005.

SAS Institute. 2012. SAS/STAT guide for personal computer. Version 9. 3rd ed. SAS Institute. Cary, NC.

Smith., C.W. and, J.T. Cothren. 1995. Cotton:Origin, History, Technology and Production. Chapter . Wiley, New York.

Steadman, R.1997. Cotton testing. Textile Progress. The Textile Institute, Manchester, UK.

Sung, F.J.M. 1978. Source-sink relationships of sorghum and cotton as effected by water stress, Ph.D. dissertation. Texas Tech University, Lubbock, Texas.

Toews, M., P. Roberts, and E. Medrano. 2010. Inter-relationships among stink bug management, cotton fiber quality and boll rot. Proceedings of the Beltwide Cotton Conferences, January 4-7, 2010, New Orleans, Louisiana.

Thibodeaux, D. and Rajasekaran, K. 1999. Development of new reference standards for cotton fiber maturity. The Journal of Cotton Science, 3:188-193.

Ulloa, M. 2006. Heritability and correlations of agronomic and fiber traits in an okra-leaf upland cotton population. Crop Science. 46:1508-1514.

USDA, 2012. Available online: http://www.ams.usda.gov/AMSv1.0/getfile?dDocName=STELDEV3099536.

Wang, Y., H. Shu, B. Chen, M. Mc.Giffen, W. Zhang, N.Xu and Z. Zhou. 2009. The rate of cellulose increase is highly related to cotton fiber strength and is significantly determined by its genetic background and boll period temperature. Plant Growth regulation 57: 203-209.

Wakelyn, P.J., A.D. French, N.R. Bertoniere, D.P. Thibodeaux, B.A.Triplett .2007. Cotton fiber chemistry and technology. Boca Raton, Florida: CRC Press.

Ware, J.1936. Plant breeding and the cotton industry. *In* "Cotton: Origin, History, Technology and Production" (C. W. Smith and J. T. Cothren, Eds.). Wiley, New York.

Ware, J.O. 1950. Origin, rise, and development of American upland cotton varieties and their status at present. Mimeo Publ. Univ. of Arkansas, College of Agric., Agriculture Experiment Station. Fayetteville, AR.*In* "Attributes of Public and Private Cotton Breeding Programs" (D.Bowman,2000) The Journal of Cotton Science 4:130-136.

Wartelle, L., J. Bardo, O. Hinojosa, and A. Pepperman. 1995. Quantitative cotton fiber maturity measurements by x-ray fluorescence spectroscopy and advanced fiber information system. Journal of Agriculture and Food Chemistry, 43: 1219-1223.

Wendel, J.F. 1989. New World Tetraploid Cottons Contain Old-World Cytoplasm. Proc National Academy of Science USA 86: 4132-4136.

Wendel, J. F., P. D.Olsen, and J. M.,Stewart.1989. Genetic diversity, introgression and independent domestication of Old World cultivated cottons. American Journal of Botany. 76: 1795–1806.

Wendel, J. F., C. L., Brubaker, and A. E., Percival. 1992.. Genetic diversity in Gossypium hirsutum and the origin of Upland cotton. American Journal of Botany. 79: 1291–1310.

Wilkins, T.A., Jernstedt, J.A. 1999. Molecular genetics of developing cotton fibers, Cotton Fibers. Developmental Biology, Quality Improvement, and Textile Processing. Chapter 9:231-269.

Xiao, J., K.Wu, D. Fang, D. Stelly, J. Yu, and R. Cantrell. 2009. New SSR Markers for Use in Cotton (*Gossypium* spp.*)* Improvement. The Journal of Cotton Science 13:75–157.

Xu, B. and Y. Huang. 2004. Image analysis for Cotton Fibers Part II: Cross-Sectional Measurements. Textile Research Journal, 74 (5): 409-416.

Zhang, J. and J.M. Stewart. 2000. Economical and rapid method for extracting cotton genomic DNA. Journal of Cotton Science 4:3:193-201.

Zhang, Y., M. Kang, and K. Lamkey. 2005. DIALLEL-SAS05: A comprehensive program for Griffing.s and Gardner-Eberhart analyses. Agronomy Journal, 97:1097-1106.

Zhang, T, Y. Yaun, J. Yu, W. Guo and R.Kohel. 2003. Molecular tagging of a major QTL for fiber strength in Upland cotton and its marker-assisted selection. Tag Theoretical and Applied Genetics, 106(2):262-268.

Zhang, J., Y.Lu, R. Cantrell and E. Hugs. 2004. Molecular marker diversity and field performance in commercial cotton cultivars evaluated in the Southwestern USA. Crop Science,45 (4) 1483-1490.

APPENDIX A

Table A. 1: ANOVA for fiber nepsize, neps, length (w), UQL (w), SFC (w), length (n), SFC (n), trash, fineness, IFC and MR (AFIS) in 2009, 2010 and 2011 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half in College Station, Texas.

		Mean Squares										
Source of variation	**Df**	**Nepsize**	**Neps**	**Length (w)**	**UQL (w)**	**SFC (w)**	**Length (n)**	**SFC (n)**	**Trash**	**Fineness**	**IFC**	**MR**
rep	2	7	9381	0.005	0.001	18*	0.015*	128**	93693	365*	7.343**	0.004**
years	2	16699**	295084**	0.019**	0.065**	124**	0.032**	1767**	21442312**	2967**	61.703**	0.059**
genotype	3	1729	171086**	2.537**	4.313**	539**	1.264**	156**	9110177**	24312**	25.344**	0.046**
rep*years	4	767	6297	0.007*	0.002	21**	0.016**	109**	68516	321**	6.317**	0.004**
genotype*years	6	2963	19596	0.039**	0.038**	55**	0.044**	165**	3721628**	1286**	17.075**	0.024**
error	412	1760	9516	0.002	0.002	5	0.003	24	137954	92	1.122	0.000

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

Table A. 2: ANOVA for fiber length (w), UQL (w), SFC (w), length (n), SFC (n), trash, fineness, IFC and MR (AFIS) in 2009, 2010 and 2011 with genotype x year and genotype x sympodial branch interaction for Acala 1517-99, FiberMax 832, TM-1 and Half and Half in College Station, TX.

		Mean Squares								
Source of variation	**df**	**Length (w)**	**UQL (w)**	**SFC (w)**	**Length (n)**	**SFC (n)**	**Trash**	**Fineness**	**IFC**	**MR**
rep	2	0.005	0.001	18.022*	0.015*	128.230**	93693	365*	7.343**	0.004**
years	2	0.019**	0.065**	124.705**	0.032**	1767.142**	21442312**	2967**	61.703**	0.059**
genotype	3	2.537**	4.313**	539.064**	1.264**	156.899**	9110177**	24312**	25.344**	0.046**
rep*years	4	0.007*	0.002	21.462**	0.016**	109.791**	68516	321**	6.317**	0.004**
genotype*years	6	0.039**	0.038**	55.524**	0.044**	165.406**	3721628**	1286**	17.075**	0.024**
genotype*rep (2009)	6	0.008**	0.012**	19.870**	0.020**	125.855**	387589**	82*	5.247**	0.003**
genotype*sympodial (2009)	36	0.001**	0.001**	13.487**	0.010**	18.824*	282780**	33	0.738	0.001
genotype*rep (2010)	6	0.008**	0.006**	29.423**	0.018**	150.155**	238113**	302**	4.859**	0.002**
genotype*sympodial (2010)	35	0.003**	0.003**	2.675	0.002*	11.033	59113	53	0.571	0.000
genotype*rep (2011)	6	0.001	0.002	2.359	0.002	13.228	103783	70	0.359	0.033**

Table A. 2: Continued

Source of variation	df	Length (w)	UQL (w)	SFC (w)	Length (n)	SFC (n)	Trash	Fineness	IFC	MR
genotype*sympodial (2011)	33	0.001	0.001	1.981	0.001	7.68	42113	57*	0.379	0.006**
error	412	0.002	0.002	5.526	0.003	24.059	137954	92	1.122	0.000

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

Table A. 3: ANOVA for fiber nepsize and nep count (AFIS) in 2009, 2010 and 2011 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half in College Station, Texas.

		Mean Squares	
Source of variation	**df**	**Nepsize**	**Neps**
rep	2	7	9381
years	2	16699**	295084**
genotype	3	1729	171086**
rep*years	4	767	6297
genotype*years	6	2963	19596
genotype*rep	11	540	27147**
genotype*sympodial	72	1303	6203
error	412	1760	9516
sympodial	12	1808	110838**

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

Table A. 4: ANOVA for fiber fineness, IFC and MR (AFIS) in 2009 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half in College Station, Texas.

		Mean Squares (2009)		
Source of variation	**df**	**Fineness**	**IFC**	**MR**
rep	2	365.887*	7.343**	0.004**
years	2	2967.541**	61.703**	0.059**
genotype	3	24312.801**	25.344**	0.046**
rep*years	4	321.123**	6.317**	0.004**
genotype*years	6	1286.100**	17.075**	0.024**
genotype*rep (2009)	5	82.559*	5.247**	0.003**
genotype*sympodial (2009)	36	33.940	0.738	0.001
error	412	92.053	1.122	0.000
sympodial (2009)	12	129.862	2.686*	0.002

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

Table A. 5: ANOVA for fiber length (w) UQL (w) SFC (w) length (n) SFC (n) and trash (AFIS) in 2009 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half in College Station, Texas.

		Mean Squares (2009)					
Source of variation	**df**	**Length (w)**	**UQL (w)**	**SFC (w)**	**Length (n)**	**SFC (n)**	**Trash**
rep	2	0.005	0.001	18.022*	0.015*	128.688**	93693
years	2	0.019**	0.065**	124.705**	0.032**	1767.946**	21442312**
genotype	3	2.537**	4.313**	539.064**	1.264**	156.899**	9110177**
rep*years	4	0.007*	0.002	21.462**	0.016**	109.791**	68516
genotype*years	6	0.039**	0.038**	55.524**	0.044**	165.406**	3721628**
genotype*rep (2009)	5	0.008**	0.012**	19.870**	0.020**	125.855**	387589**
genotype*sympodial (2009)	36	0.001**	0.001**	13.487**	0.010**	18.824*	282780**
error	412	0.002	0.002	5.526	0.003	24.059	137954
sympodial (Acala 1517-99)	12	0.002*	0.003**	3.378*	0.003*	18.186*	248501*
sympodial (FM832)	12	0.003**	0.003**	4.160*	0.005*	26.004*	290260**
sympodial (TM-1)	12	0.005**	0.005**	4.794**	0.007**	30.475*	324287**
sympodial (Half and Half)	12	0.002**	0.001*	17.444**	0.002**	43.674**	1232026**

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

Table A. 6: ANOVA for fiber SFC (w), SFC (n), fineness, IFC and MR in 2010 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half showing genotype x years and genotype x sympodial interaction at College Station, Texas.

		Mean Squares (2010)				
Source of variation	**df**	**SFC (w)**	**SFC (n)**	**Fineness**	**IFC**	**MR**
rep	2	18.022*	128.688**	365.887*	7.343**	0.004**
years	2	124.705**	1767.946**	2967.541**	61.703**	0.059**
genotype	3	539.064**	156.899**	24312.801**	25.344**	0.046**
rep*years	4	21.462**	109.791**	321.123**	6.317**	0.004**
genotype*years	6	55.524**	165.406**	1286.100**	17.075**	0.024**
genotype*rep (2009)	6	19.870**	125.855**	82.559*	5.247**	0.003**
genotype*sympodial (2009)	36	13.487**	18.824*	33.940	0.738	0.001
genotype*rep (2010)	6	29.423**	150.155**	302.755**	4.859**	0.002**
genotype*sympodial (2010)	36	2.675	11.033	53.699	0.571	0.000
error	412	5.526	24.059	92.053	1.122	0.000
sympodial	12	41.859**	222.941**	952.692**	8.845**	0.006**

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

Table A. 7: ANOVA for fiber length (w), UQL (w), length (n) and trash in 2010 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half at College Station, Texas.

		Mean Squares (2010)			
Source of variation	**df**	**Length (w)**	**UQL (w)**	**Length (n)**	**Trash**
rep	2	0.005	0.001	0.015*	93693
years	2	0.019**	0.065**	0.032**	21442312**
genotype	3	2.537**	4.313**	1.264**	9110177**
rep*years	4	0.007*	0.002	0.016**	68516
genotype*years	6	0.039**	0.038**	0.044**	3721628**
genotype*rep (2010)	6	0.008**	0.006**	0.018**	238113**
genotype*sympodial (2010)	35	0.003**	0.003**	0.002*	59113
error	412	0.002	0.002	0.003	137954
sympodial (Acala 1517-99)	12	0.004**	0.003**	0.006**	79808
sympodial (FiberMax 832)	12	0.015**	0.014**	0.019**	59462
sympodial (TM-1)	12	0.007**	0.005**	0.012**	93400
sympodial (Half and Half)	11	0.002	0.002	0.002	33719

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

Table A. 8: ANOVA for fiber length (w), UQL (w), SFC (w), length (n), SFC (n), trash and IFC (AFIS) in 2011 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half at College Station, Texas.

		Mean Squares (2011)							
Source of variation	**df**	**Length (w)**	**UQL (w)**	**SFC (w)**	**Length (n)**	**SFC (n)**	**Trash**	**IFC**	**MR**
rep	2	0.005	0.001	18.022*	0.015*	128.688**	93693	7.343**	0.004**
years	2	0.019**	0.065**	124.705**	0.032**	1767.946**	21442312**	61.703**	0.059**
genotype	3	2.537**	4.313**	539.064**	1.264**	156.899**	9110177**	25.344**	0.046**
rep*years	4	0.007*	0.002	21.462**	0.016**	109.791**	68516	6.317**	0.004**
genotype*years	6	0.039**	0.038**	55.524**	0.044**	165.406**	3721628**	17.075**	0.024**
genotype*rep (2011)	6	0.001	0.002	2.359	0.002	13.228	103783	0.359	0.033**
genotype*sympodial (2011)	33	0.001	0.001	1.981	0.001	7.680	42113	0.379	0.006**
error	412	0.002	0.002	5.526	0.003	24.059	137954	1.122	0.000
sympodial (2011)	11	0.006	0.006	9.787	0.007	39.194**	120261*	5.063**	0.006**

*significant at 0.05 **significant at 0.01

Table A. 9: ANOVA for fiber fineness and MR (AFIS) in 2011 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half at College Station, Texas.

		Mean Squares(2011)
Source of variation	**df**	**Fineness**
rep	2	365.887*
years	2	2967.541**
genotype	3	24312.801**
rep*years	4	321.123**
genotype*years	6	1286.100**
genotype*rep	6	70.00694
genotype*sympodial	33	57.560*
error	412	92.053
sympodial (Acala 1517-99)	11	364.020**
sympodial (FM832)	11	310.492**
sympodial (TM-1)	11	264.878**
sympodial (Half and Half)	11	222.189**

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

Table A. 10: ANOVA for percentage of difference in fiber length (n) among the longest and shortest fibers within the plant across Acala 1517-99, FiberMax 832, TM-1 and Half and Half in College Station, Texas, in 2009, 2010 and 2011.

		Mean Squares
Source of variation	**df**	**% difference**
genotype	3	111.153*
rep	2	49.366
years	2	86.251
rep*years	4	42.015
genotype*years	6	20.111
error	17	36.846

*significant at 0.05 **significant at 0.01

Table A. 11: ANOVA for fiber nepsize, neps, length (w), UQL (w), SFC (w), length (n), SFC (n), IFC, fineness and MR (AFIS) in 2010 and 2011 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half at Lubbock, Texas.

		Mean Squares										
Source of variation	**df**	**Nepsize**	**Neps**	**Length (w)**	**UQL (w)**	**SFC (w)**	**Length (n)**	**SFC (n)**	**Trash**	**Fineness**	**IFC**	**MR**
rep	2	613.429	46849.261*	0.047**	0.062**	43.886**	0.046**	174.521**	19275.955	233.326	2.611	0.002
years	1	2484.820	37427.021	0.0201*	0.047**	7.198	0.012	27.147	2482.065	105.096	13.447**	0.023**
genotype	3	13878.690*	23307.806	0.721**	1.038**	100.313**	0.434**	80.505**	150041.856	9408.918**	0.430	0.002
rep*years	2	576.377	47496.933*	0.022**	0.047**	4.637	0.011	7.944	65596.737	1226.315**	1.624	0.001
genotype*years	3	6073.599	9156.506	0.075**	0.153**	16.891**	0.042**	81.957**	164421.255	31.077	2.146	0.003**
error	268	4056.864	12896.286	0.003	0.005	4.192	0.003	20.106	66159.410	160.773	1.162	0.000

*significant at 0.05 **significant at 0.01

Table A. 12: ANOVA for fiber nepsize, neps, IFC and fineness (AFIS) in 2010 and 2011 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half at Lubbock, Texas.

		Mean Squares			
Source of variation	**df**	**Nepsize**	**Neps**	**Trash**	**Fineness**
rep	2	613	46849*	19275	233
years	1	2484	37427	2482	105
genotype	3	13878*	23307	150041	9408**
rep*years	2	576	47496*	65596	1226**
genotype*years	3	6073	9156	164421	31
genotype*rep	6	11514**	26238	284472**	1956**
genotype*sympodial	36	3308	15638	78354	133
error	268	4056	12896	66159	160
sympodial	12	4983	13447	80244	63

*significant at 0.05 **significant at 0.01

Table A. 13: ANOVA for fiber IFC (AFIS) in 2010 and 2011 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half at Lubbock, Texas.

		Mean Squares
Source of variation	**df**	**IFC**
rep	2	2.611
years	1	13.447**
genotype	3	0.430
rep*years	2	1.624
genotype*years	3	2.146
genotype*rep	6	7.147**
genotype*sympodial	36	1.647*
error	268	1.162
sympodial (Acala 1517-99)	12	0.918*
sympodial (FiberMax 832)	12	4.332*
sympodial (TM-1)	12	0.605
sympodial (Half and Half)	12	0.153

*significant at 0.05 **significant at 0.01

Table A. 14: ANOVA for fiber SFC (w), SFC (n) and MR (AFIS) in 2010 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half at Lubbock, Texas.

		Mean Squares (2010)		
Source of variation	**df**	**SFC (w)**	**SFC (n)**	**MR**
rep	2	43.886**	174.521**	0.002
years	1	7.198	27.147	0.023**
genotype	3	100.313**	80.505**	0.002
rep*years	2	4.637	7.944	0.001
genotype*years	3	16.891**	81.957**	0.003**
genotype*rep	4	18.956**	126.433**	0.004*
genotype*sympodial	36	5.829	25.543	0.001
error	268	4.192	20.106	0.000
sympodial	12	6.365	31.014	0.001

*significant at 0.05 **significant at 0.01

Table A. 15: ANOVA for fiber length (w), UQL (w) and length (n) (AFIS) in 2010 for Acala 1517-99, FM832, TM-1 and Half and Half at Lubbock, Texas.

		Mean Squares (2010)		
Source of variation	**df**	**Length (w)**	**UQL (w)**	**Length (n)**
rep	2	0.047**	0.062**	0.046**
years	1	0.0201*	0.047**	0.012
genotype	3	0.721**	1.038**	0.434**
rep*years	2	0.022**	0.047**	0.011
genotype*years	3	0.075**	0.153**	0.042**
genotype*rep	4	0.006*	0.002	0.017**
genotype*sympodial	36	0.004**	0.003*	0.005**
error	268	0.003	0.005	0.003
sympodial (Acala 1517-99)	12	0.001	0.001	0.002
sympodial (FiberMax 832)	12	0.011**	0.009**	0.014**
sympodial (TM-1)	12	0.001	0.000	0.002
sympodial (Half and Half)	12	0.001*	0.001*	0.000*

*significant at 0.05 **significant at 0.01

Table A. 16: ANOVA for fiber UQL (w) and SFC (n) (AFIS) in 2011 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half at Lubbock, Texas.

		Mean Squares(2011)	
Source of variation	**df**	**UQL (w)**	**SFC (n)**
rep	2	0.062**	174.521**
years	1	0.047**	27.147
genotype	3	1.038**	80.505**
rep*years	2	0.047**	7.944
genotype*years	3	0.153**	81.957**
genotype*rep	6	0.135**	125.357**
genotype*sympodial	33	0.003*	15.283*
error	268	0.005	0.003
sympodial (Acala 1517-99)	11	0.001	5.554
sympodial (FiberMax 832)	11	0.001	31.372
sympodial (TM-1)	11	0.001	11.146*
sympodial (Half and Half)	11	0.009	5.454

*significant at 0.05 **significant at 0.01

Table A. 17: ANOVA for fiber (AFIS) in 2011 for Acala 1517-99, FiberMax 832, TM-1 and Half and Half at Lubbock, Texas.

		Mean Squares (2011)			
Source of variation	**df**	**Length (w)**	**SFC (w)**	**Length (n)**	**MR**
rep	2	0.047**	43.886**	0.046**	0.002
years	1	0.0201*	7.198	0.012	0.023**
genotype	3	0.721**	100.313**	0.434**	0.002
rep*years	2	0.022**	4.637	0.011	0.001
genotype*years	3	0.075**	16.891**	0.042**	0.003**
genotype*rep	6	0.068**	34.877**	0.044**	0.002**
genotype*sympodial	33	0.002	2.523	0.002	0.000
error	268	0.003	4.192	0.003	0.000
sympodial	12	0.001	1.052	0.001	0.000

*significant at 0.05 **significant at 0.01

Table A. 18: ANOVA for fiber micronaire, uniformity ratio and elongation (HVI) in 2009, 2010 and 2011 for FiberMax 832 and Deltapine 491 in College Station, Texas.

		Mean Squares		
Source of variation	**df**	**Micronaire**	**Uniformity**	**Elongation**
rep	3	0.101	2.210	0.181
years	2	2.365**	52.948**	1.985**
genotype	1	0.028	167.472**	1.127
rep*years	6	0.426	1.042	0.293
genotype*years	2	0.229	4.086	0.228
genotype*rep	3	0.026	5.050*	0.077
genotype*sample	9	0.086	1.917	0.204
error	224	0.196	2.891	0.107
sample	9	2.744**	41.836**	0.201

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

Table A. 19: ANOVA for fiber length (HVI) in 2009, 2010 and 2011 for FiberMax 832 and Deltapine 491 in College Station, Texas.

		Mean Squares
Source of variation	**df**	**HVI Length**
rep	3	0.002
years	2	0.056**
genotype	1	0.078**
rep*years	6	0.003
genotype*years	2	0.007*
genotype*rep (2009)	3	0.002*
genotype*sample (2009)	9	0.002**
genotype*rep (2010)	3	0.004*
genotype*sample (2010)	9	0.001
genotype*rep (2011)	3	0.000
genotype*sample (2011)	9	0.001
error	224	0.002
sample(2009 FiberMax 832)	9	0.005**
sample(2009 Deltapine 491)	9	0.010**
sample(2010)	9	0.019**
sample(2011)	9	0.008**

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

Table A. 20: ANOVA for fiber strength in 2009, 2010 and 2011 for FiberMax 832 and Deltapine 491 in College Station, Texas.

		Mean Squares
Source of variation	**df**	**HVI Strength**
rep	3	1.48
years	2	196.150**
genotype	1	330.879**
rep*years	6	2.569
genotype*years	2	32.145**
genotype*rep (2009)	3	7.613*
genotype*sample (2009)	9	3.407
genotype*rep (2010)	3	7.351*
genotype*sample (2010)	9	1.741
genotype*rep (2011)	3	0.054
genotype*sample (2011)	9	2.968
error	224	5.115
sample (2009)	9	42.131**
sample (2010)	9	16.807**
sample (2011)	9	21.097**

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

Table A. 21: ANOVA for fiber nepsize, neps, SFC (w), length (n), SFC (n), trash (total), IFC, fineness, MR (AFIS) in 2009, 2010 and 2011 for FiberMax 832 and Deltapine 491 in College Station, Texas.

		Mean Squares								
Source of variation	**df**	**Nepsize**	**Neps**	**SFC (w)**	**Length (n)**	**SFC (n)**	**Trash**	**Fineness**	**IFC**	**MR**
rep	3	2508	33686	9.354	0.006	56.378	27694	52.585	1.933	0.001
years	2	28203**	312522**	235.332**	0.174**	1688.373**	6235078**	522.978**	32.424**	0.036**
genotype	1	5729	14516	215.951**	0.187**	1011.355**	585831	490.086	47.468**	0.038**
rep*years	6	1914	48068	11.109	0.003	60.849	243116	182.266	3.157	0.003
genotype* years	2	1418	25882	17.853	0.014	68.328	161173	59.632	3.258	0.002
genotype* rep	3	3738	6371	2.894	0.002	12.313	229124	20.018	1.086	0.000
genotype* sample	9	2053	8871	4.749	0.002	13.881	227952	26.001	0.725	0.000
error	224	2063	19414	6.630	0.005	28.795	432066	103.092	1.689	0.001
sample	9	5187**	197193**	94.237**	0.082**	409.996**	3788949**	1577.560**	22.697**	0.020**

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

Table A. 22: ANOVA for length (w) (AFIS) in 2009, 2010 and 2011 for FiberMax 832 and Deltapine 491 in College Station, Texas.

Source of variation	df	Mean Squares
rep	3	0.003
years	2	0.048**
genotype	1	0.127**
rep*years	6	0.001
genotype*years	2	0.012*
genotype*rep (2009)	3	0.003*
genotype*sample (2009)	9	0.003**
genotype*rep (2010)	3	0.003**
genotype*sample (2010)	9	0.000
genotype*rep (2011)	3	0.0001
genotype*sample (2011)	9	0.001
error	224	0.004
sample(2009 FiberMax 832)	9	0.009**
sample(2009 Deltapine 491)	9	0.016**
sample(2010)	9	0.035**
sample(2011)	9	0.011**

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

Table A. 23: ANOVA for length (n) (AFIS) in 2010 for FiberMax 832 and Deltapine 491 in College Station, Texas.

Source of variation	df	Mean Squares
rep	3	0.009**
genotype	1	0.187**
genotype*rep	3	0.003
genotype*sample	9	0.002
error	67	0.001
sample	9	0.039**

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

Table A. 24: ANOVA for length (w) (AFIS) in 2010 for FiberMax 832 and Deltapine 491 in College Station, Texas.

Source of variation	df	Mean Squares
rep	3	0.002
genotype	1	0.127**
genotype*rep	3	0.003**
genotype*sample	9	0.000
error	67	0.001
sample	9	0.035**

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

Table A. 25: ANOVA for lint percent in 2009, 2010 and 2011 for FiberMax 832 and Deltapine 491 in College Station, Texas.

		Mean Squares
Source of variation	**df**	**Lint Percent**
rep	3	30.015
years	2	244.019**
genotype	1	192.661**
rep*years	6	16.76
genotype*years	2	116.414**
genotype*rep (2009)	3	13.22*
genotype*sample (2009)	9	24.018**
genotype*rep (2010)	3	18.97
genotype*sample (2010)	9	9.15
genotype*rep (2011)	3	2.592
genotype*sample (2011)	9	5.89
error	224	9.324
sample(2009 FiberMax 832)	9	4.268
sample(2009 Deltapine 491)	9	40.954**
sample(2010)	9	41.602**
sample(2011)	9	7.423

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

Table A. 26: ANOVA fiber micronaire, length, UI, strength and elongation (HVI) in 2011 from diallel analysis of five parents and ten progeny (F1) in College Station, Texas.

		Mean Squares				
Source	**df**	**Micronaire**	**Length**	**UI**	**Strength**	**Elongation**
rep	3	0.053	0.001	0.539	1.073	0.037
GCA	4	0.692**	0.128**	65.468**	81.213**	1.677**
SCA	10	0.070	0.007**	7.613**	14.511**	0.204**
error	42	0.048	0.001	0.639	0.768	0.024
entry	14	0.352**	0.041**	20.488**	28.566**	0.621**

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

Table A. 27: ANOVA fiber neps, length (n), SFC, fineness, IFC, MR and Hs (AFIS) in 2011 from diallel analysis of five parents and ten progeny (F1) in College Station, Texas.

		Mean Squares						
Source	**Df**	**Neps**	**Length (n)**	**SFC**	**Fineness**	**IFC**	**MR**	**Hs**
rep	3	4857.777*	0.396	4.758	64.861*	0.283	0.000	37.529*
GCA	4	10256.117**	30.854**	20.468**	1299.066**	0.729**	0.001**	1359.446**
SCA	10	2168.590	3.855**	24.711**	33.126	0.693**	0.001**	19.498
error	42	1578.2063	0.381	2.739	19.231	0.148	0.000	10.904
entry	14	5657.495**	10.128**	24.565**	478.452**	0.997**	0.001**	437.799**

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

APPENDIX B

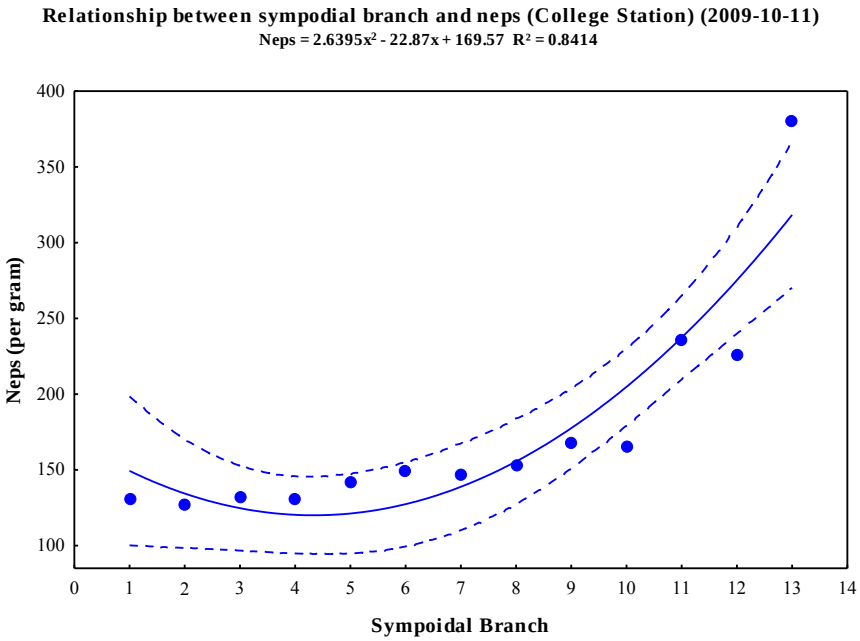

Figure B. 1: Relationship between sympodial branch and neps across genotypes in 2009, 2010 and 2011 at College Station, Texas,

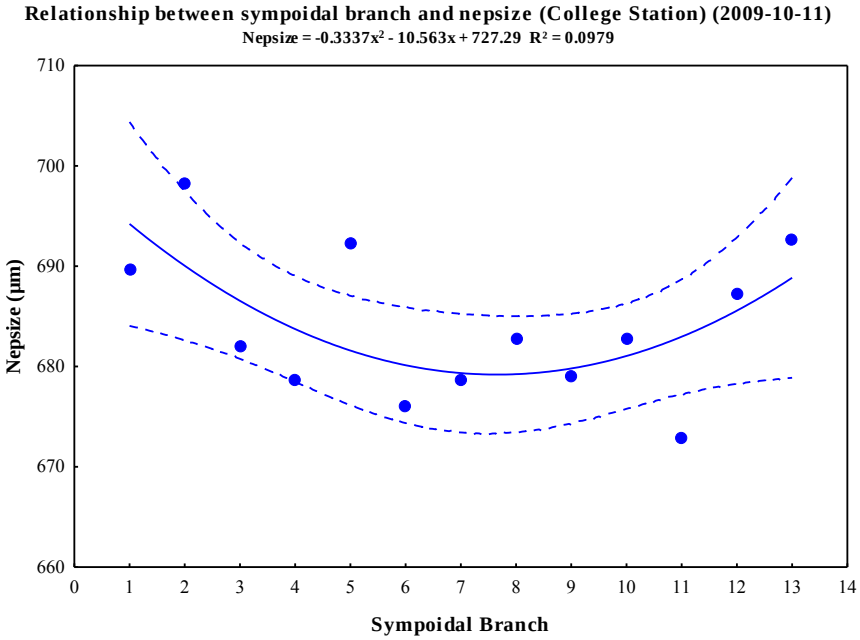

Figure B. 2: Relationship between sympodial branch and nepsize across genotypes in 2009, 2010 and 2011 at College Station, Texas.

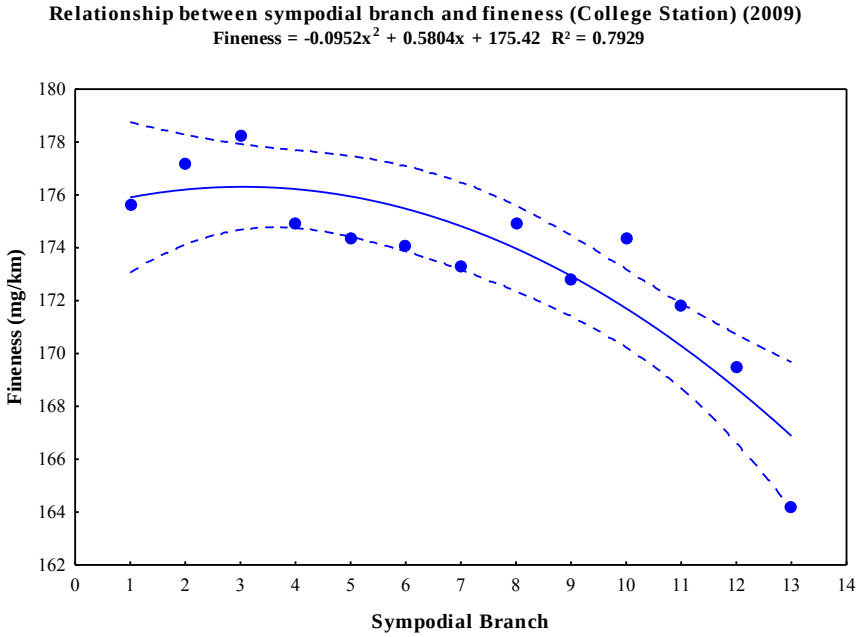

Figure B. 3: Relationship between sympodial branch and fineness (AFIS) across genotypes in 2009 at College Station, Texas.

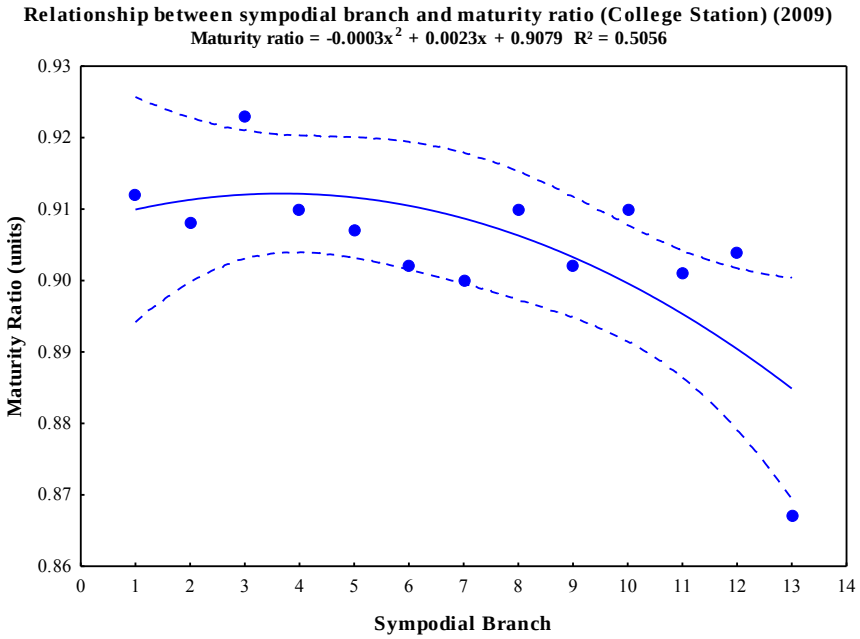

Figure B. 4: Relationship between sympodial branch and maturity ratio (AFIS) across genotypes in 2009 at College Station, Texas.

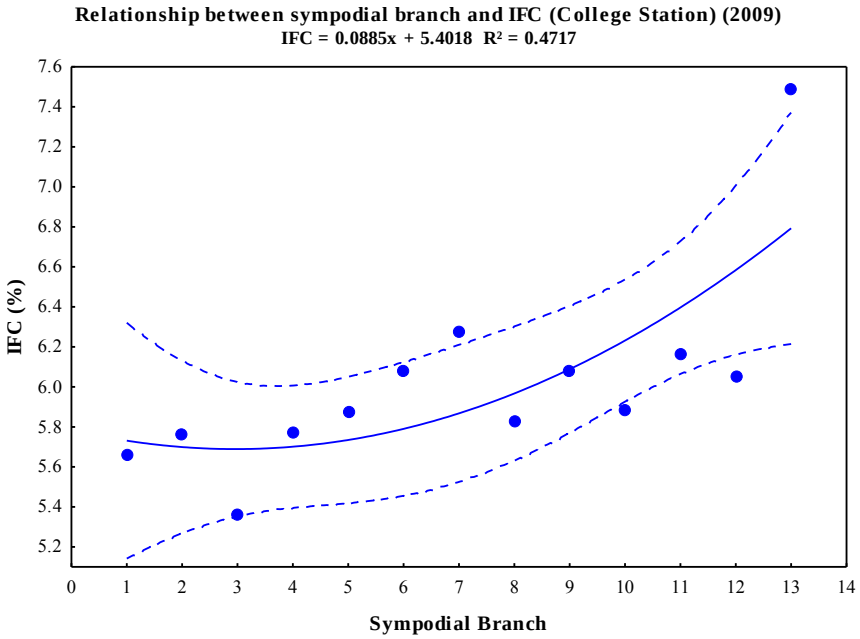

Figure B. 5: Relationship between sympodial branch and IFC (AFIS) across genotypes in 2009 at College Station, Texas.

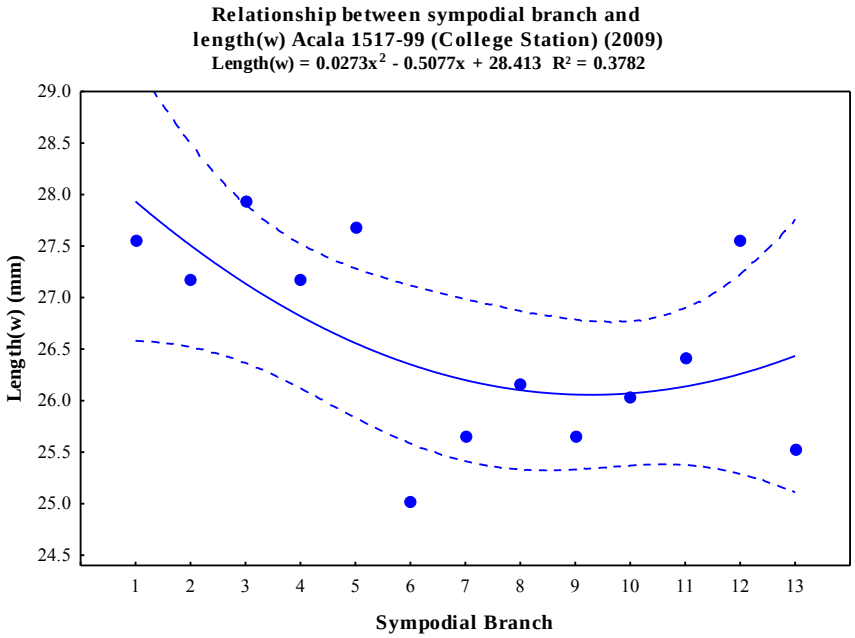

Figure B. 6: Relationship between sympodial branch and length (w) (AFIS) for Acala 1517-99 in 2009 at College Station, Texas.

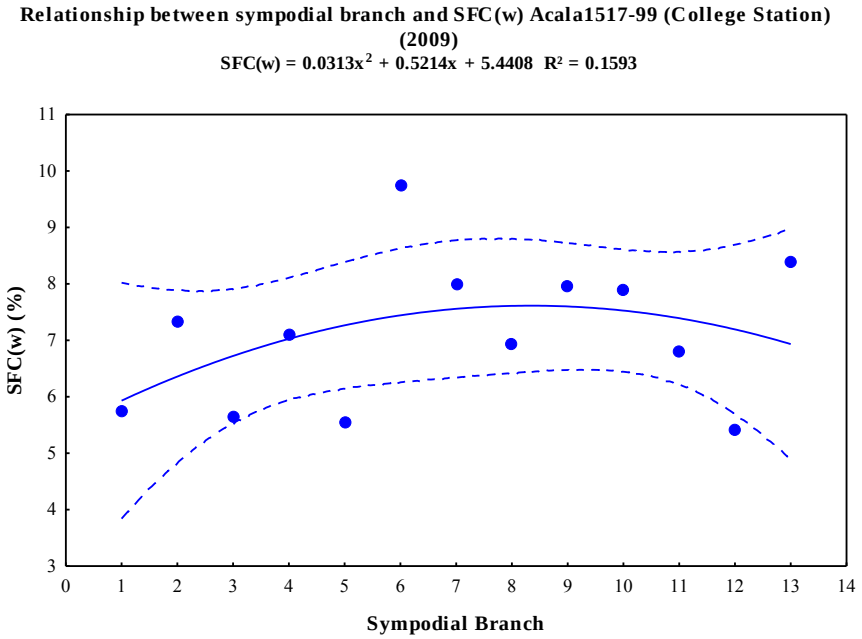

Figure B. 7: Relationship between sympodial branch and SFC (w) (AFIS) for Acala 1517-99 in 2009 at College Station, Texas.

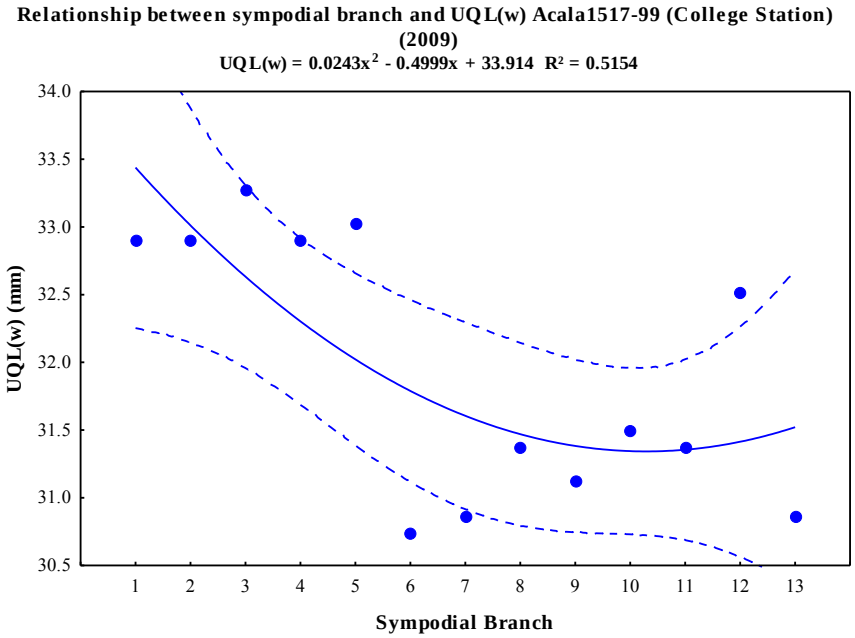

Figure B. 8: Relationship between sympodial branch and UQL (w) (AFIS) for Acala 1517-99 in 2009 at College Station, Texas.

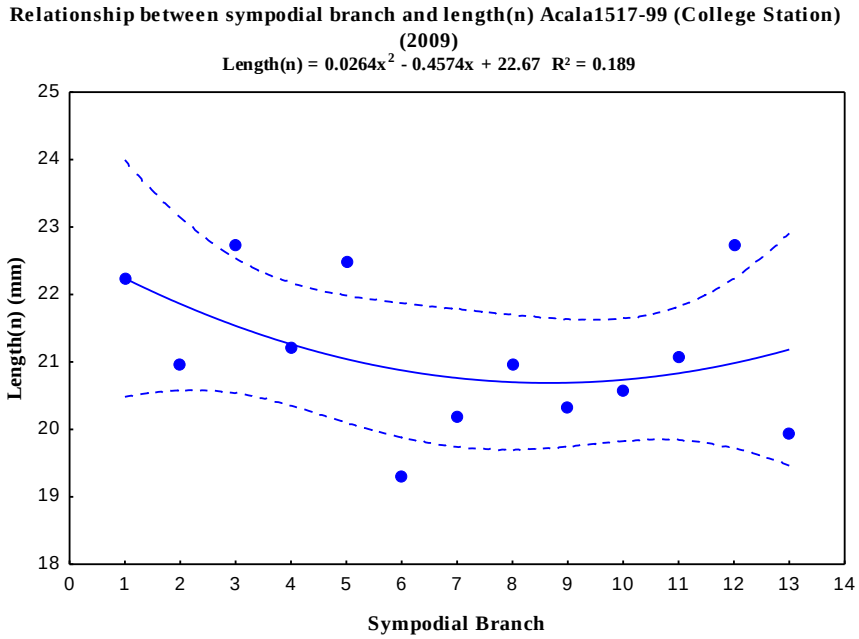

Figure B. 9: Relationship between sympodial branch and length (n) (AFIS) for Acala 1517-99 in 2009 at College Station, Texas.

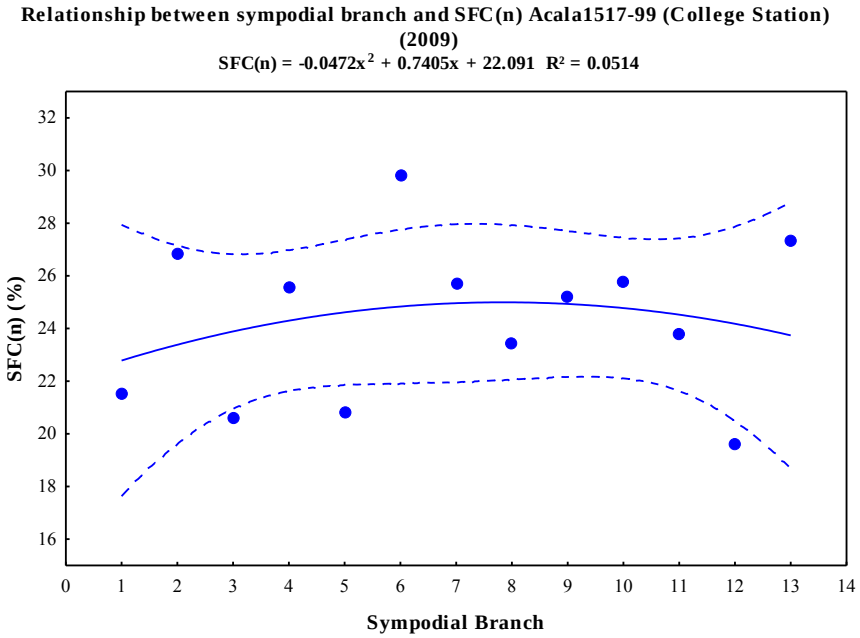

Figure B. 10: Relationship between sympodial branch and SFC (n) (AFIS) for Acala 1517-99 in 2009 at College Station, Texas.

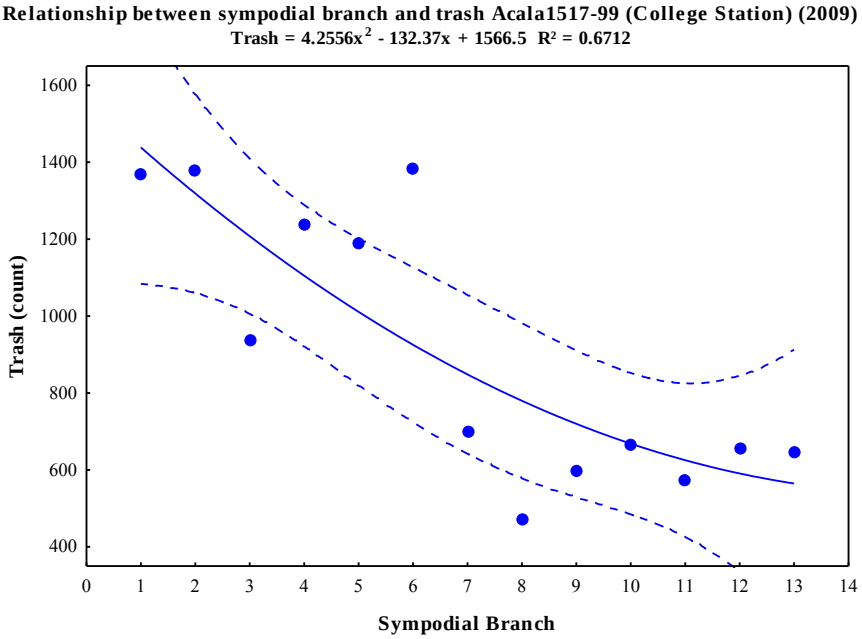

Figure B. 11: Relationship between sympodial branch and trash (AFIS) for Acala 1517-99 in 2009 at College Station, Texas.

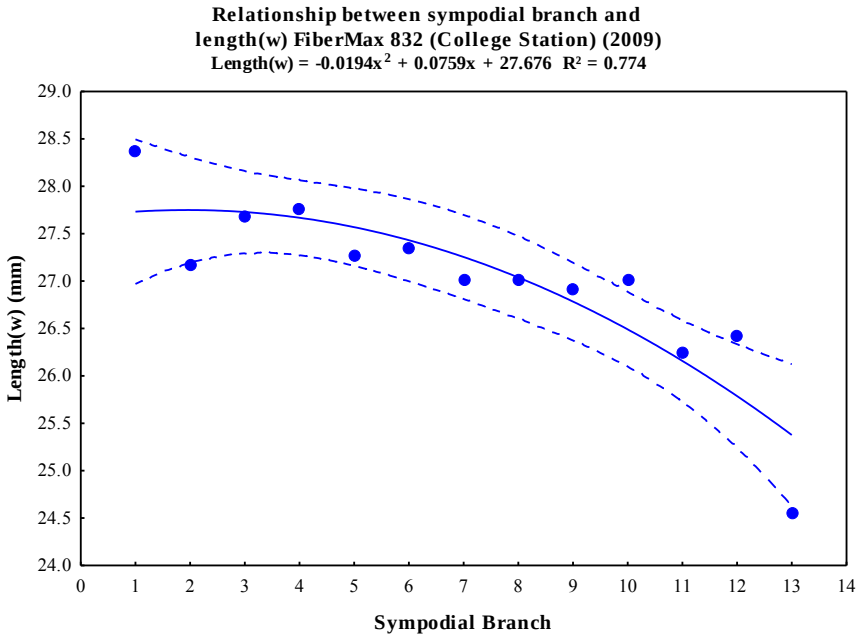

Figure B. 12: Relationship between sympodial branch and length (w) (AFIS) for FiberMax 832 in 2009 at College Station, Texas.

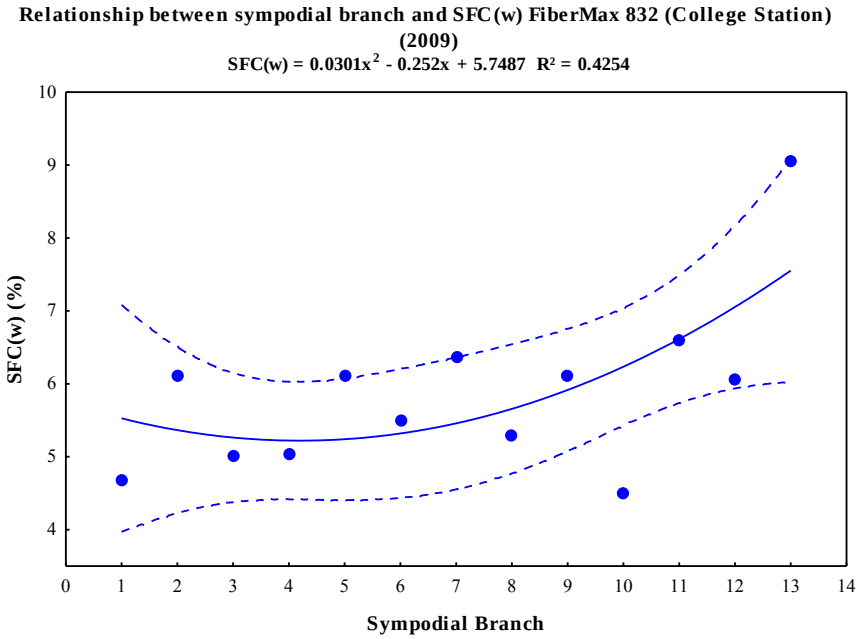

Figure B. 13: Relationship between sympodial branch and SFC (w) (AFIS) for FiberMax 832 in 2009 at College Station, Texas.

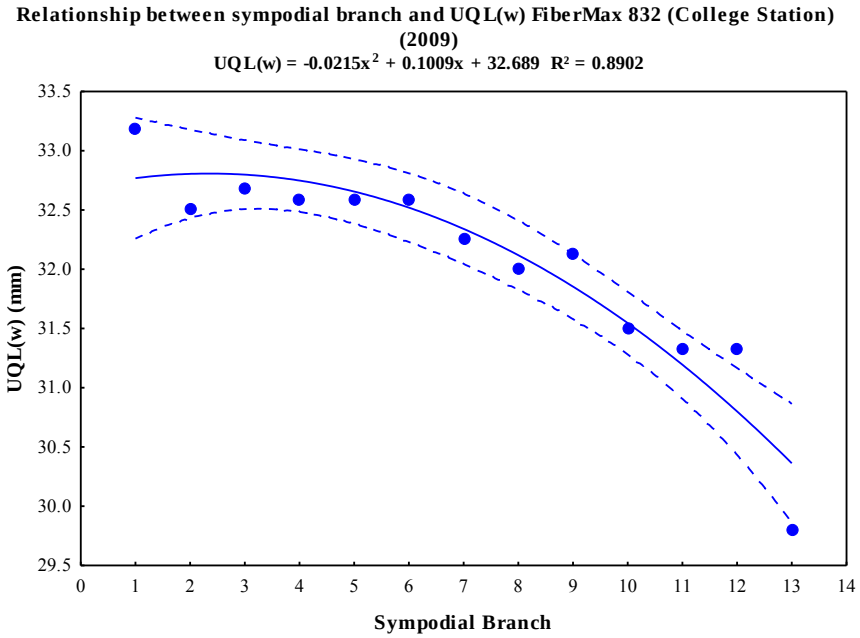

Figure B. 14: Relationship between sympodial branch and UQL (w) (AFIS) for FiberMax 832 in 2009 at College Station, Texas.

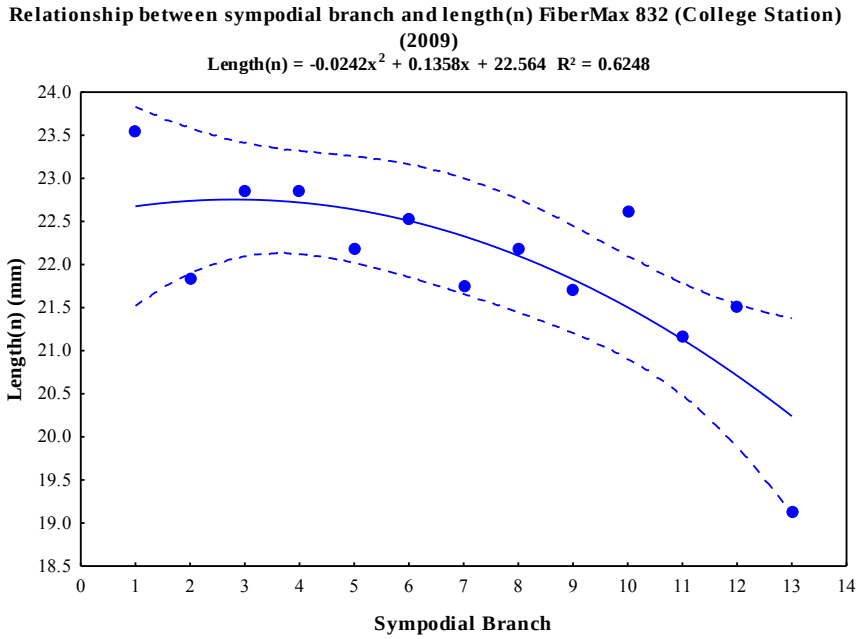

Figure B. 15: Relationship between sympodial branch and length (n) (AFIS) for FiberMax 832 in 2009 at College Station, Texas.

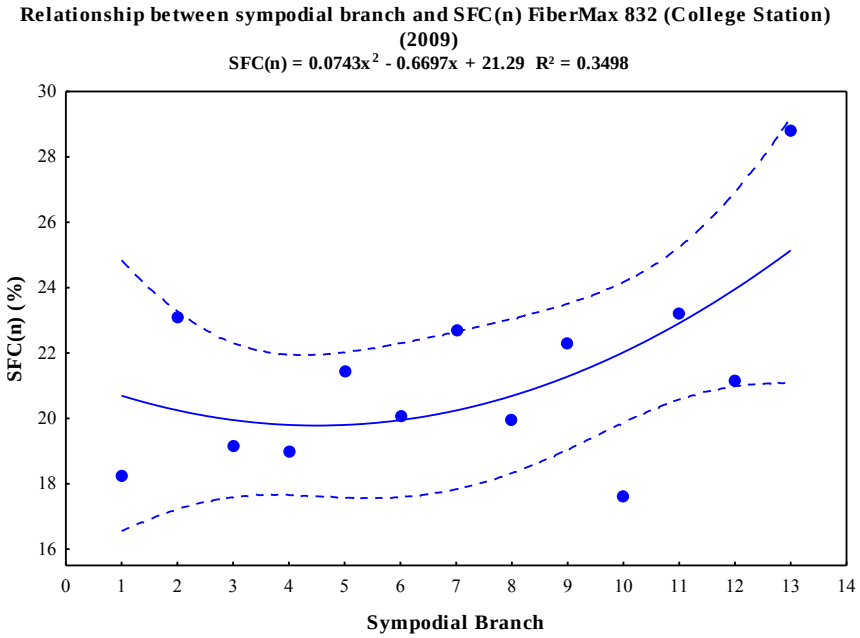

Figure B. 16: Relationship between sympodial branch and SFC (n) (AFIS) for FiberMax 832 in 2009 at College Station, Texas.

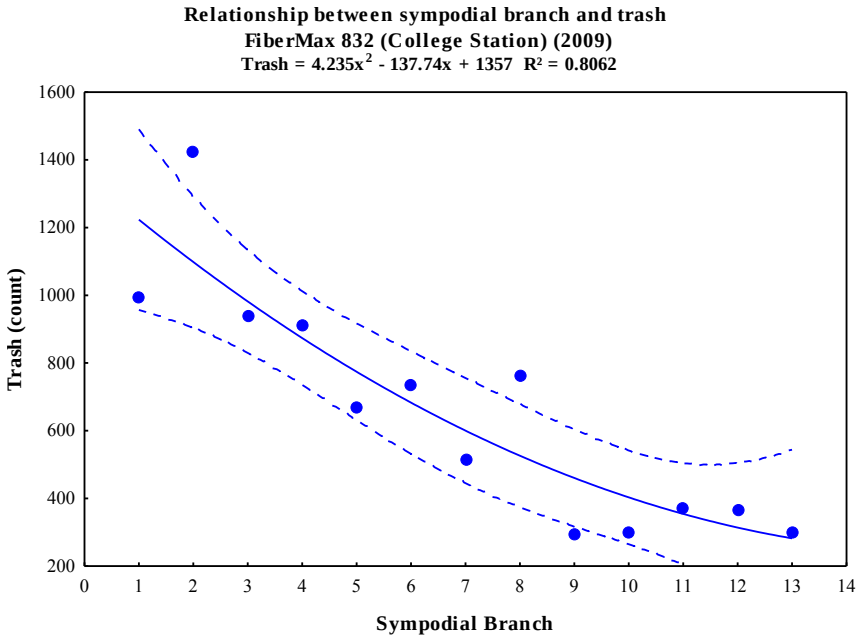

Figure B. 17: Relationship between sympodial branch and trash (AFIS) for FiberMax 832 in 2009 at College Station, Texas.

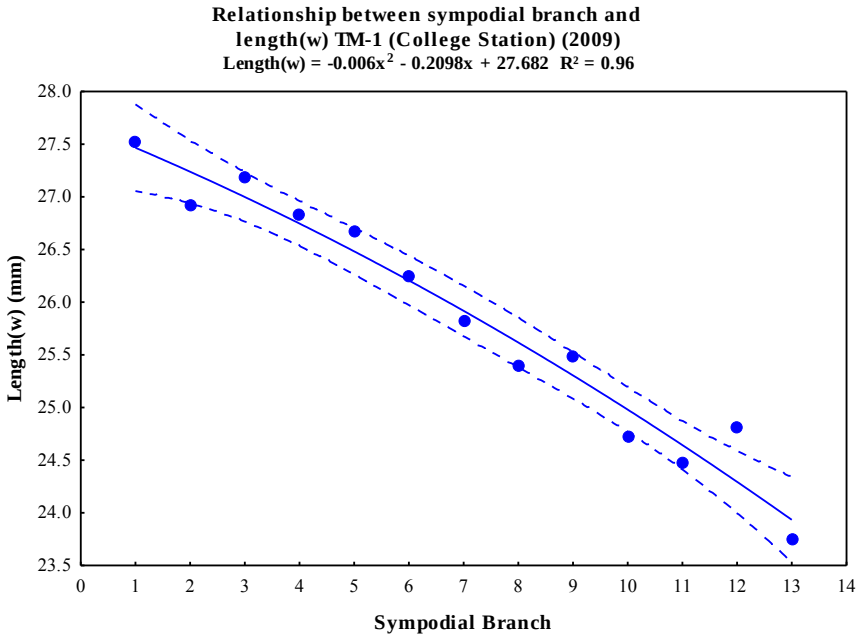

Figure B. 18: Relationship between sympodial branch and length (w) (AFIS) for TM-1 in 2009 at College Station, Texas.

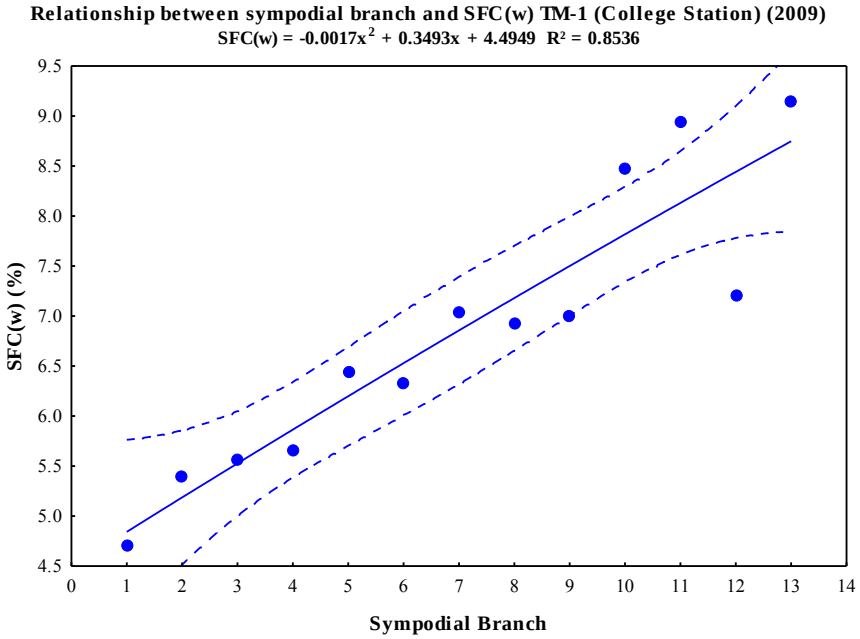

Figure B. 19: Relationship between sympodial branch and SFC (w) (AFIS) for TM-1 in 2009 at College Station, Texas.

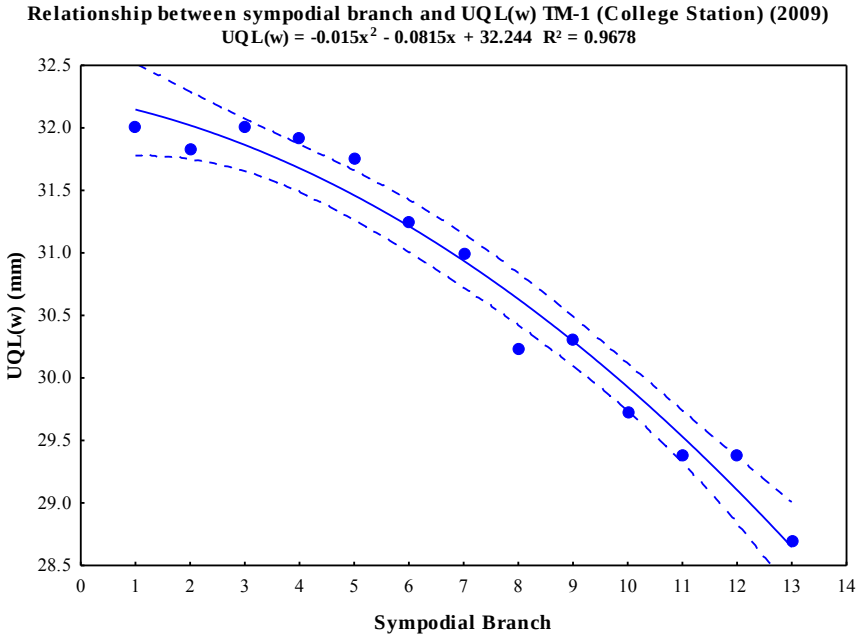

Figure B. 20: Relationship between sympodial branch and UQL (w) (AFIS) for TM-1 in 2009 at College Station, Texas.

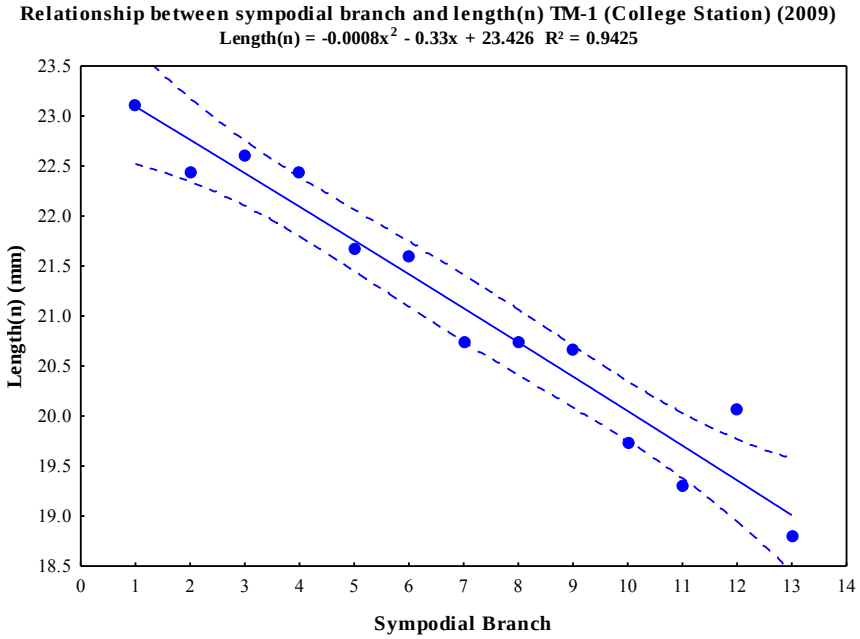

Figure B. 21: Relationship between sympodial branch and length (n) (AFIS) for TM-1 in 2009 at College Station, Texas.

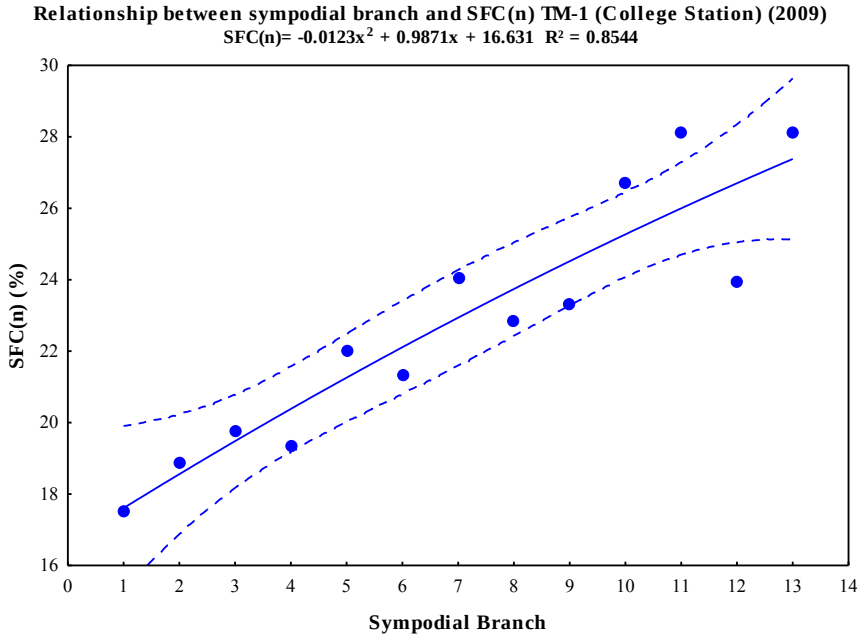

Figure B. 22: Relationship between sympodial branch and SFC (n) (AFIS) for TM-1 in 2009 at College Station, Texas.

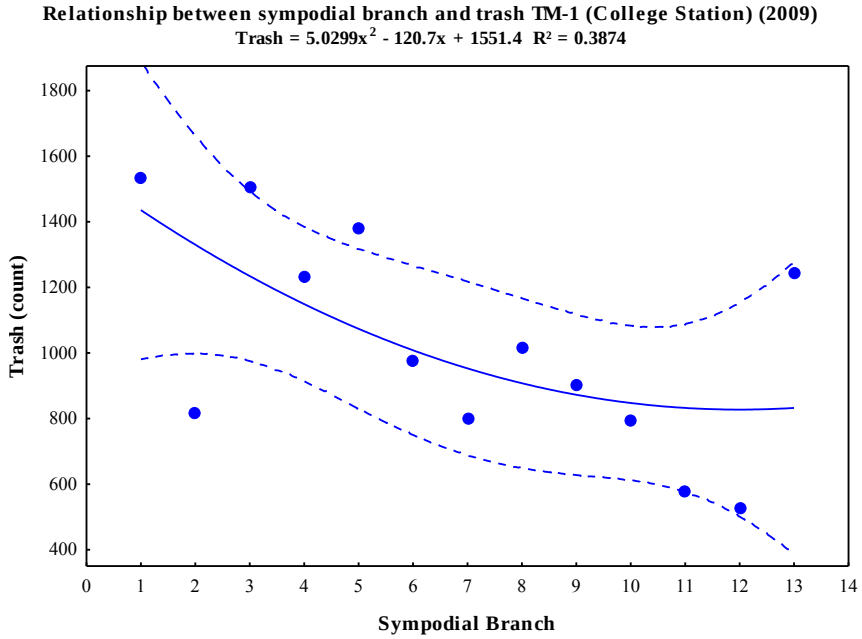

Figure B. 23: Relationship between sympodial branch and trash (AFIS) for TM-1 in 2009 at College Station, Texas.

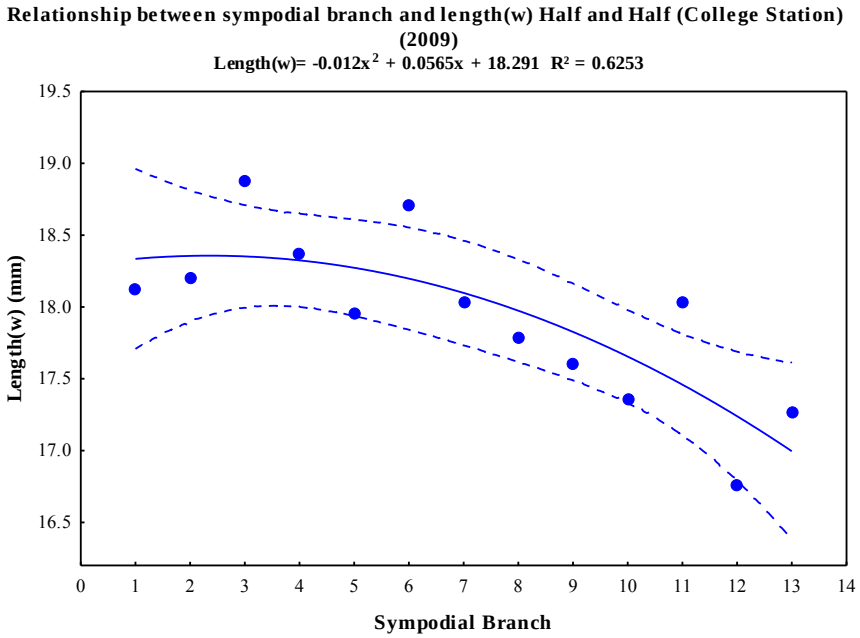

Figure B. 24: Relationship between sympodial branch and length (w) (AFIS) for Half and Half in 2009 at College Station, Texas.

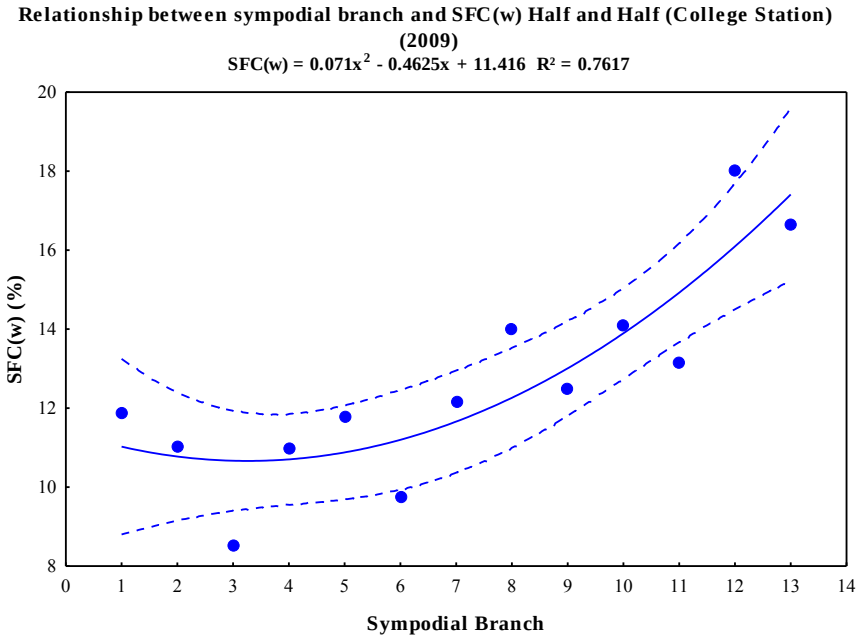

Figure B. 25: Relationship between sympodial branch and SFC (w) (AFIS) for Half and Half in 2009 at College Station, Texas.

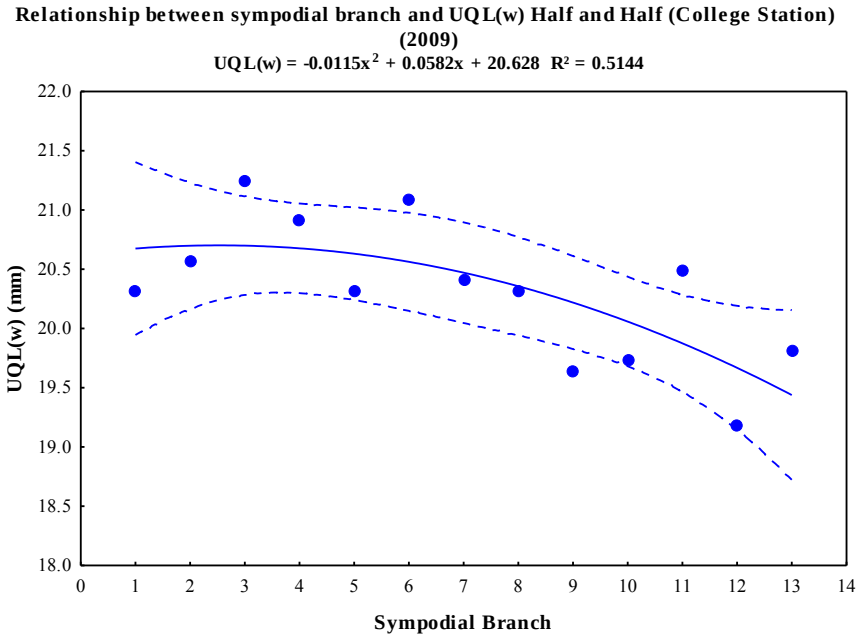

Figure B. 26: Relationship between sympodial branch and UQL (w) (AFIS) for Half and Half in 2009 at College Station, Texas.

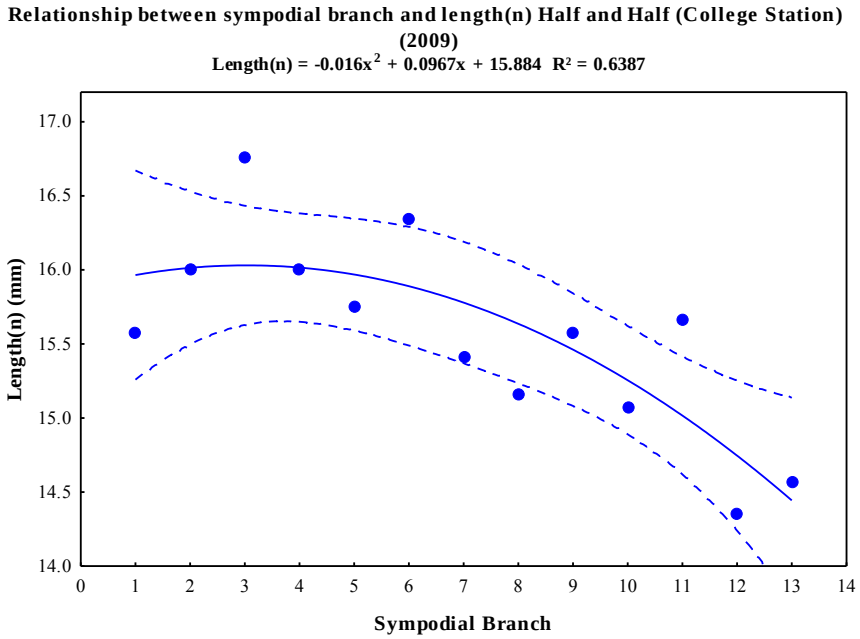

Figure B. 27: Relationship between sympodial branch and length (n) (AFIS) for Half and Half in 2009 at College Station, Texas.

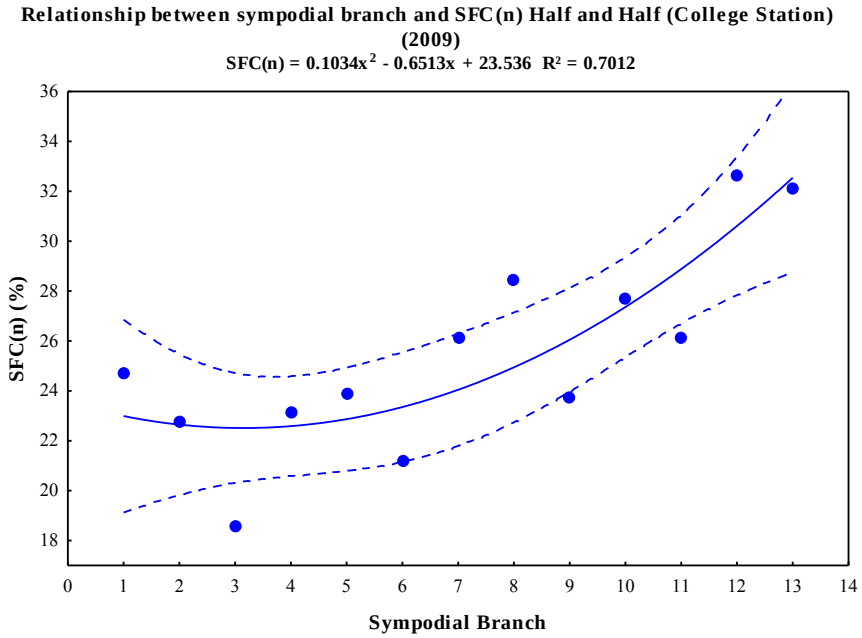

Figure B. 28: Relationship between sympodial branch and SFC (n) (AFIS) for Half and Half in 2009 at College Station, Texas.

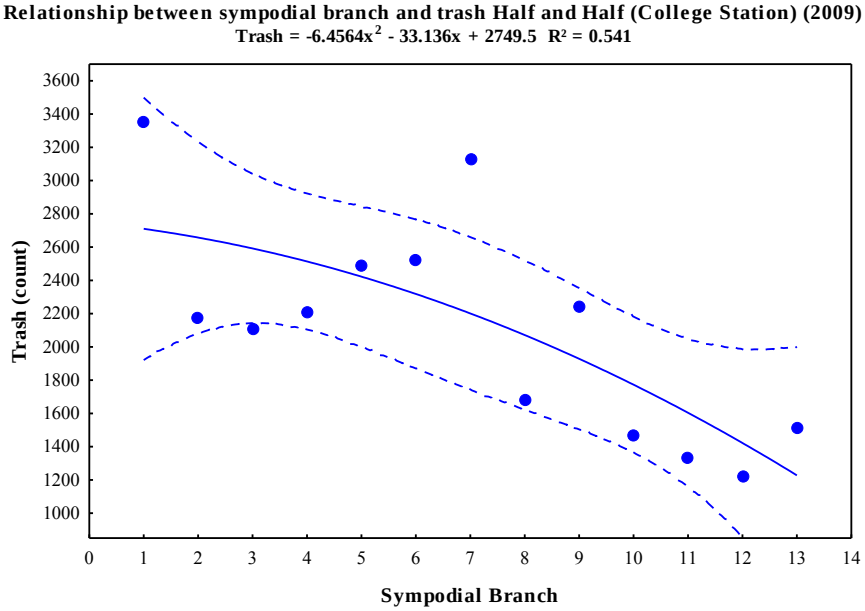

Figure B. 29: Relationship between sympodial branch and trash (AFIS) for Half and Half in 2009 at College Station, Texas.

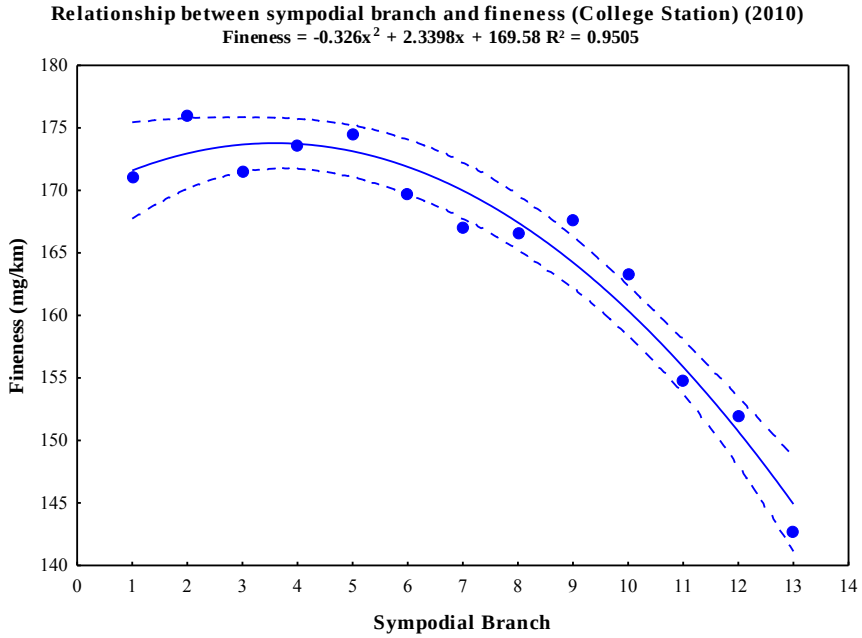

Figure B. 30: Relationship between sympodial branch and fineness (AFIS) across genotypes in 2010 at College Station, Texas.

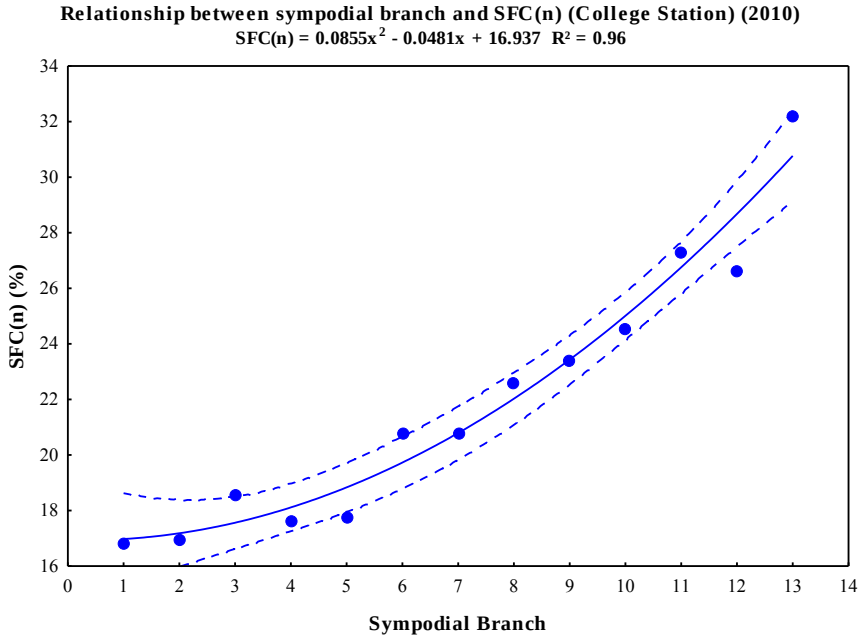

Figure B. 31: Relationship between sympodial branch and SFC (n) (AFIS) across genotypes in 2010 at College Station, Texas.

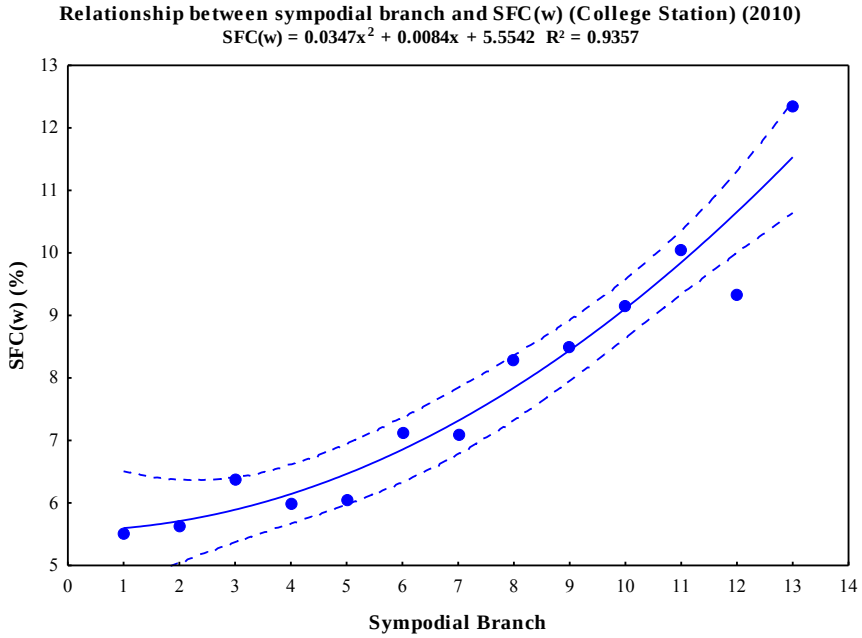

Figure B. 32: Relationship between sympodial branch and SFC (w) (AFIS) across genotypes in 2010 at College Station, Texas.

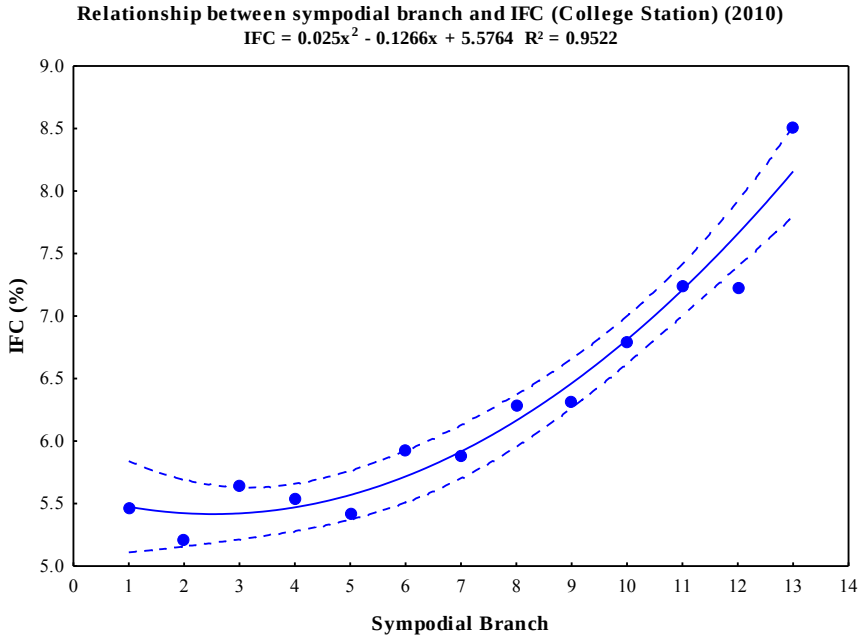

Figure B. 33: Relationship between sympodial branch and IFC (AFIS) across genotypes in 2010 at College Station, Texas.

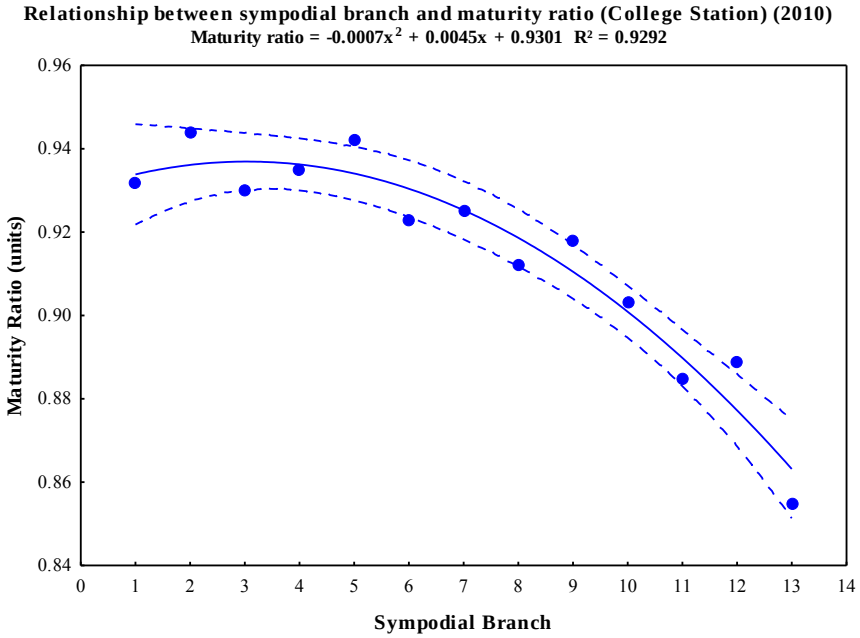

Figure B. 34: Relationship between sympodial branch and maturity ratio (AFIS) across genotypes in 2010 at College Station, Texas.

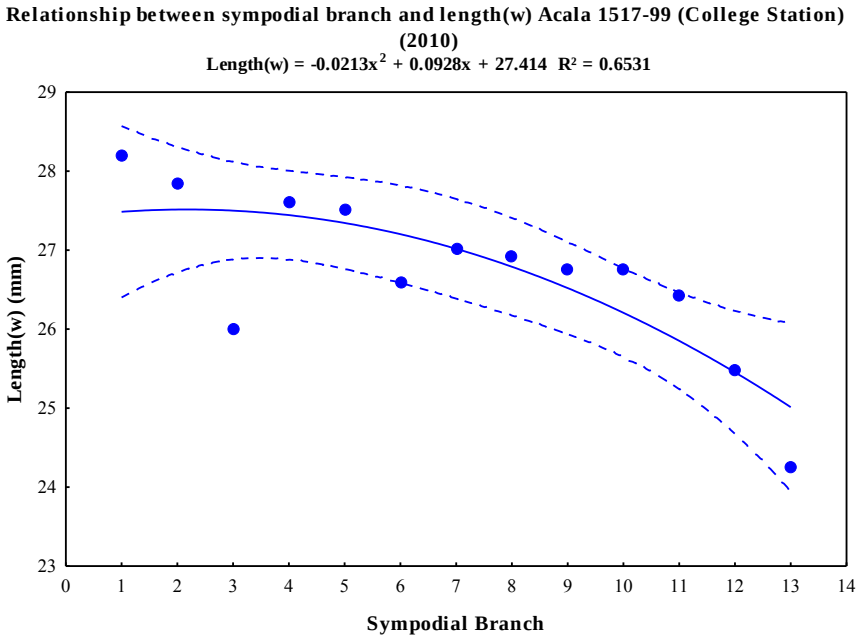

Figure B. 35: Relationship between sympodial branch and length (w) (AFIS) for Acala 1517-99 in 2010 at College Station, Texas.

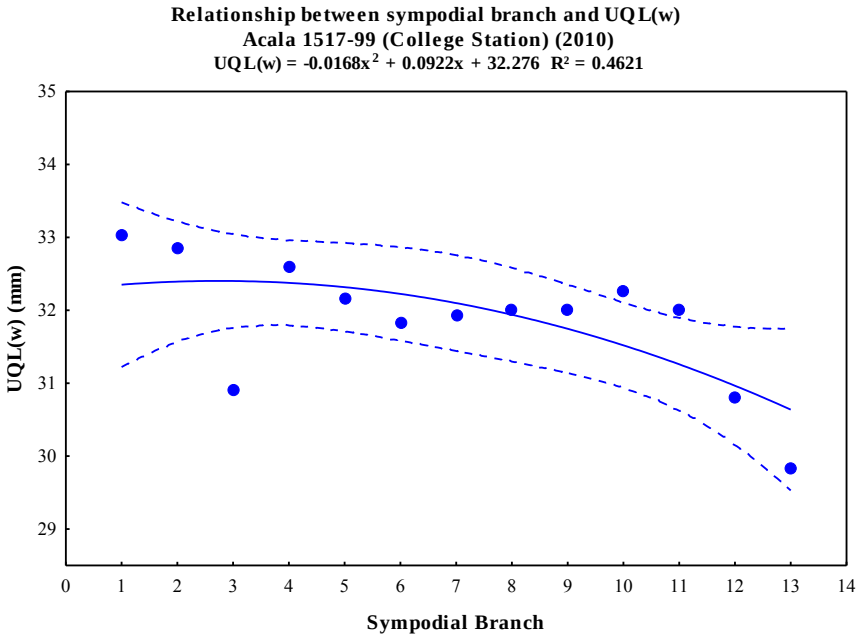

Figure B. 36: Relationship between sympodial branch and UQL (w) (AFIS) for Acala 1517-99 in 2010 at College Station, Texas.

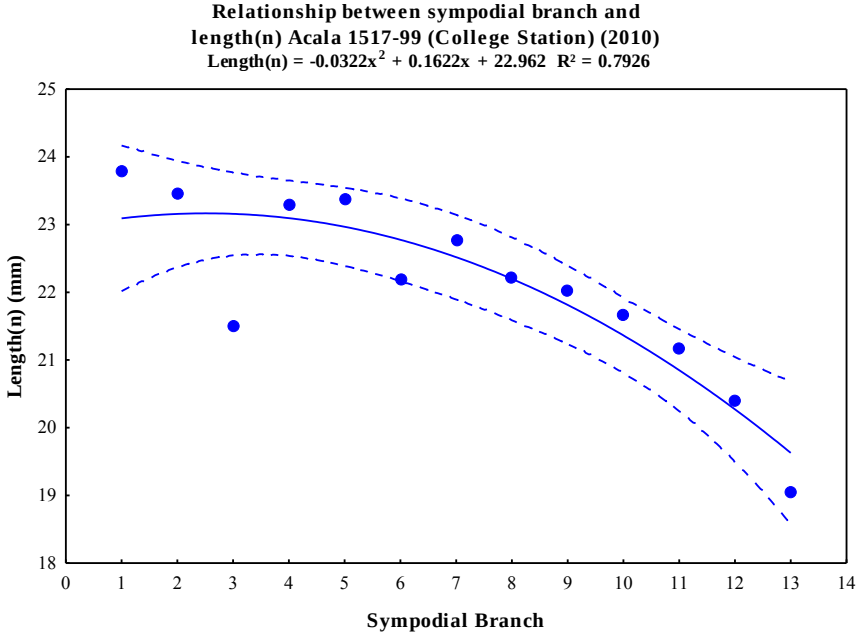

Figure B. 37: Relationship between sympodial branch and length (n) (AFIS) for Acala 1517-99 in 2010 at College Station, Texas.

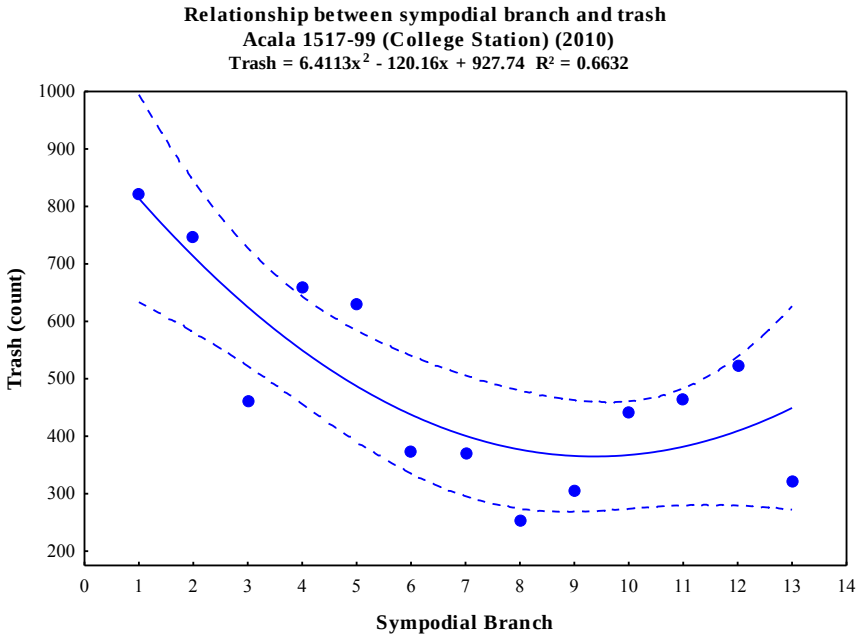

Figure B. 38: Relationship between sympodial branch and trash (AFIS) for Acala 1517-99 in 2010 at College Station, Texas.

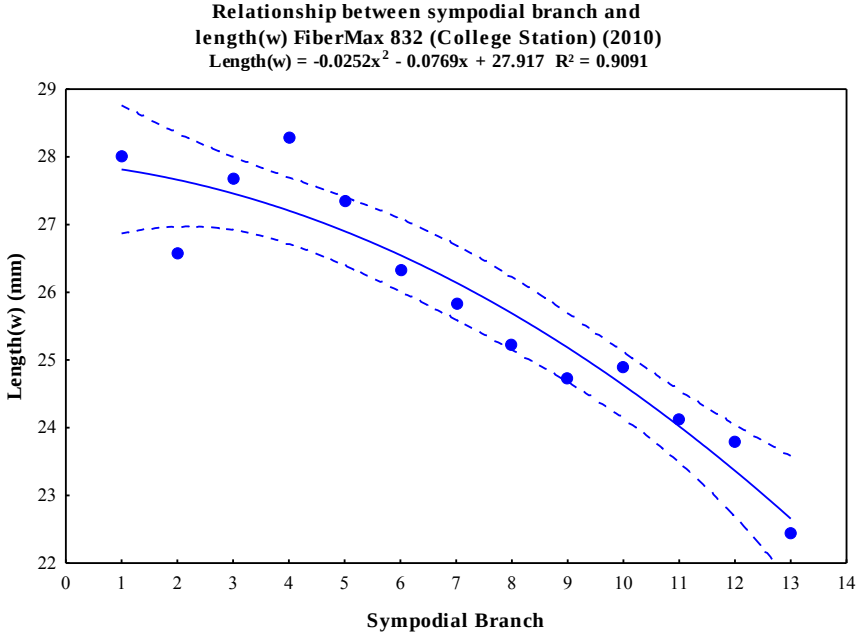

Figure B. 39: Relationship between sympodial branch and length (w) (AFIS) for FiberMax 832 in 2010 at College Station, Texas.

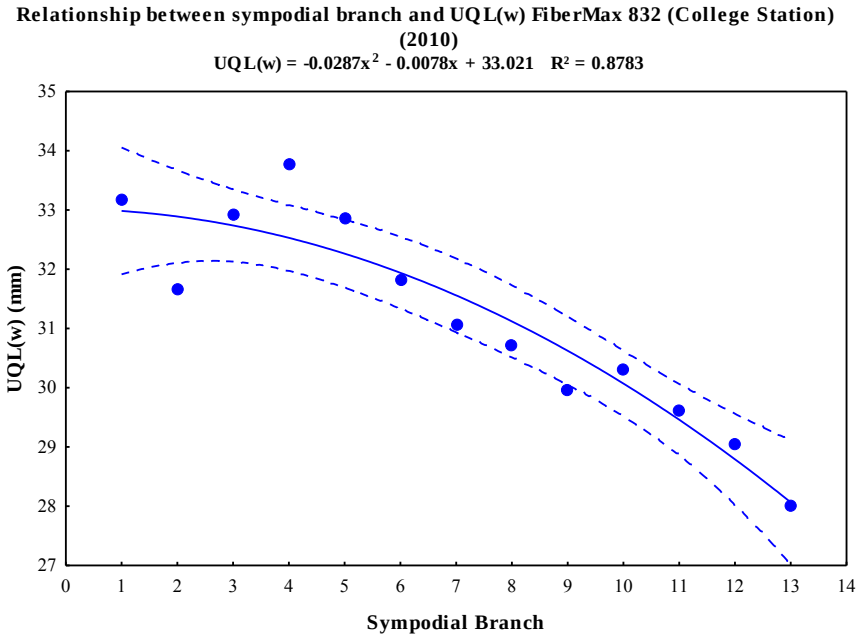

Figure B. 40: Relationship between sympodial branch and UQL (w) (AFIS) for FiberMax 832 in 2010 at College Station, Texas.

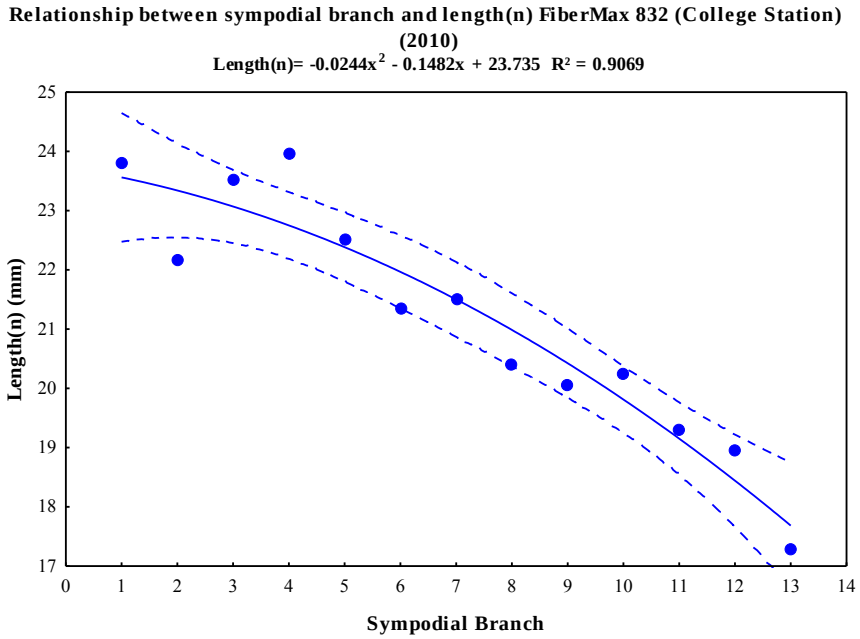

Figure B. 41: Relationship between sympodial branch and length (n) (AFIS) for FiberMax 832 in 2010 at College Station, Texas.

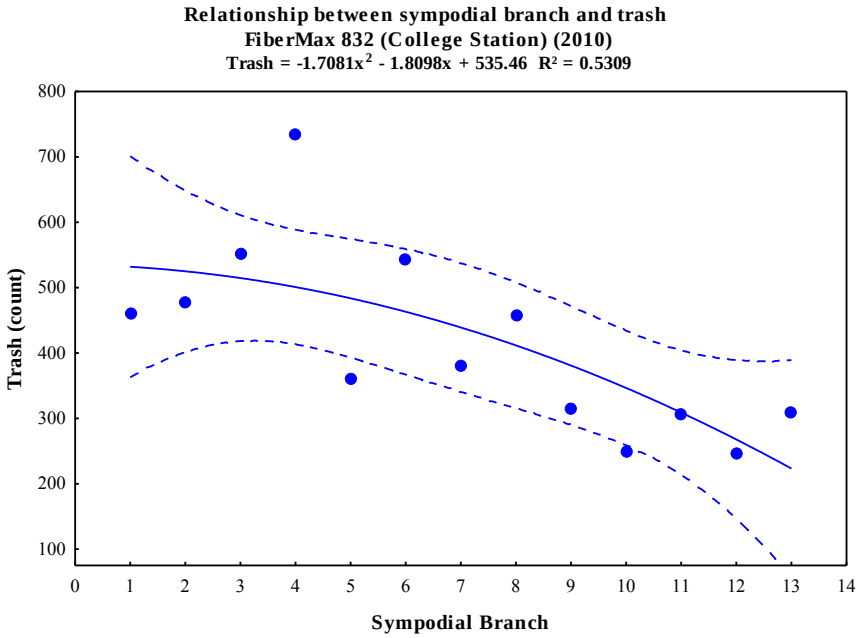

Figure B. 42: Relationship between sympodial branch and trash (AFIS) for FiberMax 832 in 2010 at College Station, Texas.

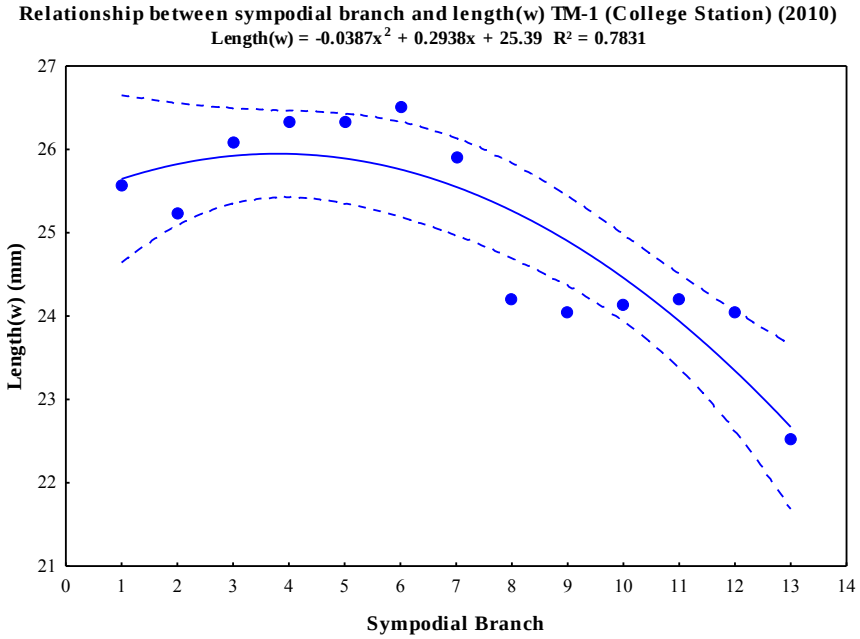

Figure B. 43: Relationship between sympodial branch and length (w) (AFIS) for TM-1 in 2010 at College Station, Texas.

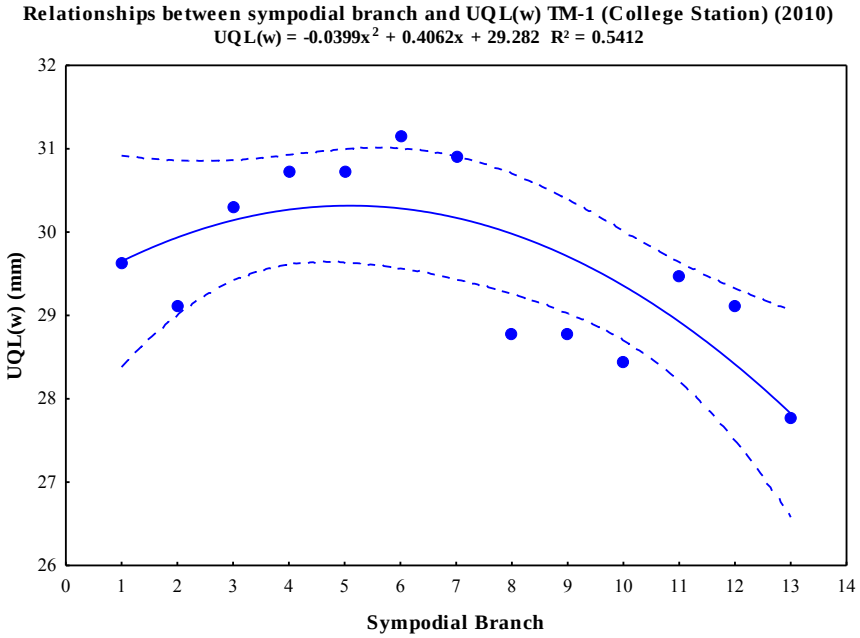

Figure B. 44: Relationship between sympodial branch and UQL (w) (AFIS) for TM-1 in 2010 at College Station, Texas.

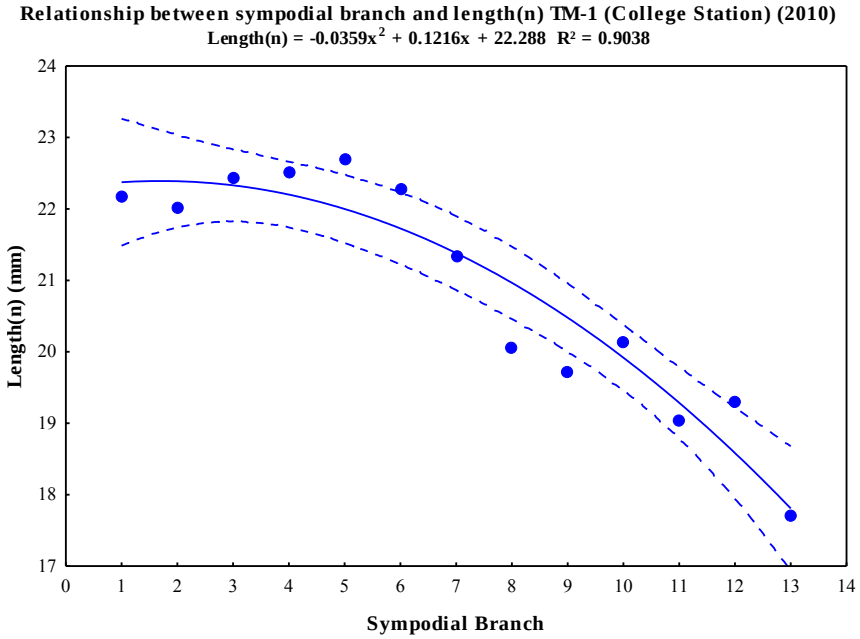

Figure B. 45: Relationship between sympodial branch and length (n) (AFIS) for TM-1 in 2010 at College Station, Texas.

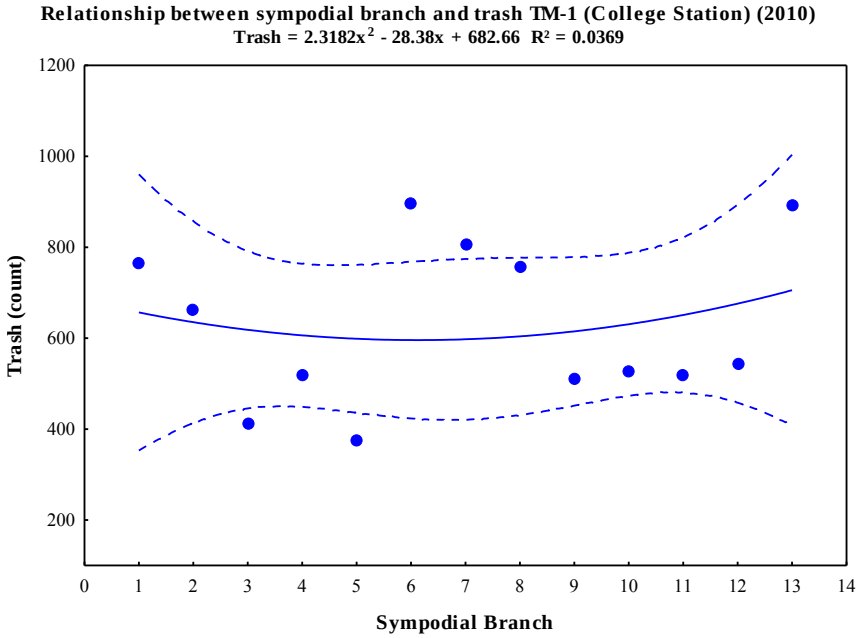

Figure B. 46: Relationship between sympodial branch and trash (AFIS) for TM-1 in 2010 at College Station, Texas.

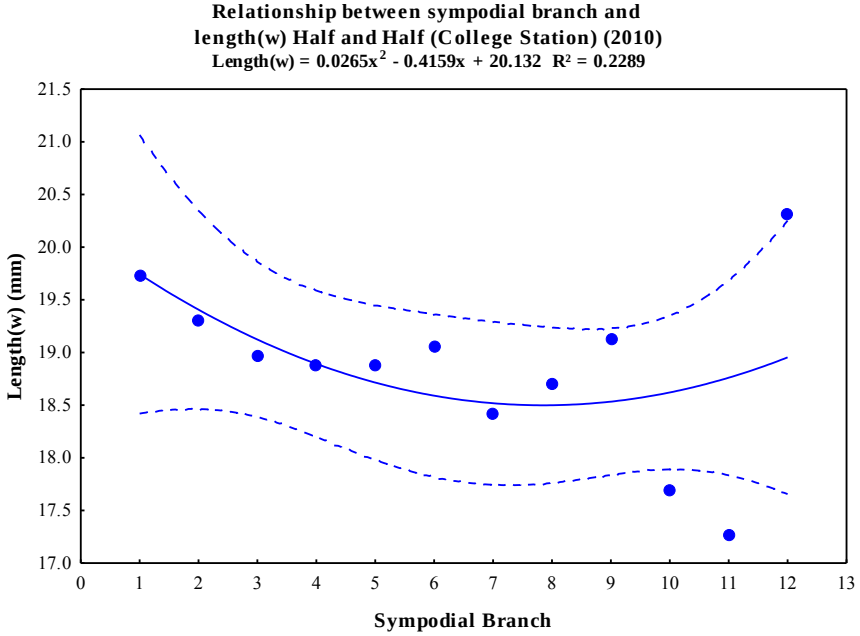

Figure B. 47: Relationship between sympodial branch and length (w) (AFIS) for Half and Half in 2010 at College Station, Texas.

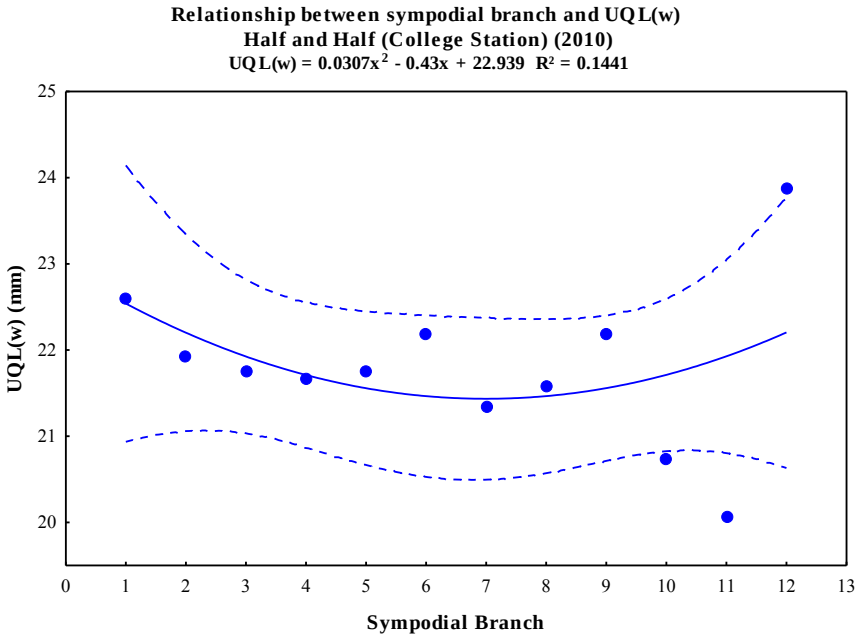

Figure B. 48: Relationship between sympodial branch and UQL (w) (AFIS) for Half and Half in 2010 at College Station, Texas.

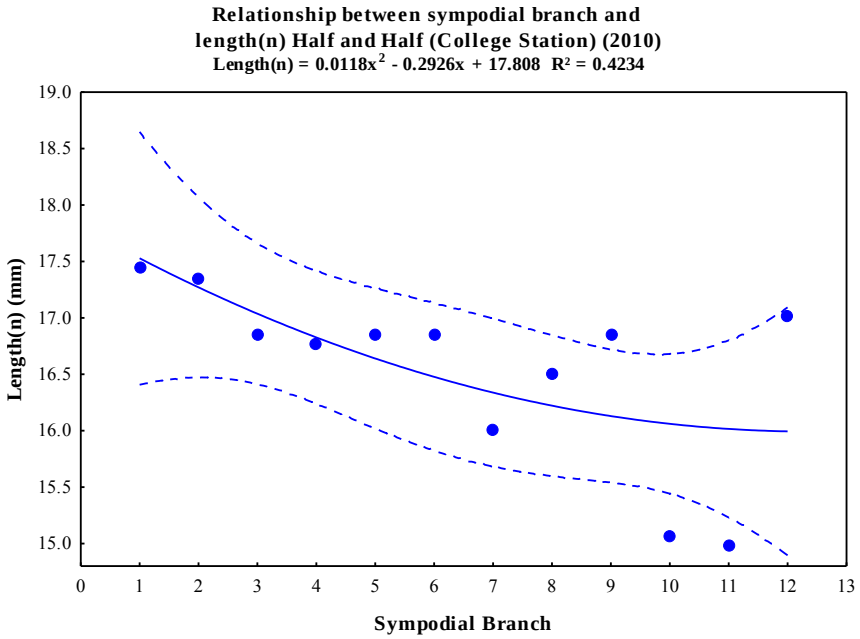

Figure B. 49: Relationship between sympodial branch and length (n) (AFIS) for Half and Half in 2010 at College Station, Texas.

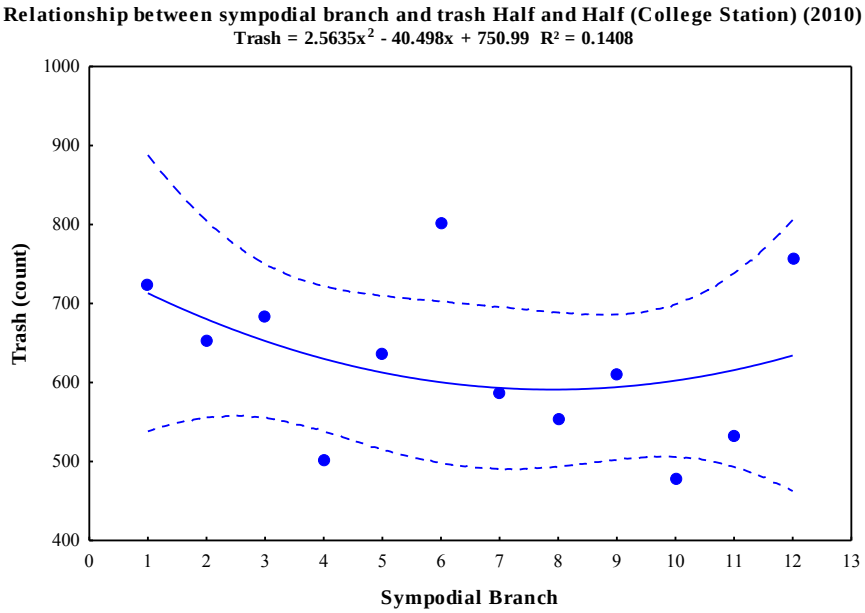

Figure B. 50: Relationship between sympodial branch and trash (AFIS) for Half and Half in 2010 at College Station, Texas.

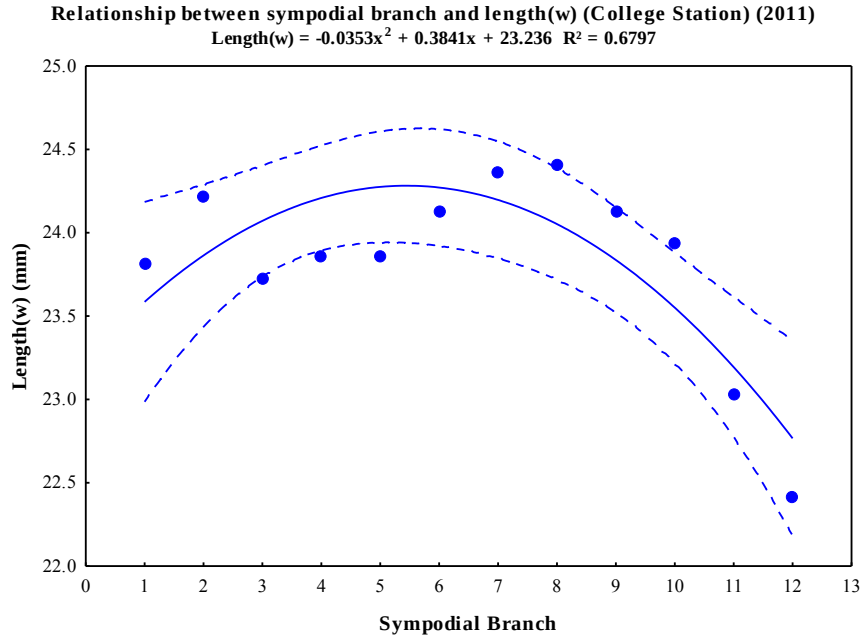

Figure B. 51: Relationship between sympodial branch and length (w) (AFIS) across genotypes in 2011 at College Station, Texas.

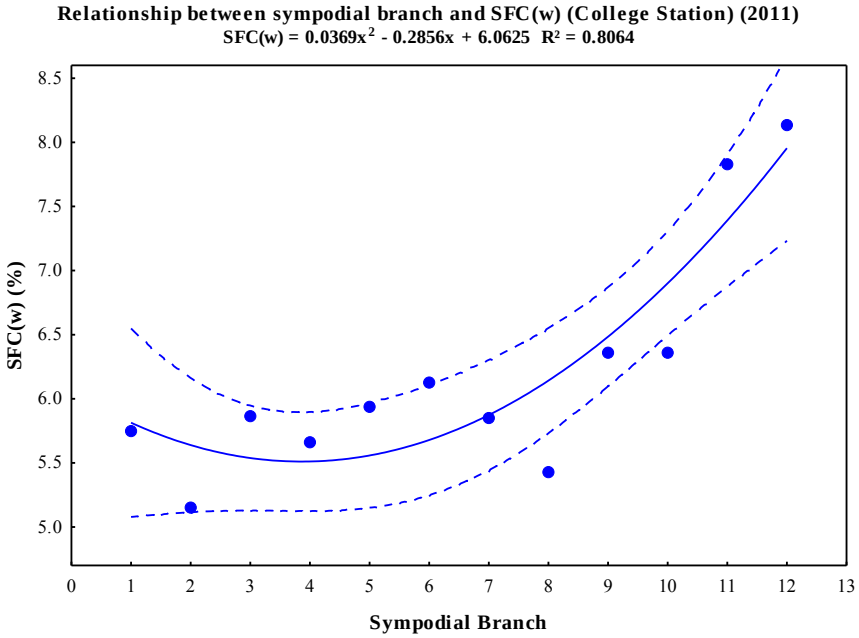

Figure B. 52: Relationship between sympodial branch and SFC (w) (AFIS) across genotypes in 2011 at College Station, Texas.

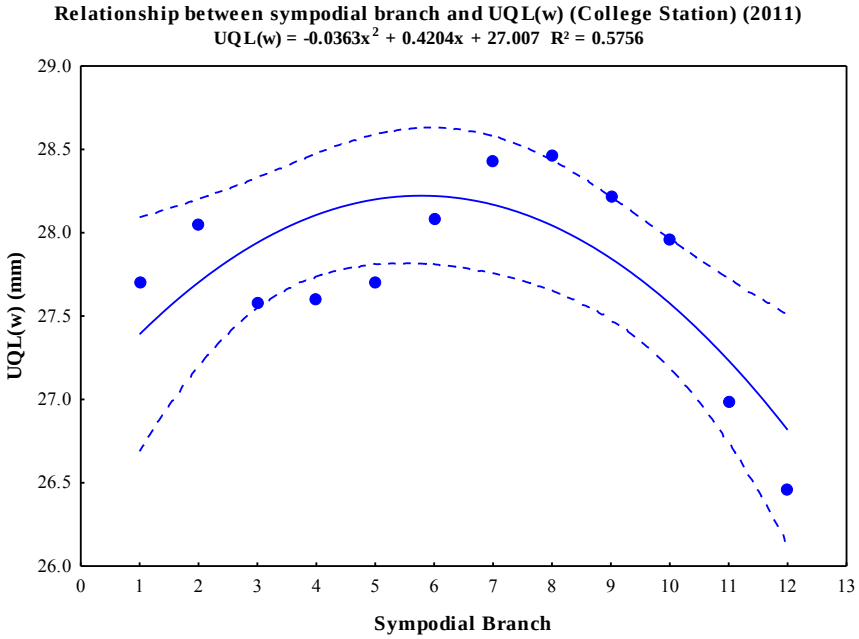

Figure B. 53: Relationship between sympodial branch and UQL (w) (AFIS) across genotypes in 2011 at College Station, Texas.

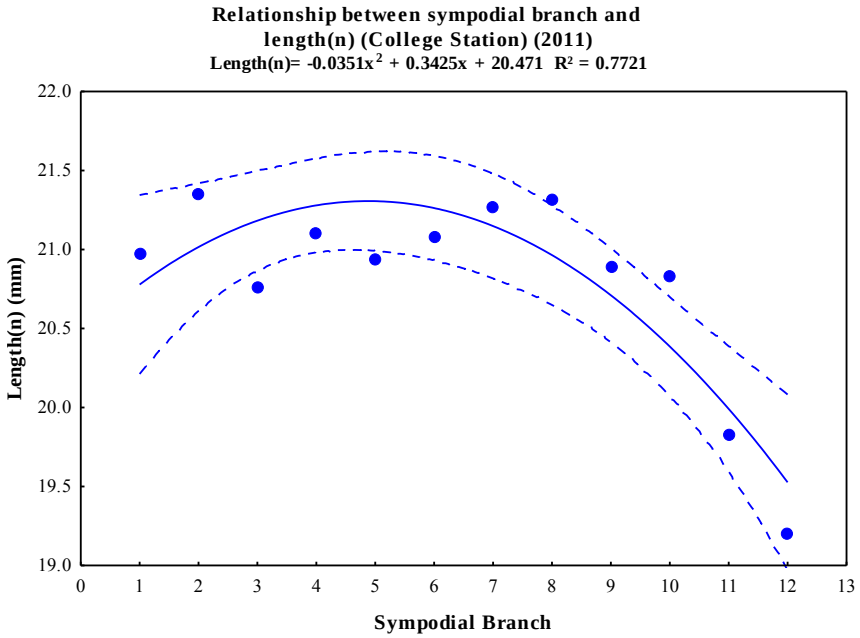

Figure B. 54: Relationship between sympodial branch and length (n) (AFIS) across genotypes in 2011 at College Station, Texas.

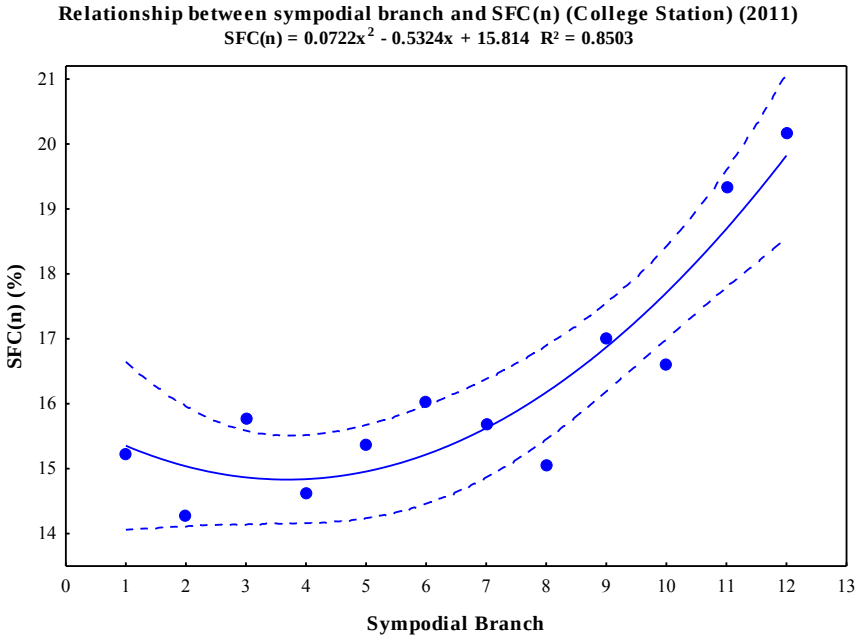

Figure B. 55: Relationship between sympodial branch and length (n) (AFIS) across genotypes in 2011 at College Station, Texas.

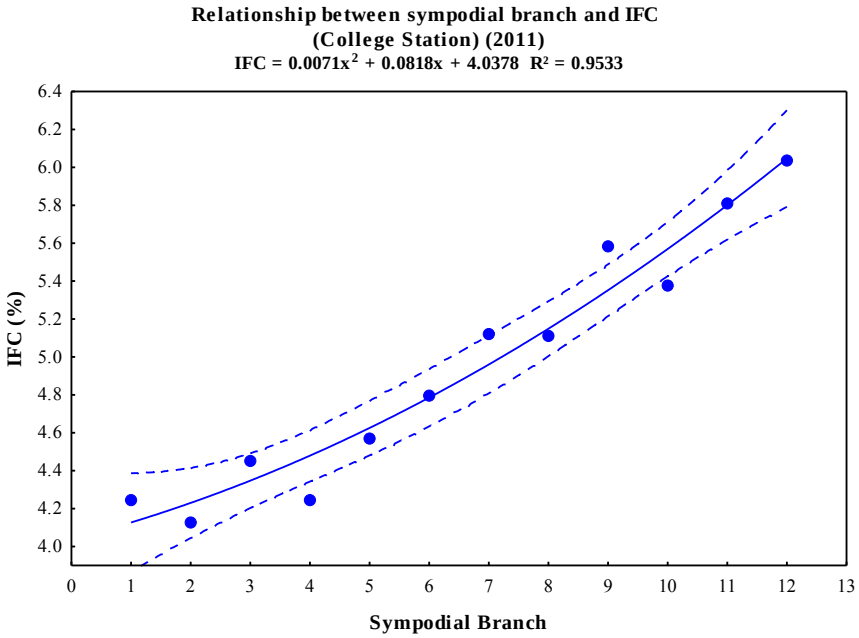

Figure B. 56: Relationship between sympodial branch and IFC (AFIS) across genotypes in 2011 at College Station, Texas.

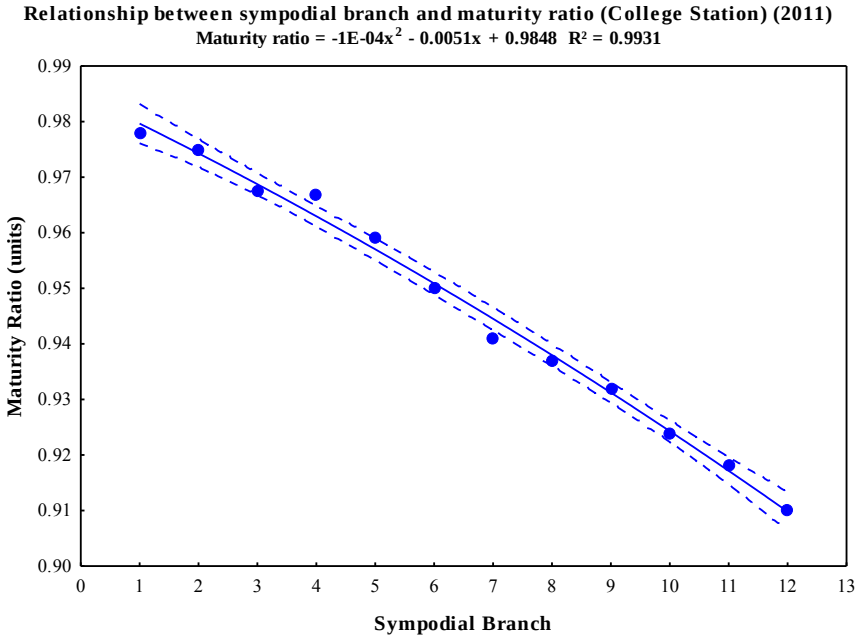

Figure B. 57: Relationship between sympodial branch and maturity ratio (AFIS) across genotypes in 2011 at College Station, Texas.

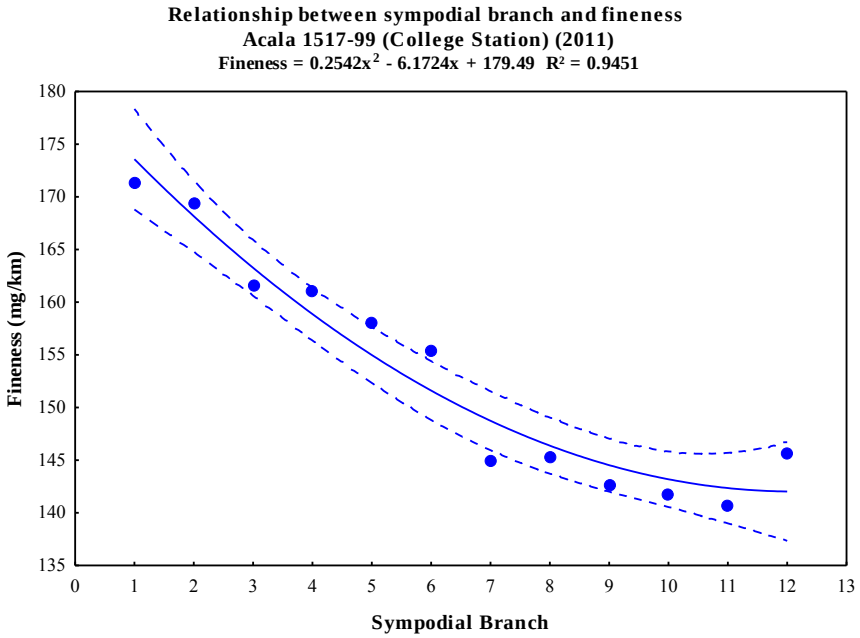

Figure B. 58: Relationship between sympodial branch and fineness (AFIS) for Acala 1517-99 in 2011 at College Station, Texas.

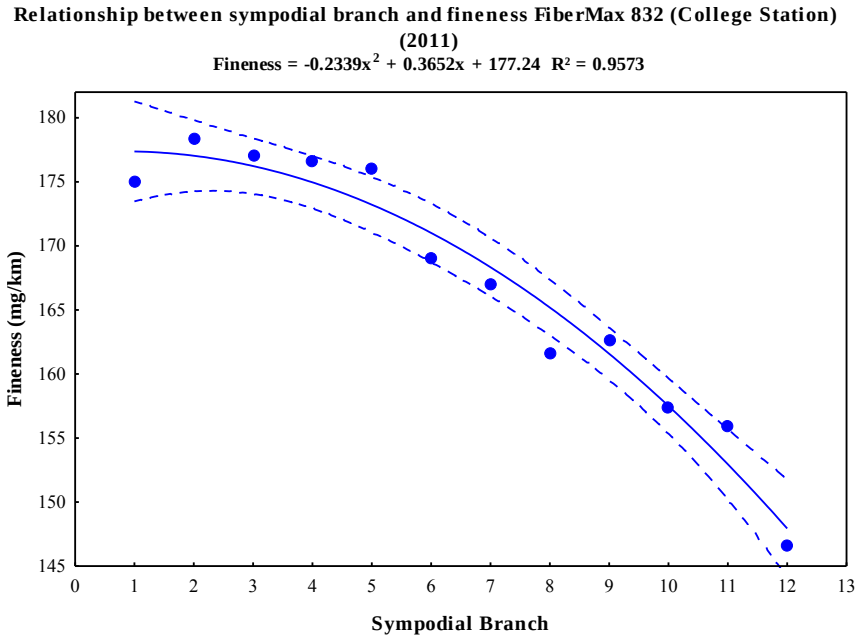

Figure B. 59: Relationship between sympodial branch and fineness (AFIS) for FiberMax 832 in 2011 at College Station, Texas.

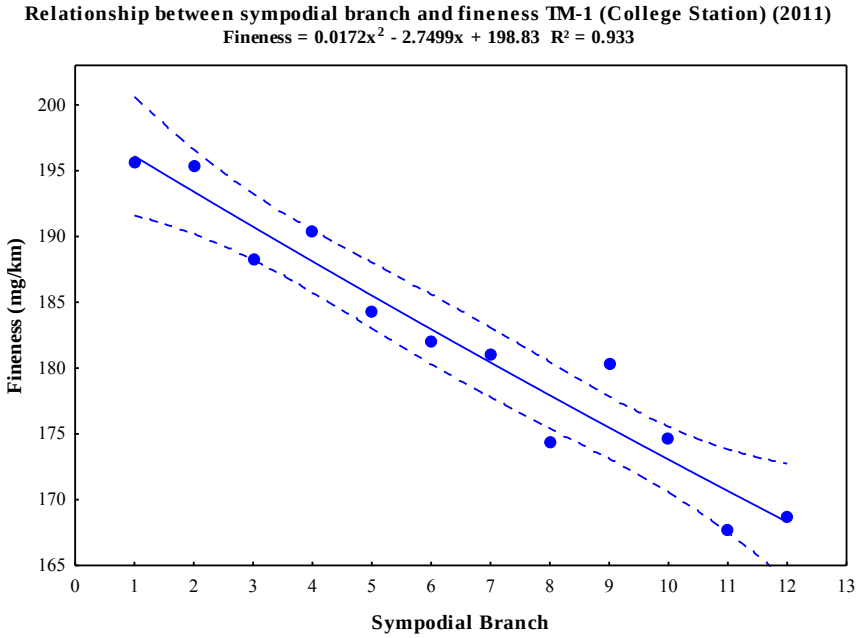

Figure B. 60: Relationship between sympodial branch and fineness (AFIS) for TM-1 in 2011 at College Station, Texas.

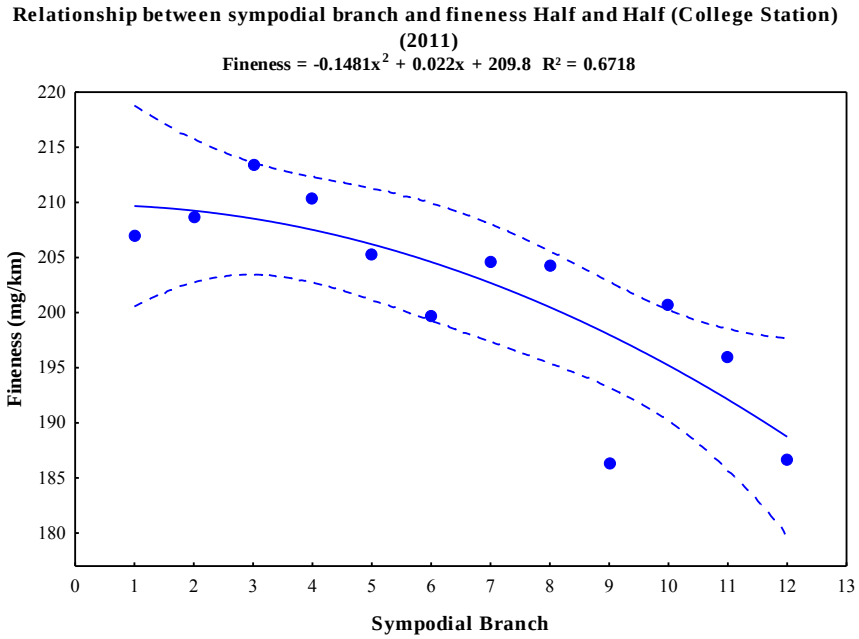

Figure B. 61: Relationship between sympodial branch and fineness (AFIS) for Half and Half in 2011 at College Station, Texas.

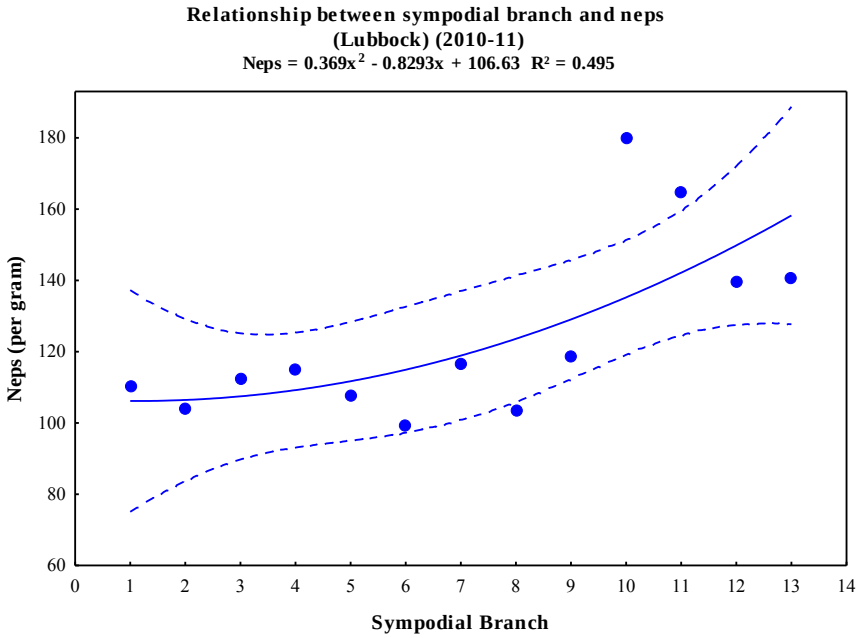

Figure B. 62: Relationship between sympodial branch and neps (AFIS) across genotypes in 2010 and 2011 at Lubbock, Texas.

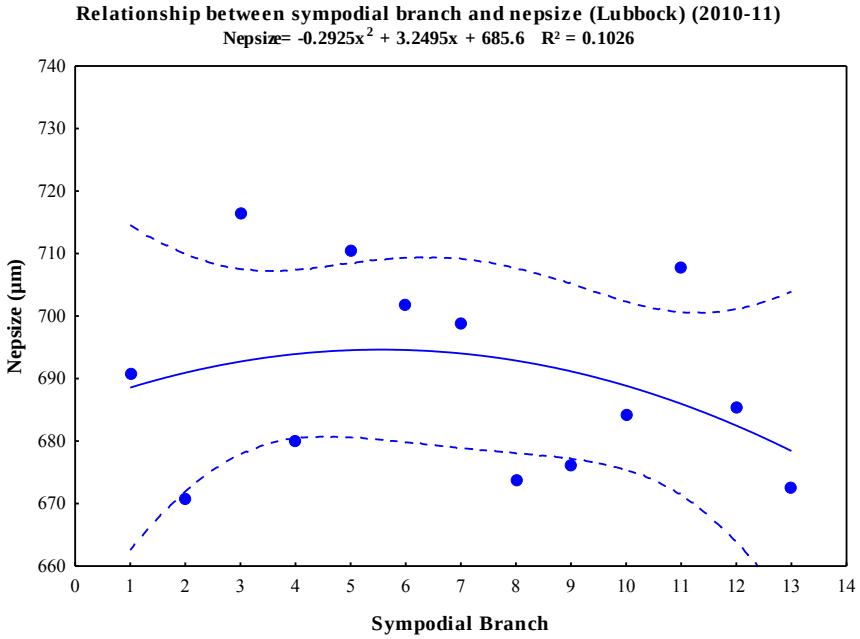

Figure B. 63: Relationship between sympodial branch and nepsize (AFIS) across genotypes in 2010 and 2011 at Lubbock, Texas.

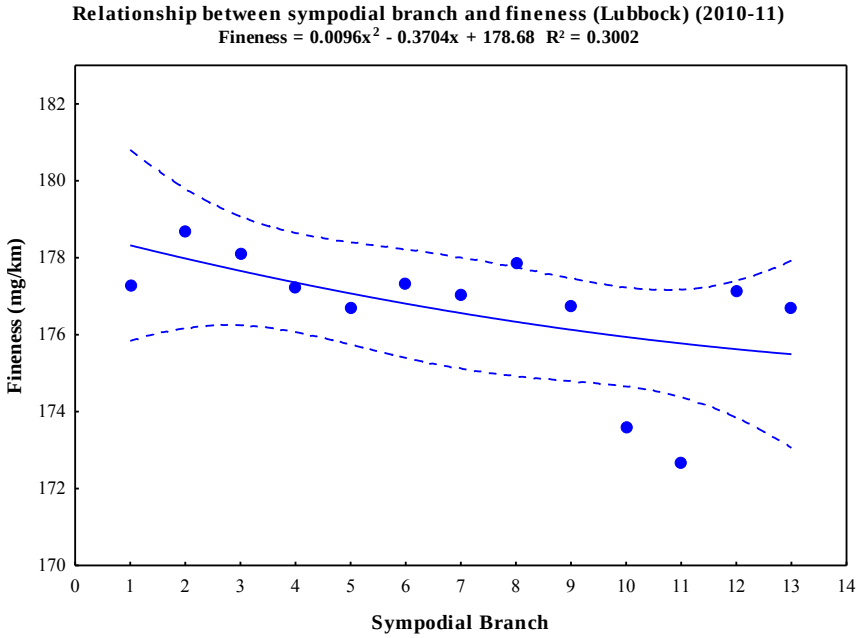

Figure B. 64: Relationship between sympodial branch and fineness (AFIS) across genotypes in 2010 and 2011 at Lubbock, Texas.

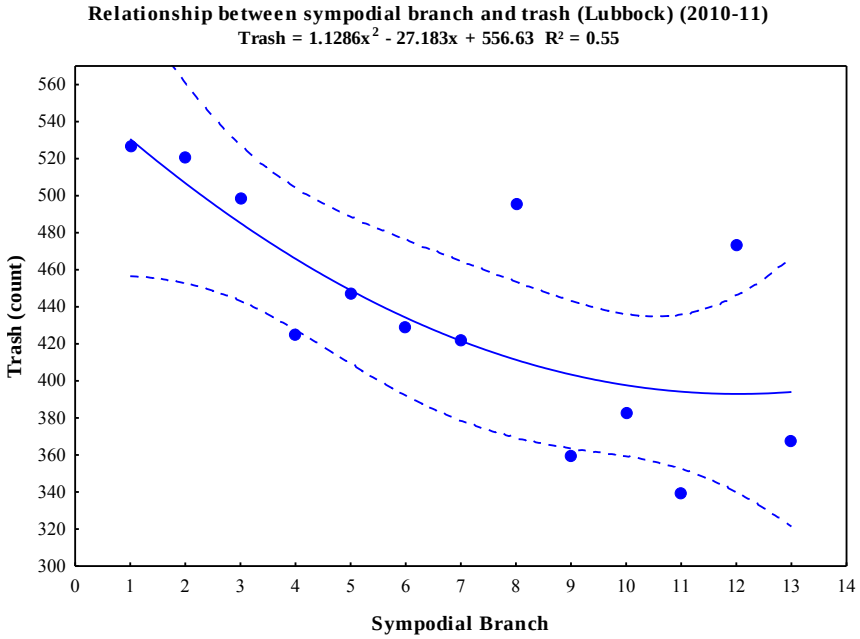

Figure B. 65: Relationship between sympodial branch and trash (AFIS) across genotypes in 2010 and 2011 at Lubbock, Texas.

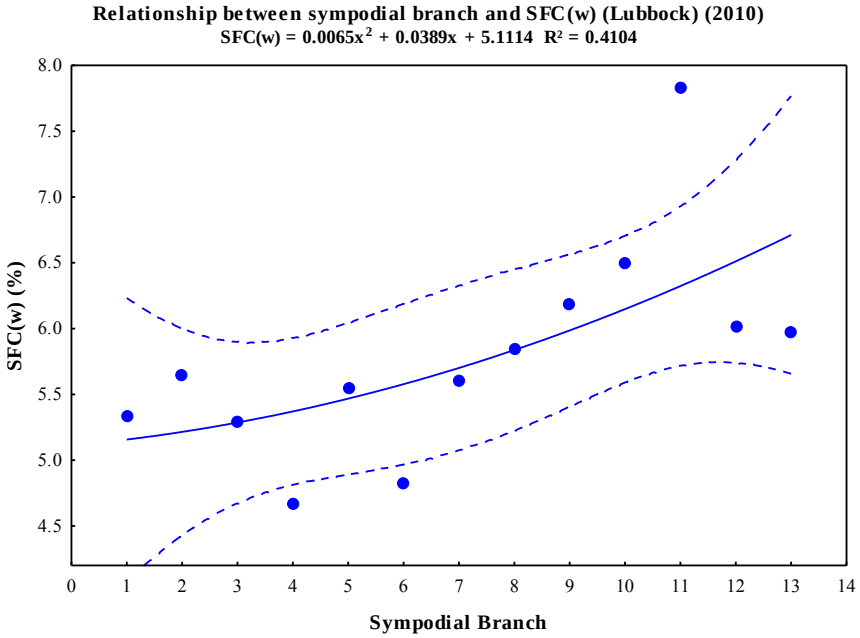

Figure B. 66: Relationship between sympodial branch and SFC (w) (AFIS) across genotypes in 2010 at Lubbock, Texas.

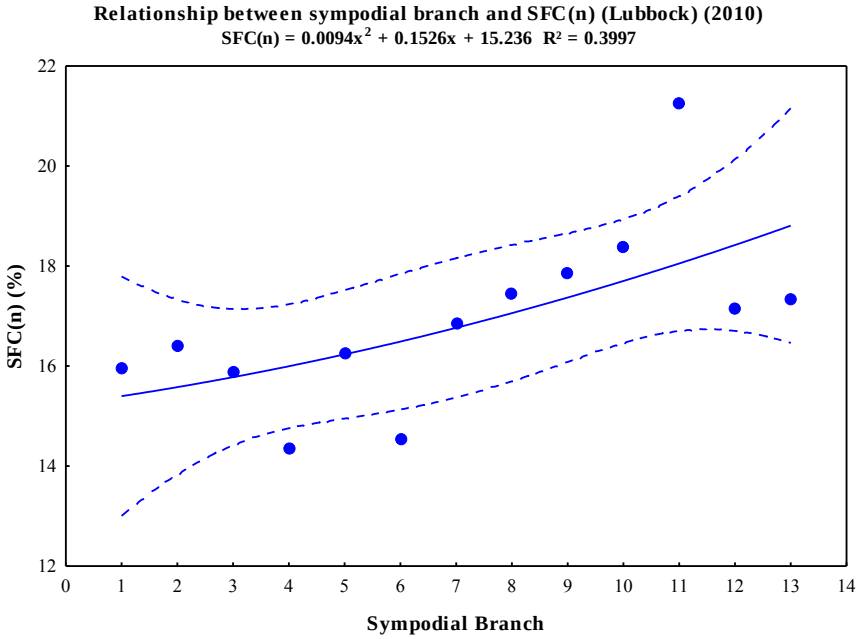

Figure B. 67: Relationship between sympodial branch and SFC (n) (AFIS) across genotypes in 2010 at Lubbock, Texas.

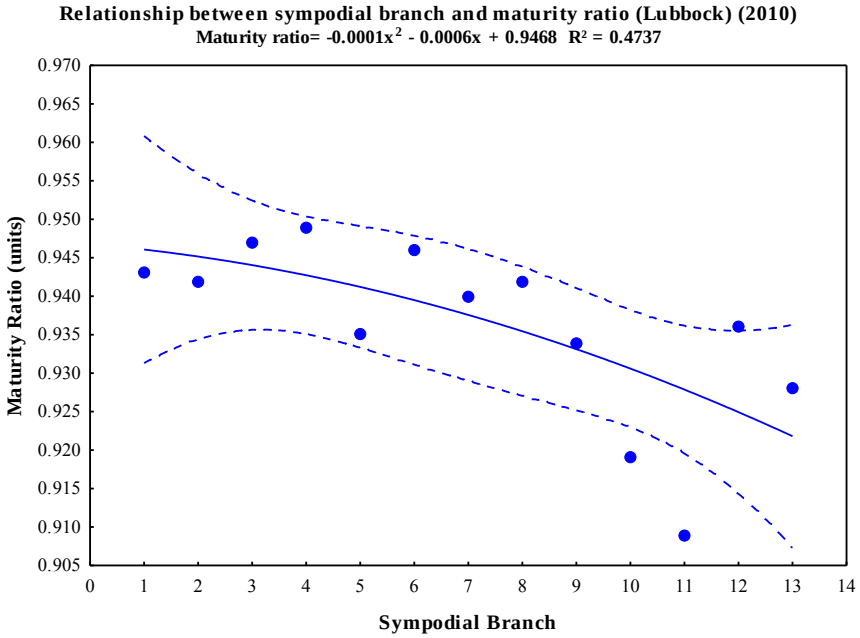

Figure B. 68: Relationship between sympodial branch and maturity ratio (AFIS) across genotypes in 2010 at Lubbock, Texas.

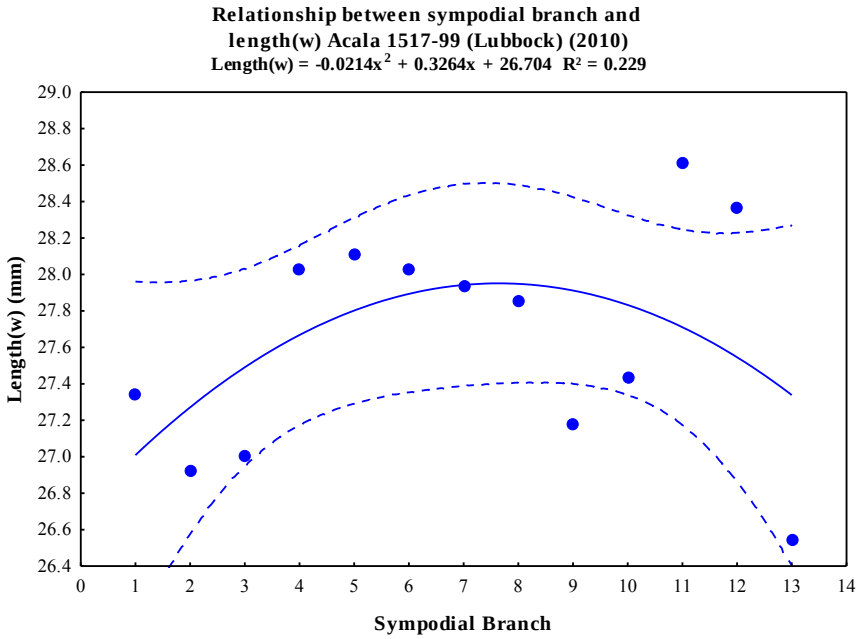

Figure B. 69: Relationship between sympodial branch and length (w) (AFIS) for Acala 1517-99 in 2010 at Lubbock, Texas.

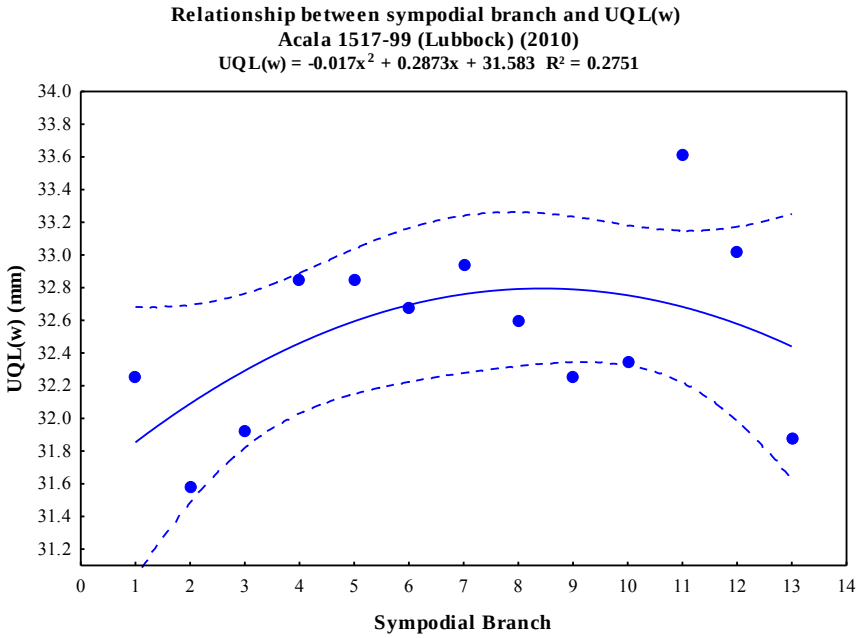

Figure B. 70: Relationship between sympodial branch and UQL (w) (AFIS) for Acala 1517-99 in 2010 at Lubbock, Texas.

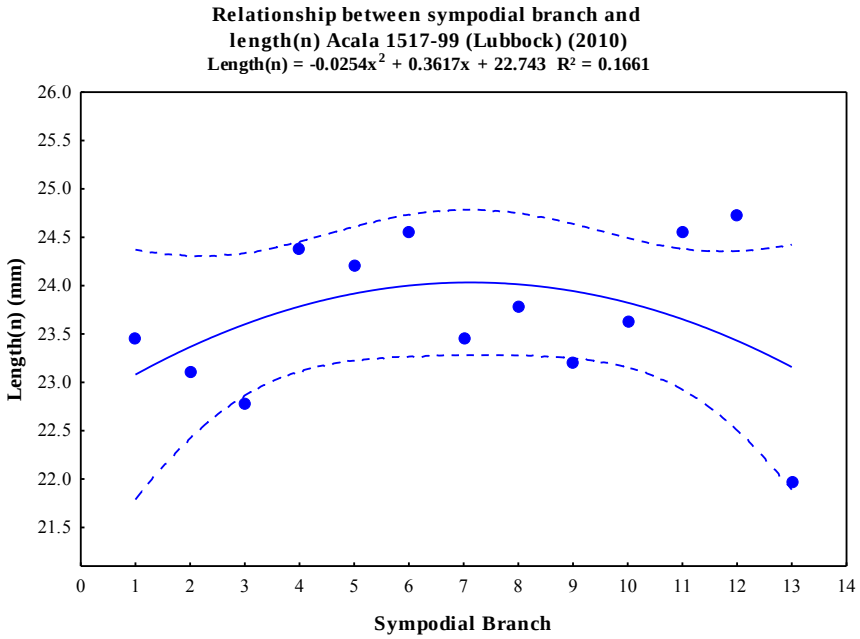

Figure B. 71: Relationship between sympodial branch and length (n) (AFIS) for Acala 1517-99 in 2010 at Lubbock, Texas.

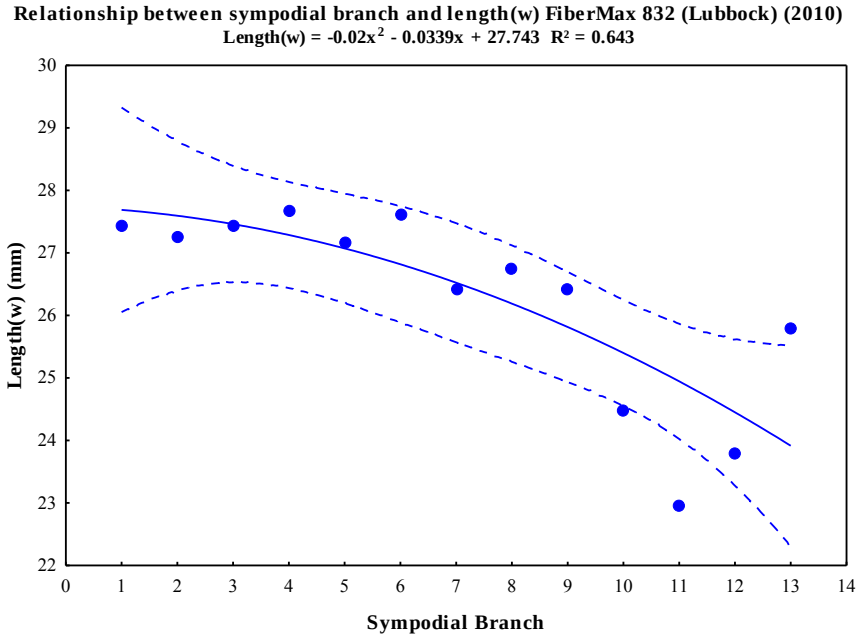

Figure B. 72: Relationship between sympodial branch and length (w) (AFIS) for FiberMax 832 in 2010 at Lubbock, Texas.

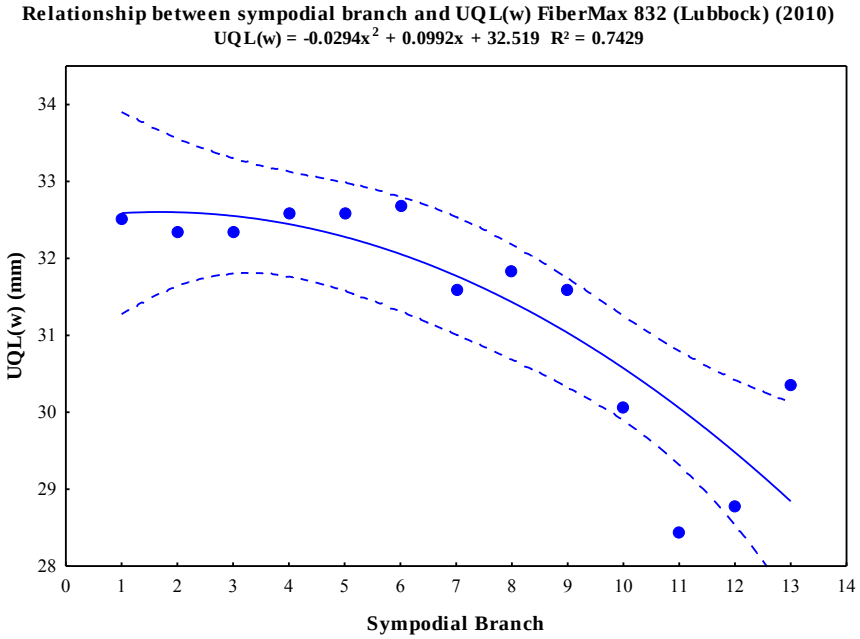

Figure B. 73: Relationship between sympodial branch and UQL (w) (AFIS) for FiberMax 832 in 2010 at Lubbock, Texas.

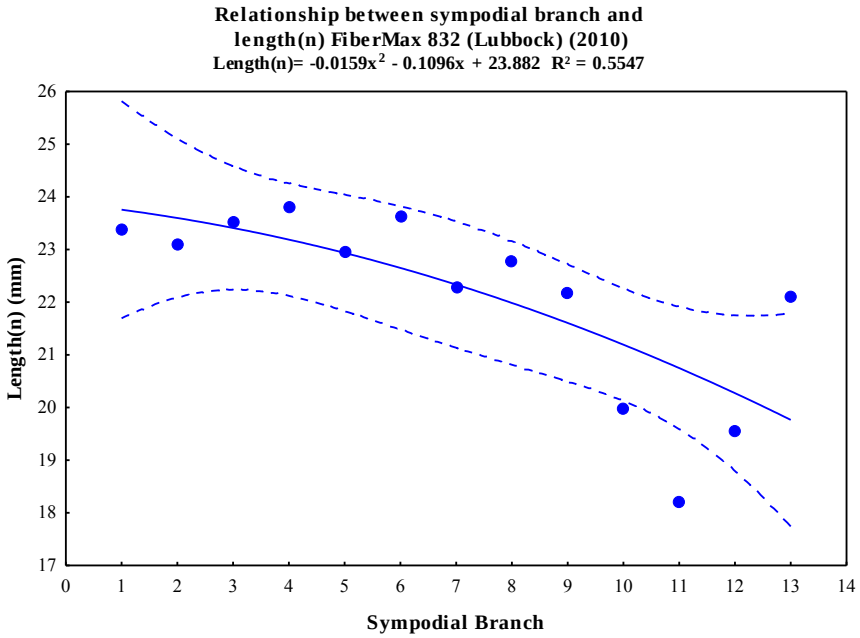

Figure B. 74: Relationship between sympodial branch and length (n) (AFIS) for FiberMax 832 in 2010 at Lubbock, Texas.

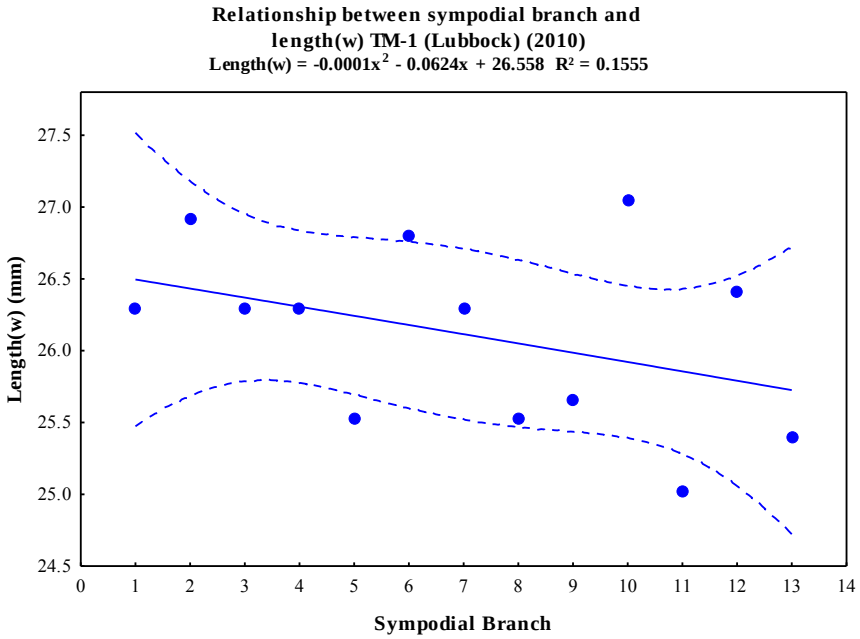

Figure B. 75: Relationship between sympodial branch and length (w) (AFIS) for TM-1 in 2010 at Lubbock, Texas.

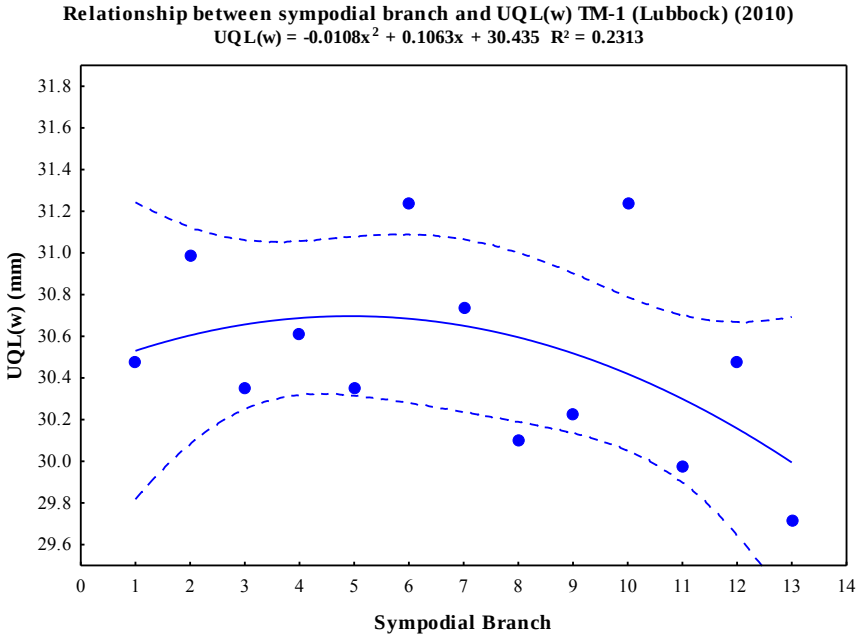

Figure B. 76: Relationship between sympodial branch and UQL (w) (AFIS) for TM-1 in 2010 at Lubbock, Texas.

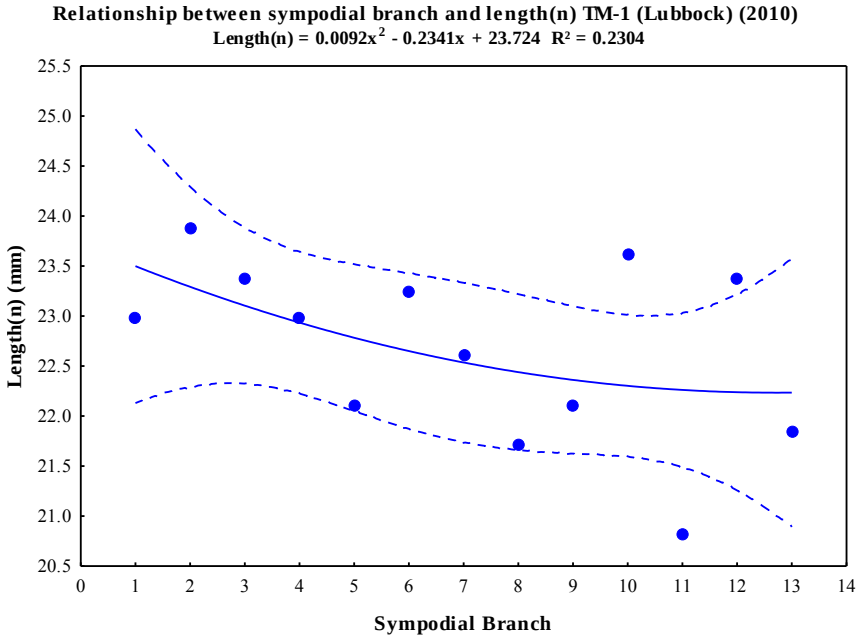

Figure B. 77: Relationship between sympodial branch and length (n) (AFIS) for TM-1 in 2010 at Lubbock, Texas.

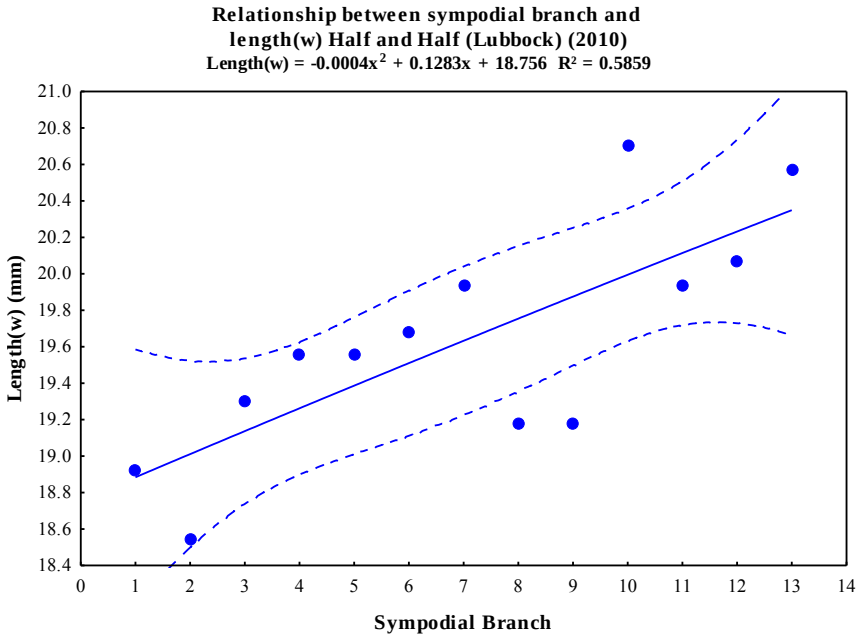

Figure B. 78: Relationship between sympodial branch and length (w) (AFIS) for Half and Half in 2010 at Lubbock, Texas.

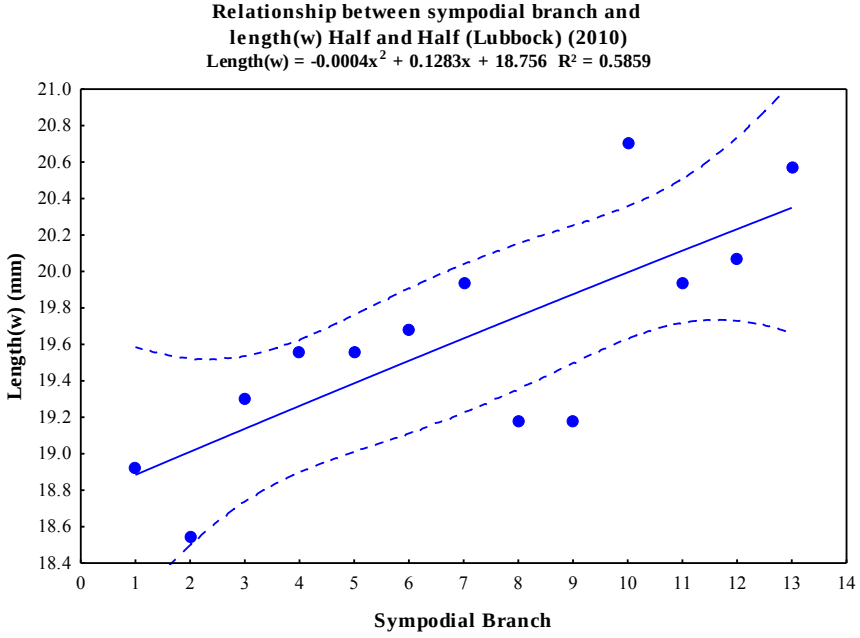

Figure B. 79: Relationship between sympodial branch and UQL (w) (AFIS) for Half and Half in 2010 at Lubbock, Texas.

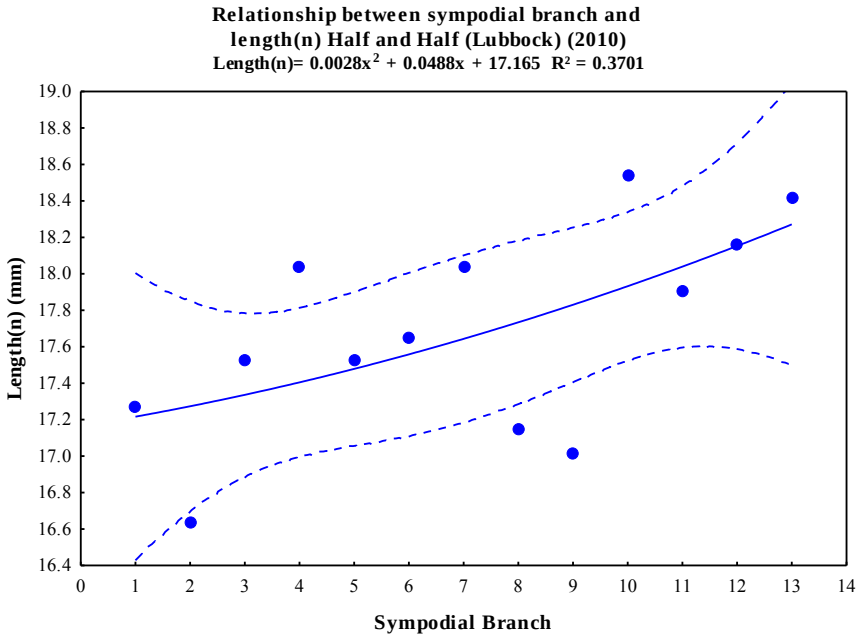

Figure B. 80: Relationship between sympodial branch and length (n) (AFIS) for Half and Half in 2010 at Lubbock, Texas.

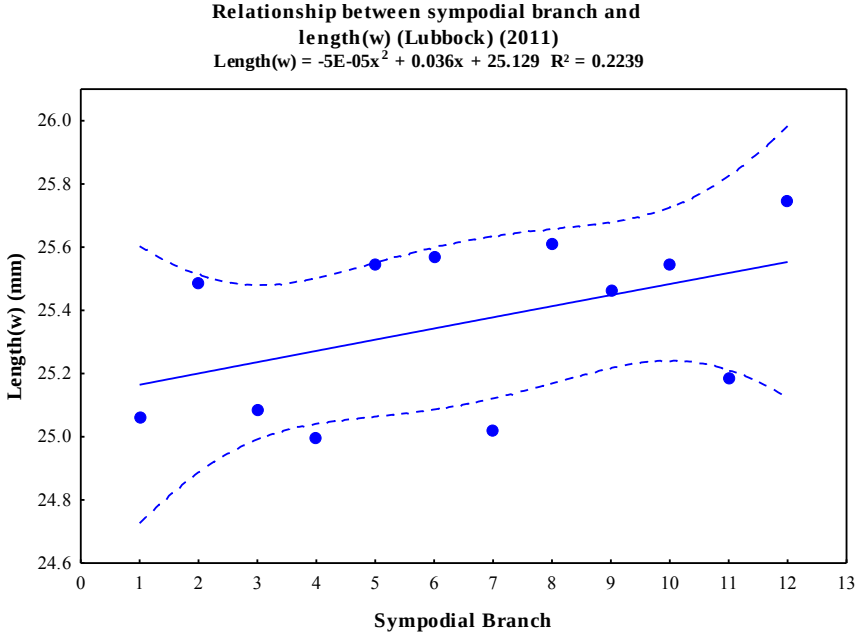

Figure B. 81: Relationship between sympodial branch and length (w) (AFIS) across genotypes in 2011 at Lubbock, Texas.

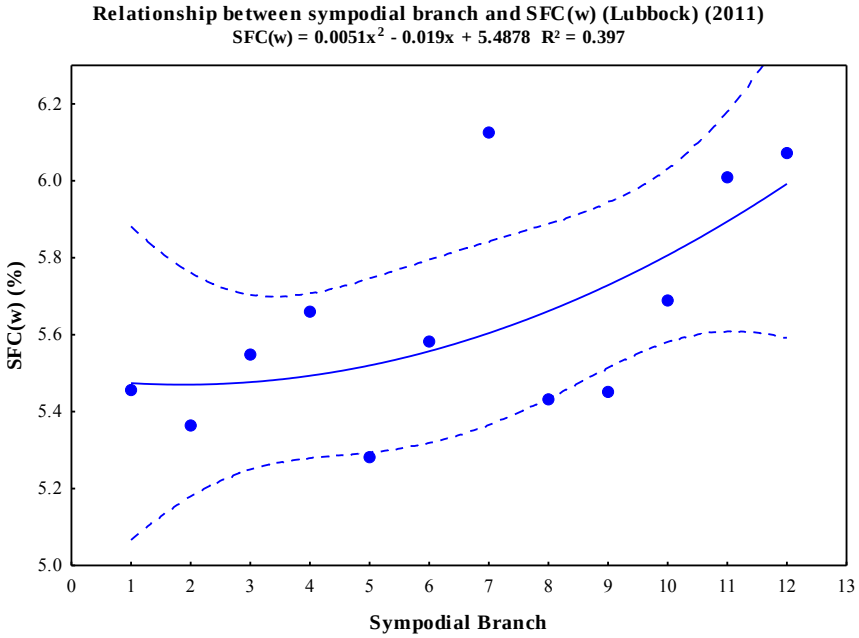

Figure B. 82: Relationship between sympodial branch and SFC (w) (AFIS) across genotypes in 2011 at Lubbock, Texas.

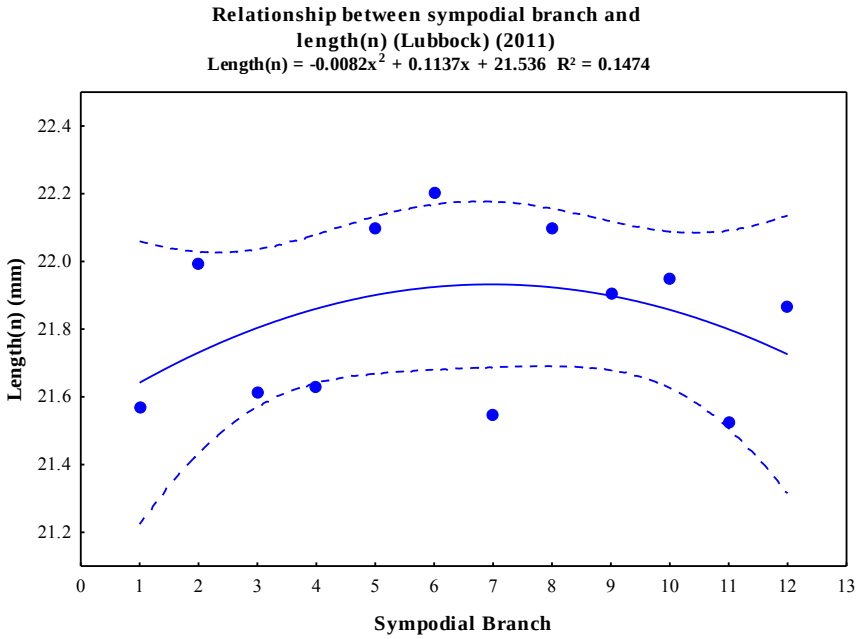

Figure B. 83: Relationship between sympodial branch and length (n) (AFIS) across genotypes in 2011 at Lubbock, Texas.

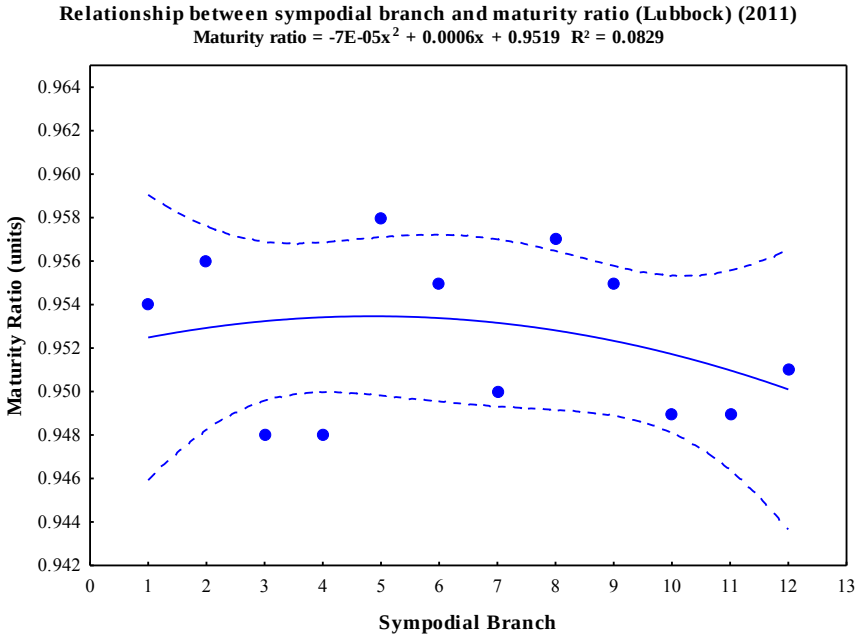

Figure B. 84: Relationship between sympodial branch and maturity ratio (AFIS) across genotypes in 2011 at Lubbock, Texas.

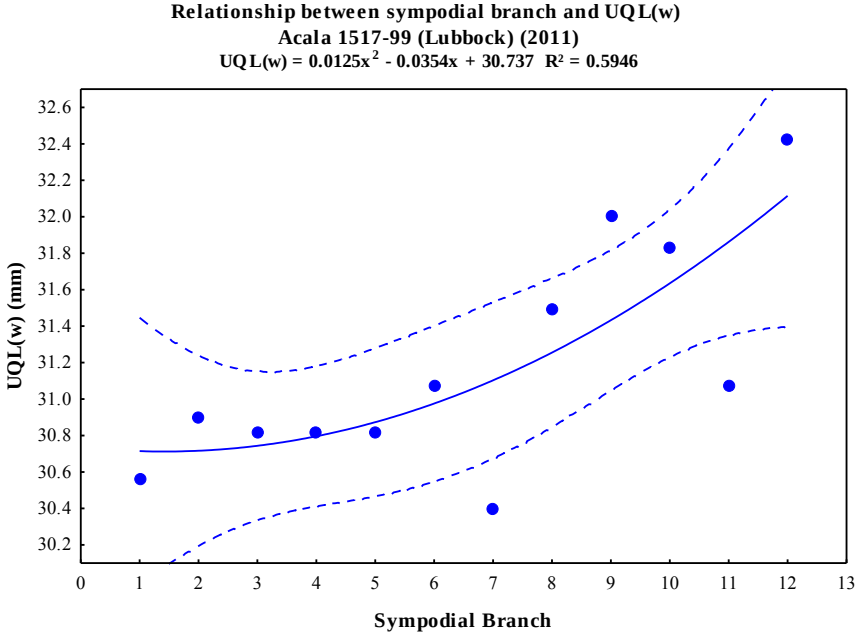

Figure B. 85: Relationship between sympodial branch and UQL (w) (AFIS) for Acala 1517-99 in 2011 at Lubbock, Texas.

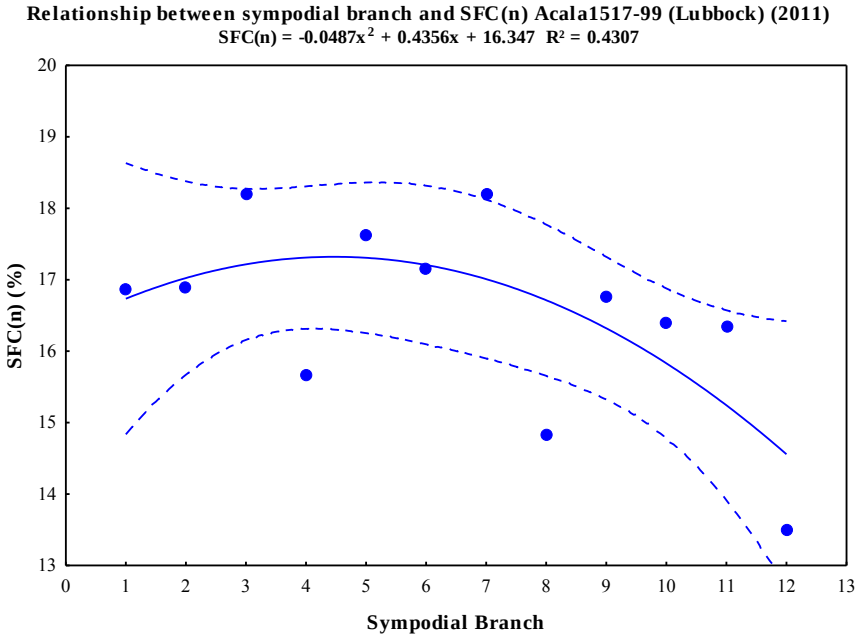

Figure B. 86: Relationship between sympodial branch and SFC (n) (AFIS) for Acala 1517-99 in 2011 at Lubbock, Texas.

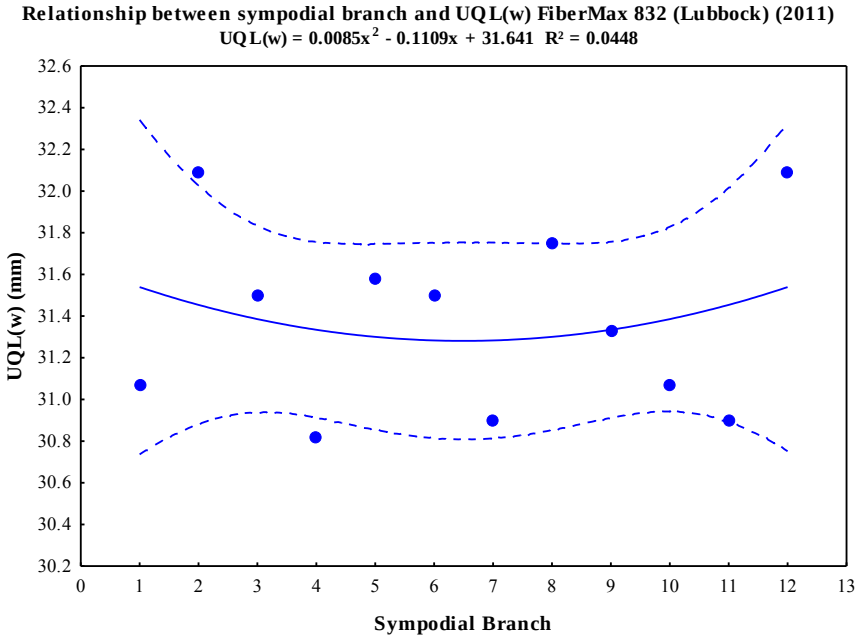

Figure B. 87: Relationship between sympodial branch and UQL (w) (AFIS) for FiberMax 832 in 2011 at Lubbock, Texas.

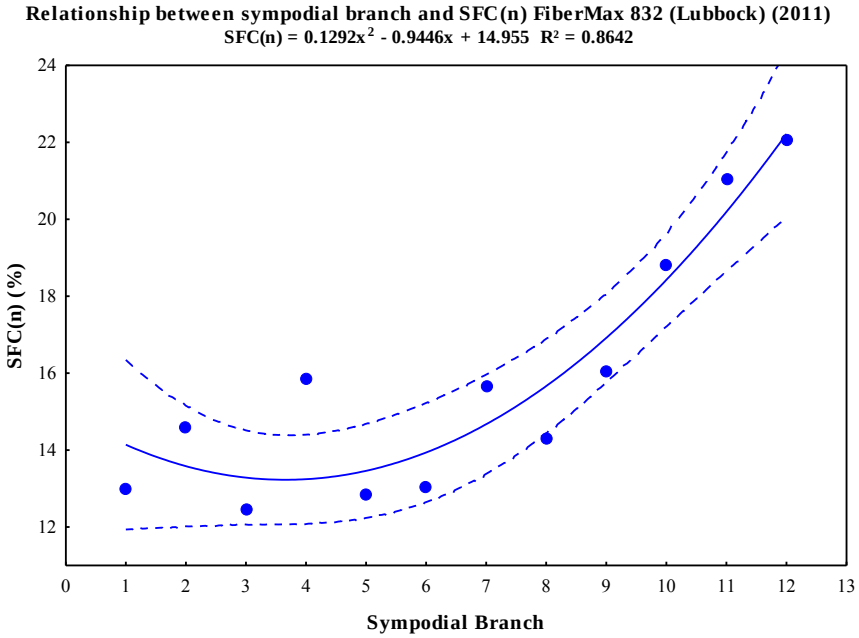

Figure B. 88: Relationship between sympodial branch and SFC (n) (AFIS) for FiberMax 832 in 2011 at Lubbock, Texas.

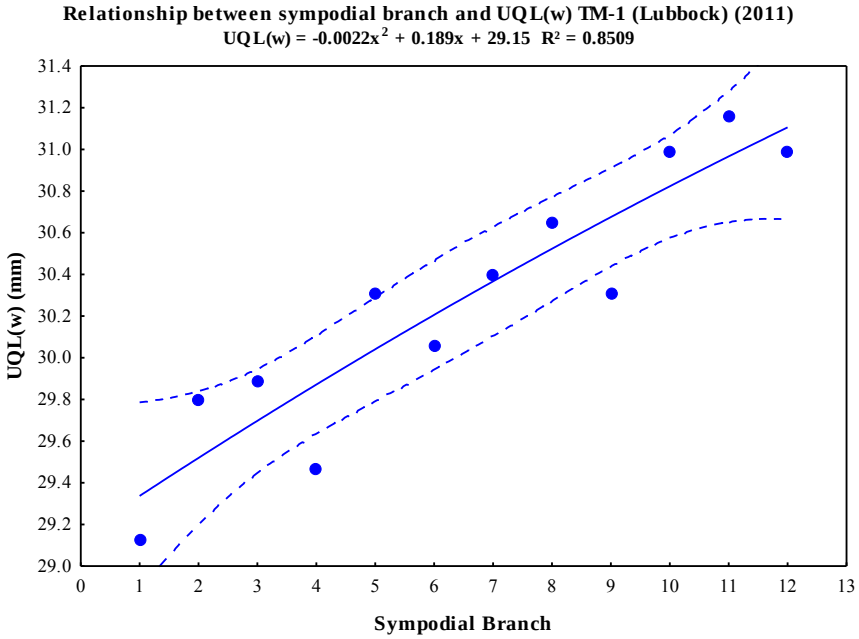

Figure B. 89: Relationship between sympodial branch and UQL (w) (AFIS) for TM-1 in 2011 at Lubbock, Texas.

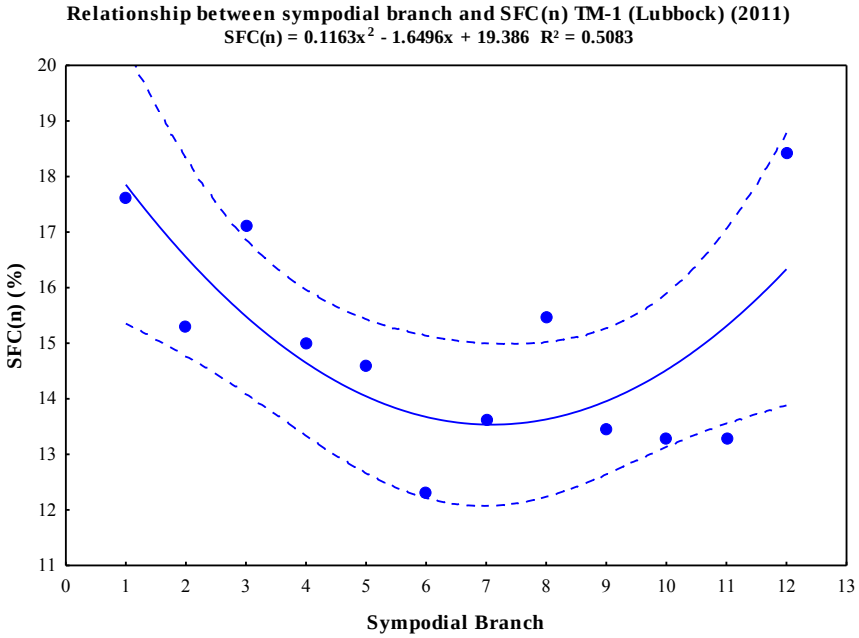

Figure B. 90: Relationship between sympodial branch and SFC (n) (AFIS) for TM-1 in 2011 at Lubbock, Texas.

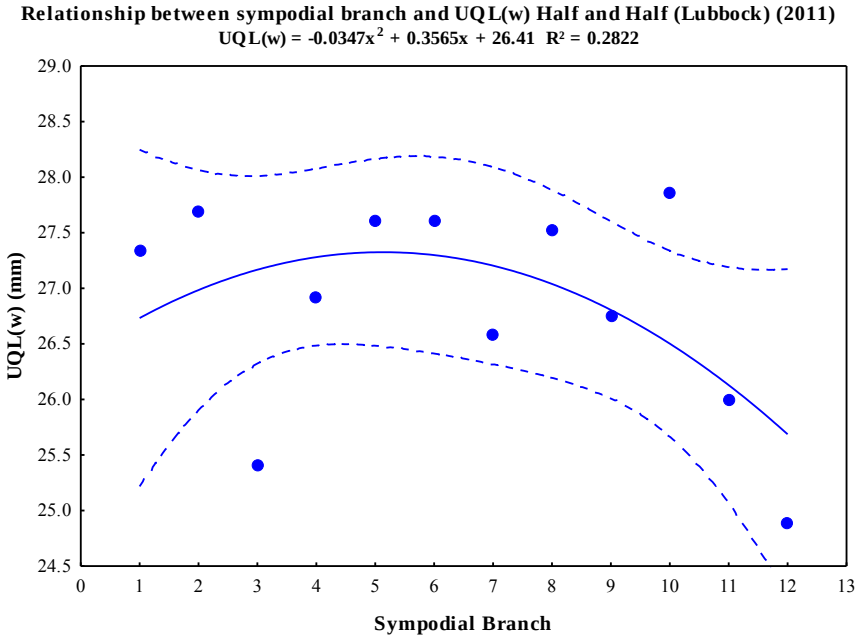

Figure B. 91: Relationship between sympodial branch and UQL (w) (AFIS) for Half and Half in 2011 at Lubbock, Texas.

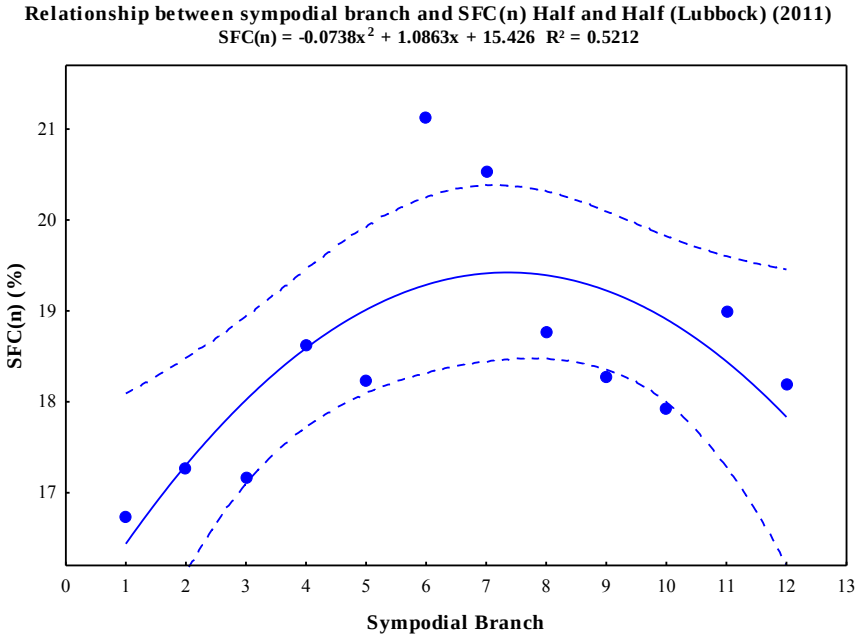

Figure B. 92: Relationship between sympodial branch and SFC (n) (AFIS) for Half and Half in 2011 at Lubbock, Texas.

VITA

Name: Nayankumar Kothari Neha

Address: Cotton Improvement Lab, Turk Road, College Station, TX 77843-2474

Email Address: nkothari@ag.tamu.edu

Education: B.Sc, Gujarat University, 2002,

M.S., Texas Tech University, 2007