A GENETIC STUDY OF FIBER PROPERTIES IN CROSSES AMONG STORMPROOF AND OPEN-BOLL VARIETIES OF COTTON USING THE DIALLEL ANALYSIS

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CHAPTER I

INTRODUCTION

In recent years, the analysis of diallel crosses, the set of all possible matings between several genotypes (14), has received considerable emphasis in many plant breeding programs because it fulfills certain specific needs of the plant breeder. The analysis provides a systematic approach for the detection of superior parents and crosses. At the same time it helps the plant breeder choose the most efficient method of selection by allowing estimates to be made of the magnitude and relative importance of various genetic parameters.

Methods of breeding are relatively simple for crops in which large amounts of hybrid seed can be obtained at reasonable cost. In these crops a high degree of specific combining ability is sought in the parents chosen. The outstanding crosses, if superior to those already in production, are repeated on a much larger scale, and the hybrid seed is then utilized commercially. For other crops such as cotton, Gossypium hirsutum L., in which cost of hybrid seed production on a commercial scale is prohibitive, the methods of breeding are more complex. In these crops general combining ability is more easily utilized in a selection program leading towards a pure-line variety than specific combining ability. For these crops crosses displaying large amounts of additive genetic variance are preferred over those with the more heterotic responses.

The stormproof upland cotton varieties grown in the Texas and Oklahoma plains area lack adequate fiber properties for current market requirements. Stormproof varieties generally have shorter and weaker fibers than the open-boll varieties. On the other hand, the open-boll varieties are unsuitable for the mechanical harvesting practices used in the plains area. Since excessive fineness of fiber is often a problem in this area, fiber coarseness as well as fiber length and strength were the traits included in this study. The purposes of this experiment were to investigate the genetic mechanisms controlling these traits and to suggest the most efficient procedures for the development of new stormproof varieties with desirable fiber properties.

CHAPTER II

REVIEW OF LITERATURE

Effect of Heredity on Fiber Quality

The principal components of fiber quality are lint length, strength, and coarseness. Each of these economically important traits exhibits quantitative inheritance (5, 40, 44, 47, 48); and each is controlled by several to many genes whose individual effects are partially masked by the environment. Relatively few reports are available in the literature on the inheritance of these traits in upland cotton, Gossypium hirsutum L. The information available is summarized below under three separate headings: fiber length, fiber strength, and fiber coarseness. Unless otherwise stated, the literature cited is concerned only with the G. hirsutum species.

A. Fiber Length. Jones and Loden (21) in a study of nine crosses detected no significant difference between the mean of the F_1 generation and the mean of the parental generation for fiber length. Miller and Lee (25) reported the average top-cross performance of fiber length in 22 crosses to be very similar to that of the mid-parent values. Ware et al. (48) in a cross between 'Florida Green Seed' and 'Rowden' determined long fiber to be partially dominant over short fiber. Barnes and Staten (4) found four crosses which had longer fiber than their higher parent out of the 43 crosses they studied. White and Richmond (49) in a five-parent diallel cross discovered five crosses in which

the fiber of the hybrid was significantly longer than its higher parent. Miller and Marani (26) in a diallel cross among eight inbred lines reported relatively small but significant amounts of heterosis above the midparent for fiber length and a significant amount of inbreeding depression from the F_1 to the F_2. Young and Murray (50) in crosses among four inbred strains identified one cross displaying heterosis for length. Their data also showed that the exhibition of significant heterosis was erratic from year to year and that fiber length exhibited a greater degree of heterosis than did strength or coarseness.

Ramey and Miller (38) detected substantial amounts of additive genetic variance and small positive estimates of dominance genetic variance in a cross between 'Empire 10' and a line six generations of backcrossing to G. hirsutum removed from the interspecific cross (G. arboreum X G. thurberi) doubled X G. hirsutum. The degree of dominance for length estimated for this cross was 0.627. Muramoto (29) recognized no significant heterosis from the mid-parent in his material though the average length of the F_1 generation did seem to approach that of the longer parent. He obtained broad-sense heritability estimates ranging from 0.0% for some crosses to 6.5% for others. Stith (44) in a cross between 'Acala' and 'Hopi' found partial dominance for fiber length. He assessed heritability estimates of 22.2% based on the genetic variance in the F_2 and 70.0% based on variance components among F_3 lines. Ramey (37) interpreted a cross between 'Half and Half' and 'Delfos 9252' as indicating both allelic and nonallelic gene interactions to be involved in the inheritance of lint length.

B. Fiber Strength. Miller and Lee (25) revealed that the average top-cross performance in 22 crosses was similar to the mid-parent mean

for fiber strength. White and Richmond (49) detected no instances of heterosis for strength in the 10 crosses studied. Ware and Harrell (46) showed that in advanced generations of Florida Green Seed X Rowden fiber strength appeared to be slightly dominant over fiber weakness. Barnes and Staten (4) identified five crosses which had higher strength than their stronger parents out of the 43 crosses studied. Young and Murray (50) detected one example of heterosis for strength among six crosses. Miller and Marani (26) in a diallel among eight inbred lines identified relatively small but significant amounts of heterosis above the mid-parent for strength though the inbreeding depression from the F_1 to the F_2 was not significant.

In a cross between 'AHA 50' and Half and Half, Self and Henderson (40) concluded that four to five pairs of genes were segregating for strength. They obtained heritability estimates of 86% based on the F_2 and 53% based on the regression of F_3 progeny mean on F_2 phenotype. Muramoto (29) disclosed that no F_1 in his material exceeded its stronger parent. Most of his crosses were intermediate in strength or were slightly closer to the stronger parent. His heritability estimates for strength ranged from 0.0% for some crosses to 57.9% for others. Ramey and Miller (38) in the cross described previously found large amounts of additive genetic variance and small positive amounts of dominance genetic variance for strength with 0.236 estimated as the degree of dominance. Stith (44) found no dominance for strength in a cross between Acala and Hopi. His heritability estimates for strength based on the genetic variance in the F_2 and on variance components among F_3 lines were 54.1% and 87.3%, respectively. Soebiapradja (41) in a diallel cross among four varieties estimated the genetic variance to be

primarily additive and/or additive by additive in nature with narrow-sense heritability estimates of 79% and 94% and with an estimate of 0.09 for the average degree of dominance.

C. Fiber Coarseness. White and Richmond (49) discovered no case of heterosis for fiber coarseness among the 10 crosses they studied. Miller and Lee (25) disclosed that average top-cross performance in 22 top-cross progenies was very similar to that of their midparent values. Ware and Harrell (47) noted that the F_1 in two crosses was generally intermediate in inheritance but that there was some tendency for fiber coarseness to be dominant over fineness. Barnes and Staten (4) revealed that 15 out of 43 crosses in their material exceeded the coarser parent. Young and Murray (50) acquired one example of heterosis out of six crosses in 1961.

Bilbro (5) obtained heritability estimates of 30.4%, 73.6%, and 60.7% in 1955, 1956, and the two years data combined, respectively. Stith (44) in a cross between Acala and Hopi reported heritability estimates of 74.6% based on genetic variance in the F_2 and of 69.9% based on variance components among F_3 lines. His material exhibited no dominance for fiber coarseness. Muramoto (29) in his material found some hybrids which approached the coarseness of their coarser parent. His broad-sense heritability estimates for this trait ranged from 50.9% for some crosses to 79.3% for others. Ramey and Miller (38) estimated large amounts of additive genetic variance and small positive amounts of dominance genetic variance in the cross previously described. They also estimated 0.314 for the degree of dominance.

Effect of Environment on Fiber Quality

In general, heredity has been found to influence the fiber properties of cotton to a greater extent than does environment (23, 27, 28, 31, 35, 36). However, environmental effects are often important enough that ignoring them can lead to serious errors in selection. Neely (31) listed the principal environmental factors which affect fiber quality as follows: soil temperature, soil moisture, soil nutrients, and disease and insect occurrence.

Hanson *et al.* (13) noted that usually in years of high temperatures and low rainfall cotton fiber tends to be shorter and stronger than in cooler, wetter seasons and that strength appeared to be affected more by changing the environment than did length. Hanson and Knisel (12) showed that cotton stressed for moisture usually has coarser and stronger fiber than if it had received adequate moisture. Pope (35) revealed that strength was modified to a large degree by small soil variations. He reported significant variety by year and variety by location interactions for fiber strength and a significant variety by location interaction for length. Miller *et al.* (27) obtained significant variety by year and variety by location by year interactions for length, a variety by location by year interaction for strength, and variety by year and variety by location interactions for coarseness. In this and in another study, Miller *et al.* (28) found the variety by environment interactions to be generally small in relation to varietal differences for these traits. Green and Stroup (10) disclosed that in Oklahoma high coarseness readings were obtained in favorable growing seasons and low readings on cotton grown under drought conditions. They also reported large

year-to-year variation at the same location and differential location effects within the same year.

Hanson and Knisel (12) noted that fiber length of varieties planted on a fine and a coarse soil increased with heavier irrigation on the fine soil but no relationship between the two variables was apparent on the coarse soil. Spooner et al. (42) determined that adequate moisture applied by irrigation increased fiber length but had no effect on strength except at one location where strength was decreased. Tabrah (45) in Oklahoma recently reported that irrigation increased fiber length and decreased strength but had no effect on coarseness.

MacKenzie and van Schaik (23) recognized that varietal differences were more important than the level of nitrogen fertilizer applied. However, Crowther (7) and Nelson (33) obtained data suggesting that increasing nitrogen applications increased fiber length. Nelson also revealed that the first increment of potassium increased fiber length and that addition of potassium increased coarseness. Perkins and Douglas (34) determined that fiber length increased with the first increment of nitrogen fertilizer applied but that length remained constant with additional applications. In contrast to these results, Spooner et al. (42) found that nitrogen levels had no significant effect on fiber length or strength. Perkins et al. (34) decided on the basis of their data that fiber strength and coarseness were unaffected by nitrogen fertilizer applications. Armstrong and Bennett (3) showed no material change in fiber length between unfertilized plots and plots fertilized with nitrogen, phosphorus, and potassium. Murray et al. (30) in Oklahoma tests acquired no significant differences for length, strength, or coarseness among the different levels of nitrogen, phosphorus, and

potassium applied. Nelson (33) also detected that phosphorus applications had little effect on fiber properties.

Grimes (11) reported that upon weathering fiber length decreased from 1/16 to 3/16 inches as exposure was prolonged. She also found losses in strength ranging from 1% to 14%, the loss in general depending upon the length of exposure and amount of precipitation. Hessler et al. (18) considered that weathering reduces fiber length but has no effect on fiber strength or coarseness.

Brown and Ware (6) stated that lint damage by disease organisms may be caused by Xanthomonas malvacearum (E. F. Sm) Dawson as well as by various species of Alternaria, Fusarium, Aspergillus, Rhizopus, Penicillium, Cladosporium, Diplodia, and Glomerella. Several of the more important insects they listed which may damage lint quality are Anthonomus grandis Boh., Pectinophora gossypiella (Saund.), and Heliothis zea (Boddie).

Santelmann et al. (39) recently showed no effect of five post-emergence herbicides on the fiber length of five cotton varieties. They did find a few cases where fiber strength and coarseness were possibly affected, but the results were not consistent for any one herbicide.

CHAPTER III

MATERIALS AND METHODS

Varieties

Ten varieties (five stormproof and five open-boll) were included in the experiment. The stormproof varieties were 'Paymaster 101,' 'Gregg,' 'Western Stormproof,' 'Lankart 57,' and '6-77.' The open-boll varieties were 'Deltapine 45,' 'Coker 100A WR,' 'Acala 44,' 'Stoneville 7,' and 'Auburn M.' Except for 6-77, all of these parental strains were standard commercial varieties of cotton. Strain 6-77 is a Bacterial Blight-resistant selection from the variety, 'Stormproof No. 1.' The 10 varieties were specifically chosen and do not represent a random sample of all upland cotton varieties. Therefore, strictly speaking, inferences derived from the data apply only to the varieties and crosses studied. The extent to which the inferences will apply to the species as a whole is uncertain.

Field Procedure

Crosses were made in Iguala, Mexico, in the winter of 1964-1965. In the following spring the 10 varieties and the 45 possible F_1 crosses among them were planted in a 7 X 8 rectangular lattice design. A dummy entry, '8948,' was also included since 56 entries are required by the design. In 1966 the 10 varieties, 45 F_1 crosses, and 45 F_2 progenies were planted in a 10 X 10 triple lattice design. In neither year were

reciprocal crosses included. The location of the tests (Perkins, Oklahoma), soil type (Vanoss loam), number of replications (three), plot size (single rows 7.5m long), and plant spacing (50 cm apart) were the same in both years. Single border rows of the variety, 'Kemp,' were planted between adjacent plots to equalize border effects between plots. Seedling diseases reduced stands considerably in 1965 but only slightly in 1966. To partially compensate for the resulting differential spacing between plants, 'De Ridder Red,' a variety with the dominant marker gene, $\underline{R_1}$, was planted in the blank hills.

Laboratory and Statistical Procedure

Two harvests were made on the material. From each plot six plants were chosen with the aid of a random number table for laboratory analysis. In plots with six or fewer than six plants, all plants were taken. Fortunately, this type of plot was relatively rare in both years. In the laboratory fiber length was measured by the upper 2.5% Span Length, fiber strength by the 1/8" Gauge Stelometer and the 0" Gauge Stelometer, and fiber coarseness by the Micronaire. Fiber samples for each harvest from each plant were analyzed separately, and then a weighted average of each fiber measurement over the two harvests was calculated for each plant based on the percentage of total lint yield per harvest. All subsequent calculations were made from these weighted averages.

The analysis of the data followed the diallel procedure described by Jinks and Hayman (14, 19, 20). Considering the length and complexity of the analysis, the procedure will be described with the results in the next chapter.

CHAPTER IV

RESULTS AND DISCUSSION

Analyses of Variance

Analyses of variance were conducted on a plot mean basis for each trait in each year. All of these analyses revealed highly significant differences among entries. A diallel analysis was then conducted for each trait in each separate year.

General Tests of the Assumptions of the Diallel Analysis

Assumptions of the diallel analysis are diploid segregation, no reciprocal differences, homozygous parents, no multiple alleles, uncorrelated gene distributions, no epistasis, and no genotype-environment interaction within locations and years (8). Since the analysis is invalidated to some degree by failure of any one of the seven assumptions, three broad, general tests were used to determine whether or not the assumptions were fulfilled by the characters. The tests were as follows:

A. Analysis of variance of the quantity $(W_r - V_r)$,

B. Analysis of the (W_r, W_r') regression, and

C. Analysis of the (V_r, W_r) regression.

V_r is the variance of the members of an individual array where an array is defined as one parent and all crosses derived from it; W_r is the covariance of the members of an array with their non-recurrent parents;

and W_r' is the covariance of the members of an array with the array means of their non-recurrent parents.

A. Analysis of Variance of the Quantity $(W_r - V_r)$. In the first test of the assumptions, the quantity $(W_r - V_r)$ is expected to be constant over arrays if all assumptions of the analysis are fulfilled (17, 20). Heterogeneity of this quantity indicates that one or more of the hypotheses are not valid for that particular character. The quantity was calculated for each of the ten arrays in each of the three replications, and then an analysis of variance was conducted upon the 30 values obtained. The results of this test for the F_1 populations in 1965 and 1966 and for the F_2 population in 1966 are summarized in Table I. The F values obtained suggest that the assumptions of the analysis were fulfilled for the traits studied except for fiber length in the F_2 in which at least a partial failure is indicated. In this test, the results obtained in the F_1 appear to be comparable from one year to the next. The performance of the F_1 in one year and the F_2 in the following year and the performance of the F_1 and F_2 in the same year were generally the same, but the results obtained here imply that one should actually conduct the test for both F_1 and F_2 populations to be certain that they do respond similarly.

B. Analysis of the (W_r, W_r') Regression. In the second test, the (W_r, W_r') regression coefficient for each trait is expected to be significantly different from zero but not significantly different from 0.5 if the assumptions are valid (1). Ninety-five percent confidence limits about the regressions were calculated by the method prescribed by Steel and Torrie (43). The results presented in Table II indicate that the regression coefficients were significantly different from zero in every

TABLE I

ANALYSES OF VARIANCE OF $(W_r - V_r)$ VALUES

		Mean Squares					
		2.5% Span Length ($\times 10^{-6}$)			Micronaire ($\times 10^{-2}$)		
Source	df	F_1 (1965)	F_1 (1966)	F_2 (1966)	F_1 (1965)	F_1 (1966)	F_2 (1966)
Arrays	9	.132415	.081429	.408827**	.212584	.017228	.089964
Replications	2	.080044	.538778**	.603990**	.024980	.090497	.134223
Error	18	.055930	.056883	.044350	.079756	.032534	.075223

		Mean Squares					
		1/8" Gauge Stelometer ($\times 10^{-4}$)			0" Gauge Stelometer ($\times 10^{-4}$)		
Source	df	F_1 (1965)	F_1 (1966)	F_2 (1966)	F_1 (1965)	F_1 (1966)	F_2 (1966)
Arrays	9	.0652	.0305	.0375	.5542	.1407	.7895
Replications	2	.5490**	.1234	.1379	3.9453**	3.5281**	.0082
Error	18	.0482	.0389	.0545	.5264	.2584	.5196

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

TABLE II

(W_r, W_r') REGRESSION COEFFICIENTS

Measurement	Slope	95% Confidence Limits
2.5% Span Length		
F_1 (1965)	.5559	.4882 - .6236
F_1 (1966)	.4377	.4020 - .4734
F_2 (1966)	.5378	.3892 - .6864
Micronaire		
F_1 (1965)	.2874	.1000 - .4748
F_1 (1966)	.4139	.0775 - .7503
F_2 (1966)	.3999	.2362 - .5636
1/8" Gauge Stelometer		
F_1 (1965)	.5047	.3870 - .6224
F_1 (1966)	.2903	.1058 - .4748
F_2 (1966)	.3179	.0095 - .6263
0" Gauge Stelometer		
F_1 (1965)	.4190	.2000 - .6380
F_1 (1966)	.4501	.3162 - .5840
F_2 (1966)	.3375	.1965 - .4785

instance. However, the regressions for the F_1 population for Micronaire in 1965, the F_1 populations for 2.5% Span Length and 1/8" Gauge Stelometer in 1966, and the F_2 population for 0" Gauge Stelometer were significantly different from 0.5. Therefore, this test implies that none of the traits strictly complies with the assumptions of the diallel. Results of this test were not consistent in the F_1 from year to year nor in the F_1 and F_2 comparisons within the same year or from year to year. If this test is used, each population for each trait must be tested in each year.

C. Analysis of the (V_r, W_r) Regression. In the third test, the (V_r, W_r) regression coefficient for each trait is expected to be significantly different from zero but not significantly different from 1.0 if all of the assumptions hold true (20). The results of this test are presented in Table III. Steel and Torrie's method (43) for computation of 95% confidence limits about the regressions was used. Two regression coefficients for Micronaire (the F_1 in 1965 and the F_2 in 1966) were not significantly different from zero, and two for length (the F_1 in 1965 and the F_2 in 1966) were significantly different from 1.0. A partial failure of the assumptions is therefore suggested by this test for these two traits while 1/8" Gauge Stelometer and 0" Gauge Stelometer appear to fulfill the assumptions. Results of this test were not consistent in comparison of F_1 populations from year to year nor in the comparison of F_1 and F_2 populations in the same year. Surprisingly, the comparison of F_1 results in 1965 were consistent with those of the F_2 in 1966.

In summary, three general tests of the assumptions of the diallel

TABLE III

(V_r, W_r) REGRESSION COEFFICIENTS

Measurement	Slope	95% Confidence Limits
2.5% Span Length		
F_1 (1965)	.5785	.3903 - 0.7667
F_1 (1966)	1.0173	.7238 - 1.3108
F_2 (1966)	.4722	.2146 - 0.7298
Micronaire		
F_1 (1965)	.3929	(-.3651)- 1.1509
F_1 (1966)	.6969	.2771 - 1.1167
F_2 (1966)	.4050	(-.2326)- 1.0426
1/8" Gauge Stelometer		
F_1 (1965)	.7751	.5209 - 1.0293
F_1 (1966)	.8209	.3687 - 1.2731
F_2 (1966)	.7009	.1244 - 1.2774
0" Gauge Stelometer		
F_1 (1965)	.9163	.2018 - 1.6308
F_1 (1966)	.9687	.6029 - 1.3345
F_2 (1966)	.9798	.4522 - 1.5074

were conducted on three populations (the F_1 in 1965 and 1966 and the F_2 in 1966) for each of the four fiber measurements. Therefore, in a sense, nine tests were conducted on each fiber measurement. 2.5% Span Length failed four of these nine tests, Micronaire three, 1/8" Gauge Stelometer one, and 0" Gauge Stelometer one. As a result, none of these traits completely fulfill the assumptions of the analysis, but 1/8" Gauge Stelometer and 0" Gauge Stelometer fulfill those assumptions more nearly than do length and Micronaire.

Specific Tests of the Assumptions of the Diallel Analysis

The pinpointing of the offending assumptions for these traits cannot be accomplished with the present data. However, certain assumptions may be considered fulfilled with some degree of confidence. Others may be tested.

A. Assumptions Which Were Not Tested. Endrizzi (9) and Kimber (22) have established with reasonable certainty that cotton, an amphidiploid, does undergo diploid segregation. As a rule, reciprocal crosses within Gossypium hirsutum L. have not been significantly different. White and Richmond (49) recently reported no significant differences between reciprocal crosses for fiber length, strength, or coarseness in a diallel cross among five, widely differing G. hirsutum strains. As a consequence, the assumptions of diploid segregation and of no reciprocal differences were considered to be fulfilled for each of these traits.

Since cotton is a predominantly self-pollinated plant and since the varieties used in this experiment were selfed for one generation prior to crossing and testing, the parents were probably relatively homozygous. However, since some heterozygosity may remain even after

many generations of self pollination (6), this assumption may account for at least part of the partial non-compliance of the traits to the assumptions. No method for testing the assumption of no multiple alleles is known to the author at present.

B. Test for Correlated Gene Distribution. The assumption of uncorrelated gene distributions may be tested (8) by the ratio $1/4\ H_2/H_1$. The symbols, H_1 and H_2, are dominance genetic variances. Their method of computation is described later in this report. The ratio, $1/4\ H_2/H_1$, is expected to equal 0.25 if the negative versus positive alleles displaying dominance are distributed equally among the parents (20). When the alleles are not distributed in such a manner, the quantity is expected to be less than 0.25. One estimate of this ratio was obtained in each replication for each trait. The ratios appearing in Table IV are means of those three ratios; and the standard errors of the mean, used in the tests of significance, were estimated by the variation of the block values around the overall mean. Only the ratio for the F_2 population of 0" Gauge Stelometer was significantly different from 0.25 indicating that the positive versus negative alleles displaying dominance were not distributed equally among the parents for this trait, i.e., the gene distribution of dominant alleles for this trait is correlated in this population. The only occasion 0" Gauge Stelometer failed to comply with expectations in the three general tests of the assumptions was in the F_2 in the second test. Lack of compliance with this assumption was at least one of the causes for that failure.

C. Test for Epistasis. Verification of the assumption of no epistasis may be accomplished using the chi-square test devised by Hayman (15). Since both F_1's and F_2's are required for this test, only

TABLE IV

MEAN 1/4 H_2/H_1 RATIOS

Measurement	F_1(1965)	F_1(1966)	F_2(1966)
2.5% Span Length	.2478	.2644	.2425
Micronaire	.2071	.2208	.2329
1/8" Gauge Stelometer	.1992	.2183	.2070
0" Gauge Stelometer	.2079	.2099	.1656**

*, **Significantly different from 0.25 at the 0.05 and 0.01 levels of probability, respectively.

the 1966 data could be used for this purpose. The formula is as follows:

$$\text{Chi-square (observed)} = k_2 [(n-1)(V_{1LX} - V_{OLX}) + n(\bar{p} - \bar{x})^2/(1 + k) + (n - 1)(V_{OLO} - 4W_{OLOX} + 4V_{OLX})/(2 + k)]$$

with $1/2\ n(n - 1)$ degrees of freedom and

where $k = nE_0/(8E_2 + 2E_1 - E_0)$ and $k_2 = n/(8E_2 + 2E_1)$.

E_0, E_1, and E_2 are estimates of the parental, F_1, and F_2 environmental variances respectively. Their method of computation is more conveniently discussed later along with H_1 and H_2. The symbol, n, equals the number of parents, $\bar{p}$ equals the mean of the parents, and $\bar{x}$ equals the overall mean of the entries in the experiment. If a table containing parental and F_1 means is defined as an L_1 table and a table containing parental and F_2 means as an L_2 table, then a $2L_2 - L_1$ table may be constructed by subtracting each term of the L_1 table from twice the term in the same position of the L_2 table. From this $2L_2 - L_1$ table V_{OLO}, V_{OLX}, V_{1LX}, and W_{OLOX} may be calculated. These estimates are analogous to V_{OLO}, V_{OL1}, V_{1L1}, and W_{OLO1} calculated from the L_1 table where V_{OLO} is the variance of the parents, V_{OL1} the variance of array means, V_{1L1} the mean variance of arrays, and W_{OLO1} the mean covariance of arrays.

The observed chi-square values were 58.0, 47.1, 42.1, and 44.3 for 2.5% Span Length, Micronaire, 1/8" Gauge Stelometer, and 0" Gauge Stelometer, respectively. None of these values were significant at the 0.05 level of probability suggesting that epistasis was either absent in or made a negligible contribution to the expression of these traits in 1966.

D. Tests for Genotype-Environment Interaction. The assumption of no genotype-environment interaction within locations and years may only partially be tested since one location and two years were used to conduct the experiment. The analysis proposed by Allard (2) was employed to test for the presence of genotype by year interactions of both the additive and dominance components of variation. It is recognized that a location effect is confounded in the results of these tests rendering them somewhat less sensitive than had an additional location been used.

The test of the additive components of variation is based on the fact that heritable differences between homozygous parents, in the absence of epistasis, are caused by the additive effects of genes. In each of the two years, one estimate of a trait's mean was obtained from each of the three replications for each of the 10 parents. A test for the constancy of the additive components was possible from an analysis of variance of the resulting 60 means in which the means from the individual replications within a single year were treated as subsamples for the purpose of error-term estimation. The results of this test are summarized in Table V. The significance of the years mean square for each of the traits has no specific genetical interpretation, since any of a large number of environmental factors could have caused the observed differences over the two seasons. In contrast, the significance of the parents mean square indicates that for each of the fiber measurements certain parents carry alleles with different additive effects. The lack of significance of the years X parents mean squares suggests that the additive effects of the genes for these traits were constant relative to one another from season to season.

TABLE V

GENOTYPE BY YEAR ANALYSES OF THE ADDITIVE COMPONENTS OF VARIATION

Source	df	Mean Squares			
		2.5% Span Length	Micronaire	1/8" Gauge Stelometer	0" Gauge Stelometer
Years	1	.080008**	8.36**	.1421**	6.2921**
Parents	9	.015412**	.50**	.1347**	.3132**
Years X Parents	9	.000630	.09	.0068	.0239
Error	40	.000326	.04	.0073	.0182

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

The test of the dominance components of variation was based on an analysis of variance of the 120 V_r and W_r estimates from the 10 arrays, three replications, and two years in which the F_1 generation was grown. Before the analysis was run, however, the individual V_r and W_r terms were divided by the variance of the parents occurring in the same replication in order to minimize the additive component of variation in the test and thereby improve the test's sensitivity in regard to dominance interaction terms. This rescaling also tends to minimize the fluctuation of basic variability in different environments which also tends to mask between-environment comparisons in genetic systems. Again, estimates from the individual replications within a single year were treated as subsamples for the purpose of error-term estimation. The results of this test are given in Table VI. Since the data was rescaled, the lack of significance of the years mean squares shows that there were no differences in mean dominance between years for any of these traits. Significance of the dominance mean square for Micronaire indicates that the mean degree of dominance for this trait is either partial dominance or overdominance. For the other traits, this test suggests either there is no dominance or dominance is not significantly different from being complete dominance. Lack of significance of the years X dominance interaction term for the traits shows that dominance, if any, was consistent over the two seasons. The significance of the arrays component for length and 1/8" Gauge Stelometer provides evidence that there are differences in dominance among the parents entering the experiment for these two traits while such differences are not apparent for Micronaire and 0" Gauge Stelometer. The lack of significance of the years X arrays term shows these relationships to be constant from

TABLE VI

GENOTYPE BY YEAR ANALYSES OF THE DOMINANCE COMPONENTS OF VARIATION

Source	df	Mean Squares			
		2.5% Span Length	Micronaire	1/8" Gauge Stelometer	0" Gauge Stelometer
Years	1	.0639	.0546	.0378	.0806
Dominance	1	.0407	1.3525**	.0677	.0170
Years X Dominance	1	.0176	.2084	.0055	.0038
Arrays	9	.1826**	.1576	.0571**	.0250
Years X Arrays	9	.0381	.0611	.0342	.0473
Dominance X Arrays	9	.0059	.0184	.0042	.0065
Years X Dominance X Arrays	9	.0083	.0355	.0021	.0016
Error	80	.0396	.0712	.0187	.0305

*, **Significant at the .05 and 0.01 levels of probability, respectively.

year to year for these traits. The non-significance of the dominance X arrays interaction provides additional evidence for the lack of epistasis for these traits, and the non-significance of the years X dominance X arrays item indicates these epistatic effects, or rather the lack of them, were constant in the F_1 over both seasons.

Estimates of the Population Parameters

When a trait exhibits a partial failure of the assumptions, estimates of the population parameters of that trait are still possible (14), although the estimates for such a trait are probably less reliable than they would have been had all assumptions been fulfilled. The more extensive the failure of the assumptions, the less reliable are the estimates of the parameters. Keeping this in mind, the parameters were estimated and are listed in Table VII. Here, each replication was treated as a separate experiment with its own estimate of environmental variation as suggested by Nelder (32). One estimate of each parameter for each trait could, therefore, be obtained from each replication. The standard errors of the mean, used in the tests of significance, were estimated by the variation of the block values around the overall mean.

As was stated previously, the parameters, E_0, E_1, and E_2, are estimates of the parental, F_1, and F_2 environmental variations, respectively. Estimates of E_0 were obtained from a between plot-within plot analysis of variance of the parental entries within each replication for each trait. Since all of the other parameter estimates in the diallel were calculated on a plot-mean basis, it was necessary to convert the estimates of E_0 to an equivalent basis by dividing the within

TABLE VII

MEAN PARAMETER ESTIMATES OF THE FIBER MEASUREMENTS

Parameter	2.5% Span Length			Micronaire		
	F_1(1965)	F_1(1966)	F_2(1966)	F_1(1965)	F_1(1966)	F_2(1966)
E_0	.000297*	.000392	-	.0251**	.0360	-
E_1	.000201**	.000235**	-	.0146*	.0222**	-
E_2	-	-	.000300**	-	-	.0265**
D	.002411*	.002693	-	.1256	.0532	-
F	.000047	.000347	-.000949	.0391	-.0033	.0053
H_1	.001513*	.000915	.004779**	.1407	.0721*	.5003*
H_2	.001489*	.000837	.004613*	.1128*	.0647*	.4523*

Parameter	1/8" Gauge Stelometer			0" Gauge Stelometer		
	F_1(1965)	F_1(1966)	F_2(1966)	F_1(1965)	F_1(1966)	F_2(1966)
E_0	.0036**	.0023*	-	.0070*	.0073**	-
E_1	.0021**	.0015**	-	.0046**	.0053**	-
E_2	-	-	.0021**	-	-	.0073**
D	.0316**	.0192*	-	.0635**	.0512*	-
F	.0101*	.0039	.0080	.0255*	.0063	.0424
H_1	.0153	.0103*	.0357*	.0424	.0205	.1627
H_2	.0124	.0087*	.0288*	.0337*	.0165	.1056

*, **Significantly different from zero at the 0.05 and 0.01 levels of probability, respectively.

plot mean square by the average number of plants within a plot in that replication. Estimates of E_1 were obtained in the same manner using the F_1 entries rather than the parental entries. Likewise, estimates of E_2 were obtained using the F_2 entries.

The remaining parameters (D, F, H_1, and H_2) are as defined by Jinks and Hayman (20) using the notation of Mather (24). D is the additive genetic variance parameter which may also include a portion of the additive X additive epistatic variance as well as the additive genetic variance itself. H_1 and H_2 are dominance genetic variance parameters which include the dominance genetic variance proper and may include dominance X dominance epistatic variance and additive X dominance variance as well as a portion of the additive X additive variance not included within D. F is an indicator of the relative frequency of dominant and recessive alleles in the parents and may take sign whereas the other parameters are expected to be positive. A negative F value results if there is an excess of recessive alleles in the parents while a positive value indicates an excess of dominant alleles. F will equal zero if the dominant and recessive alleles of each gene are distributed equally among the parents and/or if no genes exhibit dominant effects (8). Estimates of these four parameters were obtained in the F_1 by solving the equations which follow (8, 14) where n equals the number of parents:

[1] Variance of the parents = $V_{OLO} = D + E_0$.

[2] Mean covariance of arrays = $W_{OLO1} = 1/2D - 1/4F + E_0/n$.

[3] Mean variance of arrays = $V_{1L1} = 1/4D + 1/4H_1 - 1/4F + [E_0 + (n-1)E_1]/n$.

[4] Variance of array means = $V_{OL1} = 1/4D + 1/4H_1 - 1/4H_2 - 1/4F + [E_0 + (n-2)E_1]/n^2$.

Estimates of F, H_1, and H_2 were obtained in the F_2 by solving the following equations (16) where n again equals the number of parents:

[5] Mean covariance of arrays = $W_{OLO2} = 1/2D - 1/8F + E_0/n$.

[6] Mean variance of arrays = $V_{2L2} = 1/4D + 1/16H_1 - 1/8F + [E_0 + (n-1)E_2]/n$.

[7] Variance of array means = $V_{OL2} = 1/4D + 1/16H_1 - 1/16H_2 - 1/8F + [E_0 + (n-2)E_2]/n^2$.

The estimates of V_{OLO}, W_{OLO1}, V_{1L1}, and V_{OL1} are obtained from L_1 tables while W_{OLO2}, V_{2L2}, and V_{OL2} are obtained from L_2 tables. Weighted estimates of the environmental variation were used in equations [3], [4], [6], and [7] because parents and offspring do not make equal contributions to V_{1L1}, V_{OL1}, V_{2L2}, and V_{OL2}.

All estimates of environmental variation were significantly different from zero except E_0 for length and Micronaire in 1966. Furthermore, in every case the estimate of E_0 was larger than the corresponding estimate of E_1 which reinforces the statement by Hayman (16) that in cotton the variation of the parents is not equal to the variation of the F_1's. Estimates of E_2 were generally intermediate between the estimates of E_0 and E_1 obtained in the same year.

None of the estimates of D, F, H_1, and H_2 obtained from F_1 data were consistently significant or non-significant from one year to the next. In the comparisons between F_1 data in 1965 and/or 1966 and that

of the F_2, only the estimator, F, was consistent in this respect and then only in the 1966 data. Lack of significance for the various estimators could be due to one of two possible causes. Either the parameter being estimated was actually zero, and the estimates were so small that it could not be stated with a high degree of confidence that they were other than zero; or the parameter was really not zero at all, but the lack of consistency of estimates from replication to replication and the large t value associated with two degrees of freedom prevented the probability statement that they were different from zero. Since only one estimate of each parameter is possible from each replication in a diallel cross experiment, the number of estimates that can be made becomes a matter of practical concern. Usually, the number of replications that can be included is limited. Degrees of freedom are therefore small, and t values, used for setting confidence limits on means, are large which in turn creates large confidence intervals.

Estimates of D were, in general, larger than the estimates of F, H_1, and H_2 obtained in the same year in the F_1. Micronaire was a notable exception to this rule. Three out of the four estimates of dominance variance for Micronaire in the F_1 were greater in magnitude than was the D value obtained in the same year. Estimates of F, H_1, and H_2 for each of the traits were generally larger in the F_2 than in the F_1 in 1966. Perhaps, this is to be expected for these particular estimators since the F_2 is a segregating generation whereas the F_1 is not. Theory (14) states that H_2 should be equal to or smaller than H_1. In this experiment, H_2 was smaller than H_1 in every instance. Also in every case, F was smaller than D, H_1, or H_2.

Investigation of Genetic Systems

Various ratios were calculated, using the parameters estimated in Table VII, to provide further information about the genetic systems operating for each trait. An estimate of each ratio was obtained in each replication. The standard errors of the mean, used for setting confidence limits on the ratios, were estimated by the variation of the block values around the overall mean as was done for the ratios in Table IV and the parameter estimates in Table VII. These ratios are given in Table VIII.

A. Investigation of Dominance. The dominance estimators one, two, and three were estimated in the F_1 by the ratios H_1/D, $(H_1/D)^{1/2}$, and $(V_{1L1} - E)/(W_{OLO1} - E/n)$, respectively, and in the F_2 by $1/4H_1/D$, $(1/4H_1/D)^{1/2}$, and $(V_{2L2} - E)/(W_{OLO2} - E/n)$, respectively. Each of the estimators is a weighted overall measure of the degree of dominance (8) and is expected to be zero with no dominance, range between zero and one with partial dominance, be at one with complete dominance, and be above one with overdominance. All estimates for length, 1/8" Gauge Stelometer, and 0" Gauge Stelometer were within the partial dominance range though in many cases the dominance estimates were not significantly different from one (complete dominance). The situation for Micronaire is somewhat more ambiguous. Since the three estimators average 1.07 in 1965, one would hesitate to postulate in looking at one's data at the end of that year a degree of dominance other than overall complete dominance for the population of crosses studied. However, taking into consideration the average of the data from both years, 1.49, one could with perhaps some confidence suggest over-dominance for

TABLE VIII

MEAN ESTIMATOR RATIOS OF THE FOUR FIBER CHARACTERS

	2.5% Span Length					
Estimator	F_1 (1965)	95 Per Cent Confidence Limits	F_1 (1966)	95 Per Cent Confidence Limits	F_2 (1966)	95 Per Cent Confidence Limits
Dominance #1	.64	.40 - .88	.36	(- .14)- .85	.50	(- .01)-1.01
Dominance #2	.79	.62 - .96	.58	.11 -1.05	.70	.36 -1.04
Dominance #3	.78	.56 -1.00	.60	.18 -1.02	.75	.46 -1.04
K	1.64	(-1.20)-4.48	5.54	2.01 -9.07	1.08	.56 -1.60
Heritability	.49	.17 - .82	.61	(- .09)-1.30	.49	(- .10)-1.08
	Micronaire					
Estimator	F_1 (1965)	95 Per Cent Confidence Limits	F_1 (1966)	95 Per Cent Confidence Limits	F_2 (1966)	95 Per Cent Confidence Limits
Dominance #1	1.16	.68 -1.64	1.69	(-1.35)-4.74	2.89	(-2.17)-7.95
Dominance #2	1.08	.86 -1.30	1.25	.14 -2.36	1.63	.12 -3.14
Dominance #3	.98	.70 -1.26	.95	.25 -1.65	1.76	.29 -3.22
K	.37	.11 - .63	.64	(- .84)-2.11	.17	(- .19)- .54
Heritability	.40	.08 - .71	.25	(- .11)- .60	.19	(- .03)- .41

TABLE VIII (Continued)

	1/8" Gauge Stelometer					
Estimator	F_1 (1965)	95 Per Cent Confidence Limits	F_1 (1966)	95 Per Cent Confidence Limits	F_2 (1966)	95 Per Cent Confidence Limits
Dominance #1	.49	(- .10)-1.08	.55	.06 -1.04	.48	.06 - .89
Dominance #2	.69	.30 -1.08	.74	.40 -1.08	.68	.34 -1.02
Dominance #3	.64	.25 -1.03	.71	.45 - .98	.73	.53 - .93
K	.08	(- .09)- .25	.19	(- .20)- .58	.35	(- .47)-1.17
Heritability	.67	.29 -1.05	.58	.41 - .74	.62	.47 - .77
	0" Gauge Stelometer					
Estimator	F_1 (1965)	95 Per Cent Confidence Limits	F_1 (1966)	95 Per Cent Confidence Limits	F_2 (1966)	95 Per Cent Confidence Limits
Dominance #1	.69	(- .14)-1.52	.47	(- .44)-1.38	.77	.37 -1.16
Dominance #2	.81	.25 -1.37	.64	(- .09)-1.37	.87	.65 -1.09
Dominance #3	.77	.29 -1.25	.67	.16 -1.17	.90	.88 - .92
K	.37	(- .79)-1.53	.40	(- .82)-1.61	.06	(- .18)- .31
Heritability	.68	.16 -1.20	.57	.11 -1.04	.52	.22 - .82

this trait in these particular crosses. The degree of dominance predicted by these three estimators is remarkably constant. Results from the 1965 F_1 data correspond exactly with those from the 1966 F_1 data. Comparisons of F_1 results from either 1965 or 1966 with the F_2 results show anomalies only with the third estimator in the Micronaire data.

Before discussing the ratios of K and heritability given in Table VIII, the author elected to investigate the nature of the dominance estimators somewhat more fully. It was found that these are, indeed, overall estimates of the degree of dominance since all crosses do not necessarily display the same degree nor direction of dominance for the same trait. This can readily be seen in Table IX. In the table, those crosses in the column labeled "No Dominance" were not significantly different from their respective midparent values while those crosses in the other columns were. The positive direction denotes crosses having significantly longer, stronger, or coarser fiber than their midparents while the negative direction denotes those crosses having shorter, weaker, or finer fiber. Crosses in the "Complete Dominance" columns were not significantly different from their high or low parent, the particular parent being denoted by the direction of dominance. Crosses in the "Over-Dominance" columns were significantly higher or lower than their high or low parent, respectively. Significance was determined for these comparisons by use of the least-significant difference technique as outlined in Steel and Torrie (43) using t at the 0.05 probability level. The test with one exception was not sensitive enough to detect significant differences from both the parent and the midparent in crosses which were essentially intermediate in performance between them. The exception was obtained in the F_1 in 1966 for length,

TABLE IX

DIRECTION AND MAGNITUDE OF DOMINANCE IN INDIVIDUAL CROSSES

Measurement	Positive Direction		No Dominance	Negative Direction	
	Over-Dominance	Complete Dominance		Complete Dominance	Over-Dominance
2.5% Span Length					
F_1 (1965)	3	8	34	0	0
F_1 (1966)	3	18(1)	23	0	0
F_2 (1966)	1	9	34	1	0
Micronaire					
F_1 (1965)	1	8	33	3	0
F_1 (1966)	0	0	45	0	0
F_2 (1966)	1	0	42	2	0
1/8" Gauge Stelometer					
F_1 (1965)	0	0	45	0	0
F_1 (1966)	0	0	44	1	0
F_2 (1966)	0	0	44	1	0
0" Gauge Stelometer					
F_1 (1965)	0	1	42	2	0
F_1 (1966)	0	0	43	1	1
F_2 (1966)	0	2	40	3	0

and it is the cross denoted in parentheses in Table IX. Had the test been more sensitive, undoubtedly some crosses from the "Complete Dominance" and "No Dominance" columns would very likely have fallen in a "Partial Dominance" column.

Another estimate of the direction of dominance independent of the comparisons made in Table IX was obtained as a correlation of the sum $(V_r + W_r)$ for each array averaged over all three replications with the parental mean of each array averaged over all three replications for each of the traits in each of the populations studied. If this correlation is high for a particular trait, most of the dominant alleles for that trait operate in one direction, and most of the recessive alleles operate in the opposite direction. If the correlation is low, some dominant genes increase the expression of the character while other dominants decrease it, the same being true for the recessive alleles (8). The correlations obtained are given in Table X.

TABLE X

$(V_r + W_r)$ CORRELATIONS WITH PARENTAL MEANS

Measurement	Populations		
	F_1 (1965)	F_1 (1966)	F_2 (1966)
2.5% Span Length	-.78**	-.90**	-.32
Micronaire	-.45	-.03	.56
1/8" Gauge Stelometer	.45	.59	-.10
0" Gauge Stelometer	-.47	.55	-.82**

*, **Significantly different from zero at the 0.05 and 0.01 levels of probability, respectively.

With only ten paired values per correlation, relatively high correlations were required before one could state that they were significantly different from zero at the 0.05 level of probability. The F_1 correlations for length and the F_2 correlation for 0" Gauge Stelometer were the only correlations significantly different from zero, and all three were negative in sign. Since the parents having a larger number of dominant alleles for a trait are expected to have smaller array variances and covariances than those parents having a greater number of recessives, length of fiber in the F_1 according to this test is shown to be dominant to some degree over short fiber and fiber strength in the F_2 as measured by 0" Gauge Stelometer is shown to be dominant to some degree over fiber weakness. In this test, results obtained in the F_1 in 1965 were identical to those obtained in the F_1 in 1966. Results in the F_1, however, were not infallible as an indication of what to expect in the F_2.

B. Investigation of the Number of Effective Factors. The number of effective factors operating for a certain trait as defined by Mather (24) is estimated by K. This estimator measures only those factors showing some degree of dominance. The formula (19) used in the F_1 to obtain these estimates is as follows:

$$K = (\text{overall progeny mean} - \text{parental mean})^2/(1/4H_2).$$

The modified formula used in the F_2 is as follows:

$$K = (\text{overall progeny mean} - \text{parental mean})^2/(1/16H_2).$$

These assessments of effective gene number are underestimated if the dominance effects of all the genes concerned are not equal in size and

direction and/or if the distribution of the genes is correlated (19, 24). As can be seen in Table VIII, the estimates of K for Micronaire, 1/8" Gauge Stelometer, and 0" Gauge Stelometer were small while those for length were relatively higher. None of the Stelometer estimates were significantly different from zero at the 0.05 level of probability. As will be recalled from the discussion of Table IV, the only evidence for correlated gene distribution was in the F_2 for 0" Gauge Stelometer. This, at least partially, explains the relatively low estimate obtained in the F_2 as compared to the F_1 estimates for this trait. Lack of directional dominance as shown in Tables IX and X could explain the relatively low estimates of K in Micronaire, 1/8" Gauge Stelometer, and the F_1 populations of 0" Gauge Stelometer. Lack of directional dominance in the F_2 for length could also have deflated the estimate of K in that population as compared to the F_1 in the same year. Dominance effects unequal in size could have served to deflate any of these estimates.

C. Investigation of Heritability. A narrow-sense heritability estimate was calculated for each character on a plot mean basis in the F_1 using the formula (8) which follows:

$$\text{Heritability} = (1/4D)/(1/4D + 1/4H_1 - 1/4F + E).$$

In the F_2, the modified formula used was as follows:

$$\text{Heritability} = (1/4D)/(1/4D + 1/16H_1 - 1/8F + E).$$

As can be seen in Table VIII, all of the estimates were relatively high except those for Micronaire. The characters studied may be ranked by their relative heritabilities as to probable ease of selection in a

breeding program in the following order:

Micronaire << 2.5% Span Length < (1/8" Gauge Stelometer,
0" Gauge Stelometer).

Since the heritabilities for 1/8" Gauge Stelometer and 0" Gauge Stelometer were above 0.5 in every case, the majority of the variance exhibited by these traits is additive and/or additive X additive in nature. Therefore, mass selection should be an effective breeding method for improving strength within this material. Mass selection for length is expected to be somewhat less effective and for coarseness a great deal less effective. To obtain a high degree of genetic progress for Micronaire, some emphasis may have to be placed on pedigrees, sib tests, and/or progeny tests.

CHAPTER V

SUMMARY AND CONCLUSIONS

Ten varieties of upland cotton and all possible F_1 crosses among them were grown in replicated, randomized tests in 1965 and 1966. The F_2 generation progenies were also included in 1966. The characters studied were fiber length as measured by 2.5% Span Length, fiber coarseness as measured by Micronaire, and fiber strength as measured by 1/8" Gauge Stelometer and 0" Gauge Stelometer.

Analyses of variance were significant for each of the characters in both years. A diallel analysis was then conducted on each fiber measurement in each year.

In the general tests of the diallel assumptions, none of the traits completely fulfilled the assumptions of the analysis, but 1/8" Gauge Stelometer and 0" Gauge Stelometer fulfilled those assumptions more nearly than did 2.5% Span Length and Micronaire.

In the specific tests of the assumptions of the diallel, four of the individual assumptions were not tested, i.e., the assumptions of diploid segregation, no reciprocal differences, homozygous parents, and no multiple alleles. Correlated gene distributions were found in the F_2 for 0" Gauge Stelometer. Epistasis could only be tested in the 1966 data and was found to be either absent or make a negligible contribution to the fiber measurements in that year. The assumption of no genotype-environment interaction within locations and years could only partially

be tested since only one location was used in the two years the experiment was run. Additive effects of the genes for the traits studied were constant relative to one another from 1965 to 1966 as were the dominance effects.

In the estimation of population parameters, estimates of E_0 were larger in every case than were the corresponding estimates of E_1. Estimates of E_2 were generally intermediate between them. Estimates of D, F, H_1, and H_2 were fairly erratic. Estimates of D were, in general, larger than estimates of F, H_1, and H_2 except for Micronaire where three out of four estimates of H were greater in magnitude than was the D value obtained in the same year. Estimates of F, H_1, and H_2 were larger in the F_2 than in the F_1 for each of the traits. H_1, in every instance, was larger than the corresponding estimate of H_2. Also in every case, F was smaller than either H_1 or H_2.

In the investigation of dominance, three measures of the overall degree of dominance were used. All of these estimates were within the partial dominance range for length, 1/8" Gauge Stelometer, and 0" Gauge Stelometer. Over-dominance appeared to be the degree of dominance operating for Micronaire. Results of these estimators in the F_1 corresponded from year to year. Results from the F_1 to the F_2 failed to correspond only in the case of the third estimator in the Micronaire data. The estimates used were, indeed, found to be overall estimates of the degree of dominance since not all crosses displayed the same degree nor direction of dominance for the same trait. Length in the F_1 and 0" Gauge Stelometer in the F_2 appeared to have most of their dominant alleles operating in one direction and most of their recessive alleles operating in the opposite direction. The direction of dominance

was toward longer fiber for 2.5% Span Length and toward stronger fiber for 0" Gauge Stelometer.

In the investigation of effective factor number, estimates of K were generally smaller than might have been expected, were erratic in size, and were rarely significantly different from zero.

In the investigation of heritability, narrow-sense heritability estimates were such that mass selection was indicated as an effective breeding method for improving strength within this material. Mass selection for length was suggested as somewhat less effective and for coarseness a great deal less effective. To obtain a high degree of genetic progress for coarseness, some emphasis would probably have to be placed on pedigrees, sib tests, and/or progeny tests.

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VITA

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Doctor of Philosophy

Thesis: A GENETIC STUDY OF FIBER PROPERTIES IN CROSSES AMONG STORM-PROOF AND OPEN-BOLL VARIETIES OF COTTON USING THE DIALLEL ANALYSIS

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