A DIALLEL CROSS ANALYSIS OF FIBER STRENGTH

IN FOUR VARIETIES OF UPLAND COTTON

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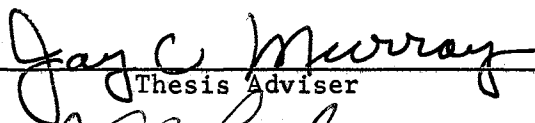Stillwater, Oklahoma
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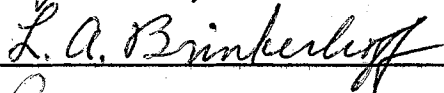for the degree of
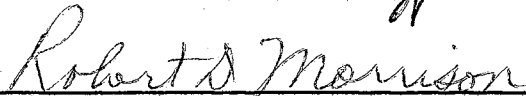DOCTOR OF PHILOSOPHY
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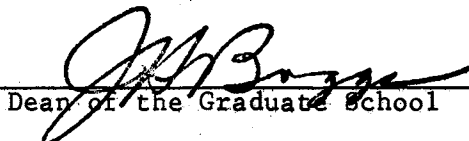Dean of the Graduate School

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ii

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TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDIX

CHAPTER I

INTRODUCTION

Cotton technologists have long recognized that the strength of raw lint cotton plays an important part in the production of high quality fabrics. Since there are varieties, which consistently produce fibers with relatively high tensile strength, it appears that the strength of the fiber of commercial cottons can be improved through breeding proper stocks.

In order to devise a breeding program for improving fiber strength, it is necessary to understand the inheritance, the heritability, and the nature of gene action governing this trait. Relatively little pertinent information concerning these subjects is available, hence, results of many more studies involving different groups of material and different methods of experimentation need to be accumulated to get a clearer picture of these phenomena.

It is the purpose of this study to provide some additional information that might contribute to a better understanding of the problem. Specifically, the objectives of this study are to obtain estimates of the diallel cross components of variance and other estimators derived therefrom, with respect to fiber strength, from a diallel cross of four commercial varieties of upland cotton grown in Oklahoma. Their breeding implications are also discussed.

CHAPTER II

REVIEW OF LITERATURE

The Inheritance of Fiber Strength

There is relatively little information available on the inheritance of fiber strength in upland cotton, Gossypium hirsutum, L. However, it has been fairly well established by early workers that fiber strength was a quantitative character being governed by a large number of genes.

Ware and Harrell (49) studied the F_1, F_2, F_3, and backcross generations of a cross between Florida Green Seed x Rowden, two stocks of upland cotton, and found that fiber strength was a quantitative character and there was slight dominance of the weak fiber.

From the data with crosses involving two varieties of upland cotton, AHA-50 x Half and Half, Self and Henderson (42) concluded that fiber strength was a quantitative trait probably governed by 4 or 5 pairs of gene. They also found that the heritability estimates for this trait were rather high.

In a rather indirect study, Ware (48) found that the X-ray diffraction patterns and the structure of cotton fiber were quantitative characters. Since there was a highly significant linear correlation between the diffraction angles and the strength of the fiber, fiber strength was also a quantitative character.

Tipton et al. (45) found in a recent study of two separate crosses of upland cotton strains, Cleveland Short Sympodia x Stardell 6-6, and Cleveland Short Sympodia x AHA-6-1-4, that fiber strength was a quantitative character presumably governed by 12 or 13 pairs of gene. They also found partial dominance of the low fiber strength and a high heritability estimate.

Heterosis and Combining Ability

Considerable interest exists among cotton breeders and geneticists on the expression of heterosis in upland cotton. Loden and Richmond (27) reviewed early works on heterosis in inter- as well as intra-specific crosses of cotton, pointing out findings ranging from no or little heterotic effects for certain characters in certain crosses to rather substantial in others.

More recent investigations on different characters (25, 32, 44, 46, 47, 50, 51) in crosses involving upland cotton varieties likewise produced variable results. Generally, in a group of materials, certain crosses exhibit substantial heterosis for certain characters as measured by comparing the F_1 with the average performance of the parental lines. However, when such F_1's are compared with the best of the parents, there are very few instances of significantly superior performances of the hybrids. Heterosis in cotton seems to be of primary importance only in yield, boll number, and boll size (32). Fiber traits occasionally showed small heterotic effects, but were generally intermediate between the parents.

There is rather meager information available on the relative magnitude of general and specific combining abilities for fiber characters

in upland cotton. Barnes and Staten (3) studied a diallel cross of seven western Acala strains, and found that specific combining ability was more important than general combining ability for fiber traits. However, from another set of diallel crosses involving south-eastern varieties, no specific combining ability was apparent. From a diallel cross among primitive and foreign strains of upland cotton, White and Richmond (51) reported a preponderance of general combining ability variance for fiber traits as compared to the specific combining ability variance.

From a diallel cross study of eight inbred lines of upland cotton, Miller and Marani (32) found a significant general combining ability variance for fiber strength and a non-significant specific combining ability variance.

Matzinger and Kempthorne (31) have shown that the general and specific combining ability variances are related to the nature of the gene action of the trait in the population under study. They reported that significant general combining ability suggests primarily additive gene action, whereas significant specific combining ability indicates the presence of dominant and epistatic effects of the character in question.

From the results of Miller and Marani (32) and of White and Richmond (51), fiber strength appears to be governed primarily by additive gene action, although the presence of heterotic effects (32) indicated the presence of dominant and epistatic effects.

Environmental Effects

Environment plays a rather important role in modifying the fiber characters, presumably due to the long maturity period of cotton fiber

(11).

Hancock (10) reported that, in general, dry and warm years tend to produce stronger and shorter fibers than do cooler and wetter seasons. However, during years of uniform rainfall distribution, the fibers tended to be both long and strong.

Pope and Ware (41) reported that fiber strength seems to be more affected by seasonal variation than do other characters of the fiber. Fiber strength appears to be significantly correlated with almost all climatic factors (12). Hesler, Lane, and Young (19) reported that the fiber development might be retarded if temperature is the limiting factor.

Spooner et al. (43) found that irrigation significantly increased fiber length, but did not significantly affect fiber strength, although there was a tendency toward lowering of strength at relatively high irrigation level.

Peebles, Den Hartog and Pressley (40) reported that somewhat weaker fibers were produced by close spacing, but the mean deficiency induced was very small and non-significant.

Limited information is available on the effect of fertilizer treatments on fiber traits. MacKenzie and van Schaik (28) found that nitrogen treatment did not affect significantly the fiber characters. Recently, Murray, Reed, and Oswalt (37) reported that various nitrogen, phosphorus, and potasium fertilizer treatments resulted in no significant differences in fiber traits.

Miller and his co-workers (33, 34, 35) have reported that fiber traits showed first and second order interactions between variety, location and year. However, in many cases the interaction components were very small relative to the variety variance component, and can be

considered unimportant.

In conclusion, fiber strength appears to be a quantitatively inherited character, governed by a large number of genes. Weak fiber appears to be partially dominant, and the heritability estimates are rather high. Presumably, the nature of gene action is primarily additive with small dominant and epistatic effects. Environment plays a part in modifying the phenotypic expression of this trait. The interactions between variety, location and year, in many cases, are small and can be considered unimportant in comparison to the varietal source of variation.

CHAPTER III

MATERIALS AND METHODS

Varieties

Four varieties of commercial upland cotton commonly grown in Oklahoma were included in this study, namely, Acala 4-42, Gregg, Lankart 57, and Stoneville 62. A short description of these varieties, as given by Brown and Ware (4), is as follows.

Acala 4-42 was developed by selection from the same general material as Acala 1517, which in turn was originally selected from Young's Acala.

Gregg was developed by selection from Macha, the latter was selected from Half and Half.

Lankart 57 is the most commonly grown variety in Oklahoma. It was developed from a Texas stormproof cotton called Lone Star.

Stoneville 62 was developed from Stoneville 2B by the Oklahoma Agricultural Experimental Station.

Under Oklahoma conditions, Acala 4-42 and Gregg produce relatively high strength fibers, while Stoneville 62 and Lankart 57 produce relatively weak fibers (36).

Experimental Procedure

All possible crosses of the four varieties were made during the summer of 1963 from a random sample of plants of each variety grown in

the field. These varieties can be considered "pure" and had been bulked for several years before. The seeds of the reciprocal crosses of any two parents were mixed together. The parental and F_1 seeds were then grown in the greenhouse in rows of 10 to 12 plants each during the winter of 1963. The parental plants were selfed and crossed in all possible combinations to obtain selfed parental and F_1 seeds. The F_1 plants were also selfed and backcrossed to both parents in order to produce F_2 and backcross seeds.

The experiment consisted of 28 entries, namely 4 parental, 6 F_1, 6 F_2, 6 B_1, and 6 B_2 generations. They were grown in the summer of 1964.

The design of the experiment was a randomized complete block with 4 replications. Each entry was grown in a single row plot of 25 feet length. The spacing between the plants in the row was 24 inches, and the rows were 40 inches apart from each other. The plants in replicates 1 and 3 were directly sown from seeds, whereas those in replicates 2 and 4 were transplanted seedlings.

The plants were cultivated in the usual practice; irrigations were applied as needed; and the plants were sprayed for insect control.

Due to the differences in maturity among the plants in the populations, the plants were harvested twice during the season. Samples of 10 bolls were taken from plants which had 10 or more bolls. The seed cotton was ginned with a saw gin, and the lint was analyzed for their fiber properties. The strength of the fiber reported in this study was measured in T_0 unit, namely, the strength of a bundle of fibers measured on a Stelometer with two jaws holding the bundle tightly appressed. The strength is expressed in grams/grex.

Statistical Procedure

A. Analysis of Variance. Analysis of variance was conducted to test the differences in fiber strength among the entries, and to provide an estimate of error variance, which will be used in testing the presence of heterosis and inbreeding depression.

B. Test of Heterosis and Inbreeding Depression. To test the presence of significant heterotic effect the mean of the F_1 of each cross was compared with the mean of each of its mid-parents (MP) value. By assuming that the mid-parents values are normally distributed and have equal error variance as the F_1, t-tests were conducted on each of the mean of $(F_1 - MP)$ values.

Inbreeding depression was tested by comparing the mean of F_2 and that of F_1 of each cross. Similarily, the error variances of F_1 and F_2 values are assumed to be equal, and t-tests were conducted on each of the mean of $(F_2 - F_1)$ values.

In addition, the direction of the average degree of dominance in the parents was determined from the sign of the mean of $(F_1 - MP)$ values. On the assumption that these differences are normally distributed, the confidence limits of the mean of $(F_1 - MP)$ were set.

C. Diallel Cross Analysis. The diallel cross analysis employed in this study is the one developed by Jinks and Hayman (23) and later elaborated by Hayman (13, 14, 15, 16) and Jinks (20, 21, 22), and recently used and discussed by Crumpacker and Allard (6), Johnson (24), White and Kohel (50), and Whitehouse, Thompson and Do Valle Ribeiro (52).

Hayman's model is based on several assumptions, each of which must hold true for the analysis to be valid. These assumptions are (6):

1. Homozygous parents

2. Diploid segregation

3. No reciprocal differences

4. No genotype - environment interaction

5. No non-allelic gene interaction

6. No multiple alleles

7. Uncorrelated gene distributions

The first four assumptions appear to be valid for G. hirsutum.

G. hirsutum can be considered as a mostly-self-pollinated crop.
With controlled pollination, a homozygous condition can be more assured.
The parental plants used in this study are samples of rather "pure" var-
ieties, which had been bulked for several years, and selfed for one
generation. Consequently, the parental plants are considered to be
fairly homozygous.

Although G. hirsutum is an amphidiploid, according to Endrizzi (9)
and Kimber (26), it segregates in a diploidal manner.

For most characters of cotton, many authors consider that there
are no differences between reciprocal crosses. Recently, White and
Richmond (51) reported no significant differences between reciprocal
crosses for fiber strength and other fiber properties.

The fifth assumption can be tested using the method given by Hayman
(14), which are presented later in this chapter.

The last two assumptions, in fact all of these assumptions, can
be tested by the diallel cross or (Vr, Wr) graph (14, 20, 23). This
test is presented later in this chapter.

When these assumptions are valid, the contribution of each locus
to the family means in a diallel cross can be described in terms of the

genetic parameters $\underline{u}$, $\underline{v}$, $\underline{d}$, and $\underline{h}$ (23, 29), where:

u and v = respectively, frequencies of positive and negative alleles.

$$o \leqslant u, v, \leqslant 1; \quad u + v = 1$$

d = additive effect. $\quad o \leqslant d \leqslant c_1$

h = dominant effect. $\quad c_2 \leqslant h \leqslant c_3; \quad c_2 \leqslant o, \quad c_3 \geqslant o$

c_1, c_2 and c_3 = constant values (for each gene).

Then a number of statistics can be calculated from the parental, F_1, F_2, and backcross family means. For a number of genes, say $\underline{k}$, the genetic contents of certain statistics, in terms of the genetic parameters, from the parental and F_1 family are as follows (13, 23):

$$\text{Var.[1] of parents} = Vp = V_{0L0} = 4 \sum u_i v_i d_i^2 \tag{a}$$

$$\text{Var. of the } r^{th} \text{ array[2]} = Vr = \sum_{i=1}^{j} u_i v_i (d_i - h_i)^2 + \sum_{j+1}^{k} u_i v_i (d_i + h_i)^2 \tag{b}$$

$$\text{Mean var. of arrays} = V_{1L1} = \sum \left[u_i v_i \left\{ d_i^2 + h_i^2 - 2 d_i h_i (u_i - v_i) \right\} \right] \tag{c}$$

$$\text{Var. of array means} = V_{0L1} = \sum \left[u_i v_i \left\{ d_i - h_i (u_i - v_i) \right\}^2 \right] \tag{e}$$

$$\text{Covar.[3] of the } r^{th} \text{ array} = Wr = 2 \sum_{i=1}^{j} u_i v_i d_i (d_i - h_i) + 2 \sum_{j+1}^{k} u_i v_i d_i (d_i + h_i) \tag{f}$$

$$\text{Mean covar. of arrays} = W_{0L01} = 2 \sum \left[u_i v_i d_i \left\{ d_i - (u_i - v_i) h_i \right\} \right] \tag{g}$$

$i = 1, 2, \ldots, k$; j = the number of negative alleles; $j < k$

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[1]Var. = variance.

[2]Array. = All crosses which have a common parent, including the parent itself.

[3]Covar. = Covariance of the rth array and their non-recurrent parents.

The subscript L refers to the diallel cross mating system, and the subsequent number(s), beginning from 0 for the parents, refer to the generations under consideration. In variances of individual measurements, the number preceding L is the same as the one following, whereas in variances of means and in covariances, the number(s) preceding L refers to the generation(s) of the common parents. The summations are over all values of i, except for Vr and Wr.

Jinks and Hayman (23) defined the diallel crosses components of variance or the diallel cross parameters as:

$$D = 4 \sum u_i v_i d_i^2 \tag{p}$$

$$H_1 = 4 \sum u_i v_i h_i^2 \tag{q}$$

$$H_2 = 16 \sum u_i^2 v_i^2 h_i^2 \tag{r}$$

$$F = 8 \sum \left[u_i v_i (u_i - v_i) d_i h_i \right] \tag{s}$$

Taking into account the environmental variances, the expectations of the variances and the covariances of the family means, in terms of the diallel cross components of variance, are as follows:

For parental and F_1 families (13, 20):

$$V_{0L0} = D + E_0$$

$$V_{0L1} = \tfrac{1}{4}D + \tfrac{1}{4} H_1 - \tfrac{1}{4}H_2 - \tfrac{1}{4}F + E_0 + (n - 2)E_1/n^2$$

$$V_{1L1} = \tfrac{1}{4}D + \tfrac{1}{4} H_1 - \tfrac{1}{4} F + E_0 + (n - 1)E_1/n$$

$$W_{0L01} = \tfrac{1}{2}D - \tfrac{1}{4}F + E_0/n$$

where: E_0 and E_1 are the environmental variances for the parental and F_1 families.

   n is the number of parents in the diallel cross.

For parental and F_2 families (14, 22):

$$V_{0L2} = \tfrac{1}{4}D + (1/16)H_1 - (1/16)H_2 - (1/8)F + E_0 + (n - 2)E_2/n^2$$

$$V_{1L2} = \tfrac{1}{4}D + (1/16)H_1 - (1/8)F + E_0 + (n-1)E_2/n$$

$$V_{2L2} = \tfrac{1}{4}D + (1/8)H_1 + E_2$$

$$W_{0L02} = \tfrac{1}{2}D - (1/8)F + E_0/n$$

where: E_2 is the environmental variance for the F_2 family, and E_0,

E_1, and $\underline{n}$ are as defined above.

For the parental and backcross populations (22):

In the absence of non-allelic interactions, there exists a relation-ship between the F_2 family mean and the means of the two reciprocal back-cross families, namely $\overline{F}_2 = \tfrac{1}{2}(\overline{B}_1 + \overline{B}_2)$. Thus, in the absence of non-allelic interactions, the expected statistics for the means of the reciprocal backcross families are identical with those for the F_2 family means (22).

Estimates for each set of these statistics can be calculated from the tables consisting of the means of the parents and F_1's, the means of the parents and F_2's, and the means of the parents and the average of the reciprocal backcrosses. These three tables will, respectively, be called the L_1, L_2, and B_1 tables.

Since the estimates of environmental variances can be obtained from replicated experiments, the estimates of the diallel cross parameters can be solved from each set of equations given previously. These equa-tions can be solved by a method given by Mather (29) and Hayman (13). The normal equations of the diallel cross parameters are obtained and their coefficients are set in a square matrix that is symmetrical about the main diagonal. This matrix is then inverted to obtain the covar-iance matrix. The latter is used to provide estimates of D, H_1, H_2, and F. In this solution, V_{0L0}, V_{0L1}, V_{1L1}, and W_{0L01} are assumed to be independent and normally distributed.

To avoid these assumptions, Nelder (38) and Crumpacker and Allard (6) suggested that each replication be treated as a separate experiment with its own environmental component of variance. Then by assuming that the estimates of these parameters from each block are samples of normal population, the standard error of the mean of each of these parameters can be estimated from the variation of the block values around the overall mean. This is considered desirable, since the distribution of the sample means tends toward normality with increasing size of samples, eventhough the individual varieties may not be distributed normally. The estimates of the diallel cross parameters in this study are made according to Nelder's suggestion with separate estimates of environmental variances.

A number of important estimators that may be derived from the diallel cross parameters (22) among others are:

1. H_1/D, an estimator of the average degree of dominance, since $H_1/D = \sum u_i v_i h_i^2 / \sum u_i v_i d_i^2$. This quantity is weighted in favor of the genes which have both alleles represented equally in the parents and have large $\underline{h}$ effects (6). With average partial dominance, H_1/D is expected to have a value between 0 - 1. The square root of H_1/D is a weighted measure of the average degree of dominance at each locus.

2. $(V_{1L1} - E)/(W_{0L01} - E/n)$ is another estimate of the average degree of dominance. It is a weighted estimator in the same sense as H_1/D, and with partial dominance it will also fall between 0 and 1.

3. The sign of $(\overline{F}_1 - \overline{MP})$, an indicator of the average direction of dominance. The variation of the individual $(\overline{F}_1 - \overline{MP})$ around the mean of $(\overline{F}_1 - \overline{MP})$ was used to estimate the standard error for the mean of $(\overline{F}_1 - \overline{MP})$.

4. $\frac{1}{4}H_2/H_1$, an estimator for the average frequency of negative versus positive alleles in the parents, since $\frac{1}{4}H_2/H_1 = (\sum u_i^2 v_i^2 h_i^2)/$ $(\sum u_i v_i h_i^2) = \overline{u}\overline{v}$. It has a maximum value of $\frac{1}{4}$ when $u = v = \frac{1}{2}$. If the negative and the positive alleles are not equally distributed among the parents, $uv < \frac{1}{4}$. This estimator is weighted in favor of the genes with large $\underline{h}$ effects. No information is provided for the genes that have no dominant effects.

5. The parameter $F = 8\sum \left[u_i v_i (u_i - v_i) d_i h_i\right]$. Its sign depends on the sign of $(u_i - v_i) h_i$, and the magnitude of each of these parameters. If no genes exhibit dominant effects, or if the dominant and the recessive alleles of each gene are distributed equally among the parents, $F = 0$. In the excess of dominant alleles F will be positive, whereas an excess of recessive alleles will cause F to be negative. Thus the sign of F is an indicator of the relative frequencies of dominant and recessive alleles in the parents. When the $\underline{h}$ effects of each gene are unequal, the sign of F will be weighted in favor of the genes with large $\underline{h}$ effects.

6. $\underline{K}$, the effective factors $= (\overline{F}_1 - \overline{P})/\frac{1}{2}H_2$.

An effective factor has been defined by Mather (29) as the smallest unit that is capable of being recognized by the methods of biometrical genetics. It may be a group of closely linked genes or, at the lower limit, a single gene. The value of $\underline{K}$ will be underestimated unless the $\underline{h}$ effects of all genes are equal in sign and size, and the distribution of the genes is uncorrelated (20, 29). It also gives no information on the genes with no dominant effects.

Most of these estimators are ratios, and the question of their biasness immediately arises. This problem is a troublesome one. However,

the approximate standard errors of these ratios can be estimated similar to Nelder's suggestion in estimating the standard error for the diallel parameters, namely, from the variation of the ratios calculated from each block around the over-all mean of the ratios. For example, the ratio of H_1/D is determined for each block and the block values are used to estimate the mean, and the standard error of the mean of H_1/D.

D. Diallel Cross Graph. Consider equations (b), (f), (p), and (q). The quantity $Wr - Vr$ is equal to $\frac{1}{4}(D - H_1)$ and is expected to be constant over all arrays, independent of $\underline{r}$, if the basic assumptions are valid and environmental effects are negligible. Thus, Wr = contant + Vr, under these conditions. By plotting Wr on Vr, the regression of Wr upon Vr is a straight line with unit slope (7, 23).

Consider equations (a), (b), and (f). Jinks and Hayman (23) have shown that there is an inequality of $Wr^2 \leqslant Vp\ Vr$. This means that all Wr and Vr points on the (Vr, Wr) graph should lie inside the parabola $Wr^2 = Vp\ Vr$.

Thus, the regression of Wr on Vr in the diallel cross or (Vr, Wr) graph can be used to test the validity of the basic assumptions, supported by the fact that all values of Vr and Wr should lie inside the $Wr^2 = Vp\ Vr$ parabola.

Furthermore, the (Vr, Wr) graph is also a means to make some genetic analysis. Consider again the equation $Wr = \frac{1}{2}(D - H_1) + Vr$. When $Vr = 0$, then $Wr = \frac{1}{2}(D - H_1)$. Thus on the (Vr, Wr) graph, the Wr intercept is an indicator of the average degree of dominance in the experimental materials. With partial dominance, $H_1 < D$, the Wr intercept will be positive, whereas in overdominance, $H_1 > D$, the Wr intercept will be negative. With average complete dominance, $H_1 = D$, the regression line

will pass through the origin. In the case of no dominance, all points of the (Vr, Wr) graph will estimate one single point, Wr = 2 Vr (6, 7, 23). Dickerson and Jinks (7) illustrated these situations with certain values of dominance (Fig. 1).

The positions of the array points along the line of regression of Wr on Vr depend upon the relative proportion of dominant and recessive alleles present in the common parent of each array (13, 20). Parents with a preponderance of dominant effects will have a low array variance and covariance, and will lie near the origin. Highly recessive parents will have a large array variance and covariance, and will lie on the part of the regression line, away from the origin. If the dominant effects of the genes are unequal, the position of an array point will be weighted in favor of genes with large dominant effects.
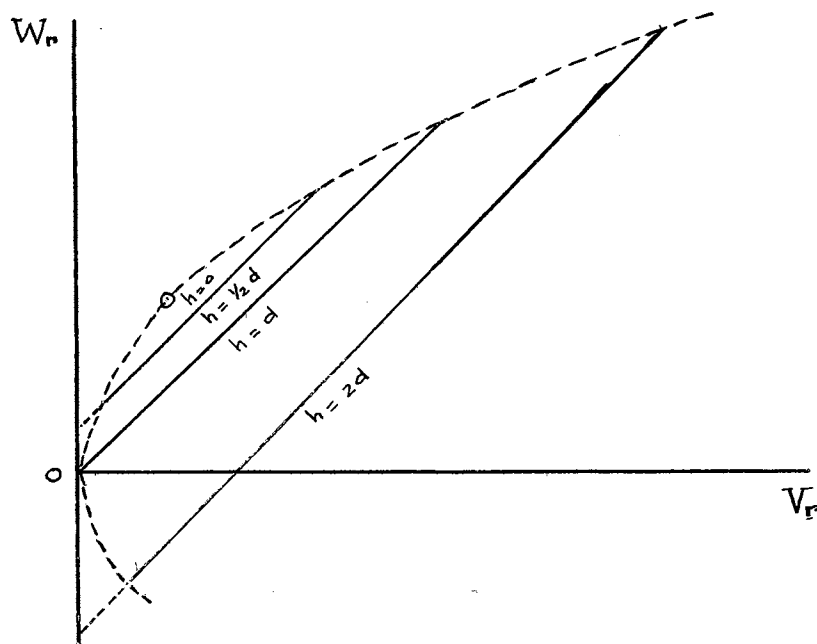
Fig. 1. The regression lines of Wr on Vr with varying degrees of dominance. After Dickinson and Jinks (7).

The analysis by means of the (Vr, Wr) graph can be applied and interpreted similarly to the F_2 family (15, 23). Further, the graph of F_1 array variances or covariances on the F_2 variances or covariances should be on a straight line of slope $\frac{1}{2}$ (15, 23).

Thus, the (Vr, Wr) graph provides a test of the validity of the basic assumptions ($b_1 = 1$), the presence of dominance, and the average degree of dominance (the sign of b_0), where b_1 is the slope of the regression line and b_0 is the Wr intercept.

Failure of any of the basic assumptions will cause deviation of the (Vr, Wr) points from the regression line with unit slope. With increasing proportion of heterozygosity in the parents, there will be a proportional shifting of the regression line upwards and to the left. The effect of this shift is to simulate a lower level of dominance. The deviation of the regression line from unit slope may be significant (7, 23). Similar bias may be due to allele frequencies correlation, or linkage (7). Non-allelic interaction, particularly complementary gene action, results in deviation of the points corresponding to the arrays of the interacting parents from the expected regression line. Hence, in such cases, the actual regression line will usually deviate from unit slope. It may cause extreme deviation of the corresponding points to the right and below the expected regression line (7, 13, 23).

E. Test of Non-allelic Interactions. One of the many recent explanations of heterosis is the joint action of favorable combinations of genes at different loci, that is non-allelic interactions or epistasis. Comstock and Robinson (5) pointed out that non-allelic interactions could inflate intra-allelic interactions. Jinks (21) suggested that apparent over-dominance may be due to epistasis. Henderson (18) suspected that

non-allelic interactions might be partly responsible for heterotic effects.

Due to the importance of non-allelic interactions, Hayman (14) introduced a method to test the significance of these interactions in the diallel cross experiment, when the F_2 is included. It is a kind of Chi-square test for fit that can be calculated from the $2L_2 - L_1$ table. This table is similar to the L_1 or L_2 table, and as the name suggests, it is constructed by subtracting each term of the L_1 table from twice the term, in similar position, of the L_2 table.

The Chi-square value for $\frac{1}{2}n(n - 1)$ degrees of freedom is (14):

$$\text{Chi-square} = k_2 \left[(n - 1)(V_{1LX} - V_{0LX}) + n(\bar{p} - \bar{x})/(1 + k) + (n - 1)(V_{0L0} - 4W_{0L0X} + 4V_{0LX})/(2 + k) \right]$$

Where: V_{0L0}, V_{0LX}, V_{1LX}, and W_{0L0X} are analogous to V_{0L0}, V_{0L1}, V_{1L1}, and W_{0L01}, calculated from the $2L_2 - L_1$ table.

$k = nE_0/(8E_2 + E_1 - E_0)$

$k_2 = n/(8E_2 + 2E_1)$

E_0, E_1, E_2, and $\underline{n}$ are as defined before on page 12.

$\bar{p}$ = the mean of parents

$\bar{x}$ = the grand mean (of parents, F_1, and F_2).

A significant Chi-square value indicates the presence of significant non-allelic interactions. It can be investigated in detail, whether it is manifested in the F_1, or F_2 families. Then the epistatic crosses can also be classified into duplicate or complementary epistasis (14, 52).

CHAPTER IV

RESULTS AND DISCUSSION

In this experiment, the plants grown from seedlings survived better than those grown by direct seeding in the field. Many of the plants in replication 1 and replication 3 did not grow well, some had no or less than 10 open bolls during the harvest time. The number of observations or subsamples in replicate 1 varied from 0 to 13, whereas that in replicate 3 varied from 3 to 13. The smallest number of subsamples in replicate 2 and replicate 4 are 6 and 8, respectively. The complete number of subsamples for each entry in each replicate is given in Table I.

Due to the missing observation of the Gregg population in replicate 1, and the presence of very small (three) subsamples in replicate 3, only the analysis based on replicate 2 and replicate 4 is presented in this report. To avoid any effects of unequal subsamples in the diallel analysis, random samples (except for the entry that has the smallest number of subsamples) of 6 observations were taken from each population for statistical analysis.

Analysis of Variance

The analysis of variance based on these two replications is given in Table II. There are highly significant differences among the populations. Block effects, experimental and sampling errors are relatively small in comparison to the variation of the population. The differences

TABLE I

NUMBER OF SUBSAMPLES

Generation	Entry	Replicate				Total
		1	2	3	4	
Parents	A	7	9	10	10	36
	G	0	12	3	10	25
	L	10	12	5	12	39
	S	9	12	8	12	41
F_1	A x G	6	10	8	9	33
	A x L	12	12	9	11	44
	A x S	9	11	8	12	40
	G x L	13	12	10	12	47
	G x S	9	8	5	9	31
	L x S	9	9	9	11	38
F_2	A x G	10	11	8	9	38
	A x L	9	11	5	11	36
	A x S	9	9	11	12	41
	G x L	5	13	8	11	37
	G x S	6	13	10	11	40
	L x S	11	12	5	9	37
B_1	(A x G) x A	6	12	5	10	33
	(A x L) x A	7	10	6	11	34
	(A x S) x A	8	12	8	8	36
	(G x L) x G	10	6	7	8	31
	(G x S) x G	9	11	5	9	34
	(L x S) x L	9	10	9	12	40
B_2	(A x G) x G	5	13	5	9	32
	(A x L) x L	6	12	5	9	32
	(A x S) x S	5	13	5	13	36
	(G x L) x L	2	12	8	10	32
	(G x S) x S	6	12	8	10	36
	(L x S) x S	8	12	3	10	33

Legend: A = Acala 4-42
        G = Gregg
        L = Lankart 57
        S = Stoneville 62

These abbreviations will be used in many instances in this report.

TABLE II

ANALYSIS OF VARIANCE

Source of variation	d.f.	Sums of Squares	Mean Squares
Total	335	349.6630	
Replicate	1	0.3523	0.3523
Population	27	237.4092	8.7829**
Experimental error	27	12.6669	0.4691
Sampling error	280	99.2346	0.3544

**Significant at 1% probability level.

among the populations are likely to occur, since two of the parents have high tensile strength, and the other two have low tensile strength.

Heterosis and Inbreeding Depression

The means of parents, mid-parents, $\overline{F}_1$, $\overline{F}_2$, $(\overline{F}_1 - \overline{MP})$, and $(\overline{F}_2 - \overline{F}_1)$ are given in Table III. The estimate of the standard error of the difference between two means is 0.39. None of the calculated t - values of each of $(\overline{F}_1 - \overline{MP})$ and of $(\overline{F}_2 - \overline{F}_1)$ exceeds the tabulated t-value at 5% probability level. Thus, heterotic effect and inbreeding depression are not significant at 5% probability level.

All of the differences of the F_1 and the mid-parent values have negative signs. The standard error of the mean of these differences is estimated to be 0.015. The 99% confidence limits on the mean of the differences are -0.11 and 0.01. Thus the sign of the average degree of dominance in the parents is negative, or the low tensile strength is dominant over the high tensile strength. This confirmed the findings of earlier workers (42, 45, 48).

TABLE III

MEANS OF PARENTS (P_1, P_2), MID-PARENTS (MP), F_1
F_2, (F_1 - MP) AND (F_2 - F_1) OF INDIVIDUAL
CROSSES, IN GRAMS/GREX

Crosses	P_1	P_2	MP	F_1	F_2	(F_1 - MP)	(F_2 - F_1)
A x G	4.00	4.10	4.05	4.02	4.04	-0.03	0.02
A x L	4.00	3.23	3.62	3.54	3.57	-0.08	0.03
A x S	4.00	3.47	3.75	3.64	3.50	-0.10	-0.14
G x L	4.10	3.23	3.67	3.61	3.72	-0.06	0.11
G x S	4.10	3.47	3.79	3.77	3.80	-0.02	0.03
L x S	3.23	3.47	3.35	3.34	3.50	-0.01	0.16
Mean			3.70	3.65	3.69	-0.05	0.04

In conclusion, no heterotic effects and inbreeding depression are detected, at 5% probability level, in individual crosses of the materials studied, although there are highly significant differences among the populations. The direction of the average degree of dominance in the parents is toward the low tensile strength, or on the average there is dominant effects of low tensile strength over high tensile strength.

Diallel Cross Graph

Before proceding to the estimation of the diallel cross parameters, it is essential to see that the basic assumptions are valid. A method to test the validity of these assumptions is by analyzing the diallel cross or the (Vr, Wr) graph (7, 13, 23).

The means, overall replicates, of the parents, F_1, and F_2 are given in Table IV and Table V, which are the L_1 and the L_2 tables, respectively. The means of parents are in the diagonal, and those of the crosses are in the off-diagonal positions in the respective table.

TABLE IV

MEANS OF PARENTS AND F_1, IN GRAMS/GREX

Parent	A	G	L	S
A	4.00	4.02	3.54	3.64
G		4.10	3.72	3.80
L			3.23	3.35
S				3.47

TABLE V

MEANS OF PARENTS AND F_2, IN GRAMS/GREX

Parent	A	G	L	S
A	4.00	4.04	3.57	3.50
G		4.10	3.72	3.80
L			3.23	3.50
S				3.47

Estimates of variance of parents (Vp), variance of each array, (Vr), and covariance of each array (Wr) were calculated for the F_1 and F_2 generations from the L_1 and L_2 tables, respectively. For each of the array variance or covariance, r was substituted with a, g, l, and s, which stands for Acala 4-42, Gregg, Lankart 57, and Stoneville 62 arrays, respectively. The values of these estimates are given in Table VI.

The Vp, Vr, and Wr values calculated from the L_1 and L_2 tables were plotted into the (Vr, Wr) graphs, respectively, in Figure 2 and Figure 3. In both graphs, all points lie inside the theoretical parabola $Wr^2 = 0.1746\ Vr$. The slopes of the regression lines of Wr on Vr (b_1)

TABLE VI

ESTIMATES OF Vp, Vr, AND Wr

| Statistics | Generation | |
	F_1	F_2
Vp	0.1746	0.1746
Va	0.0605	0.0795
Vg	0.0510	0.0337
Vl	0.0303	0.0420
Vs	0.0342	0.0242
Wa	0.1027	0.1110
Wg	0.0941	0.0765
Wl	0.0725	0.0786
Ws	0.0758	0.0423

in both graphs are not significantly different from one, and the Wr intercepts (b_0) in both graphs are positive, but only in the F_1 generation is it significantly different from zero at 5% probability level. The complete regression analyses following the method given by Ostle (39) are in Appendix A and Appendix B.

From the results of the regression analysis, it seems likely that the basic assumptions are valid. However, the positions of the array points along the regression lines in figure 2 and figure 3 are not constant. This provides evidence that some of the basic assumptions are not strictly valid.

The position of the regression lines toward the hypothetical parabola in both graphs show that, on the average, the dominance effects are not complete. As previously shown, the direction of the average degree of dominance is negative; hence, there is partial dominance of the low over high tensile strength. This was also found by earlier workers
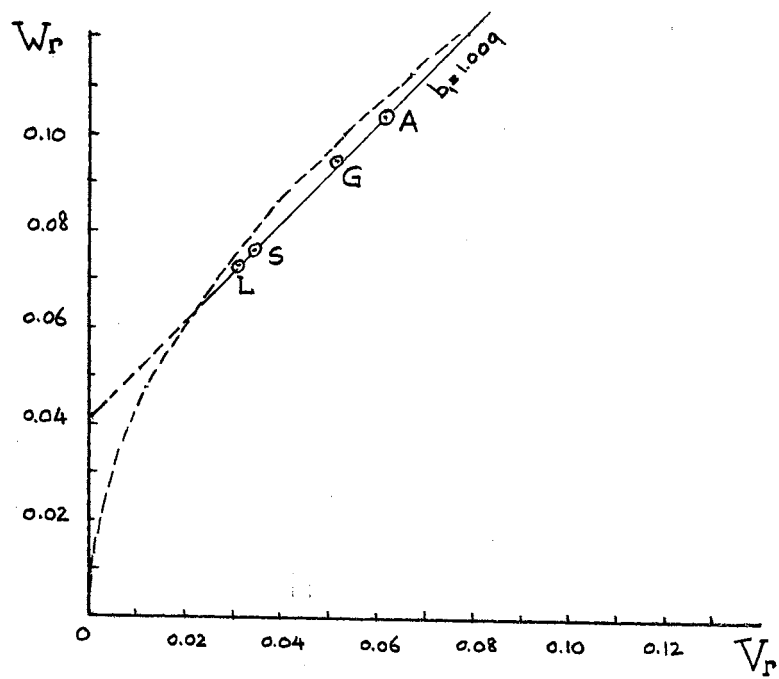
Fig. 2. The (Vr, Wr) graph of the F₁ family.
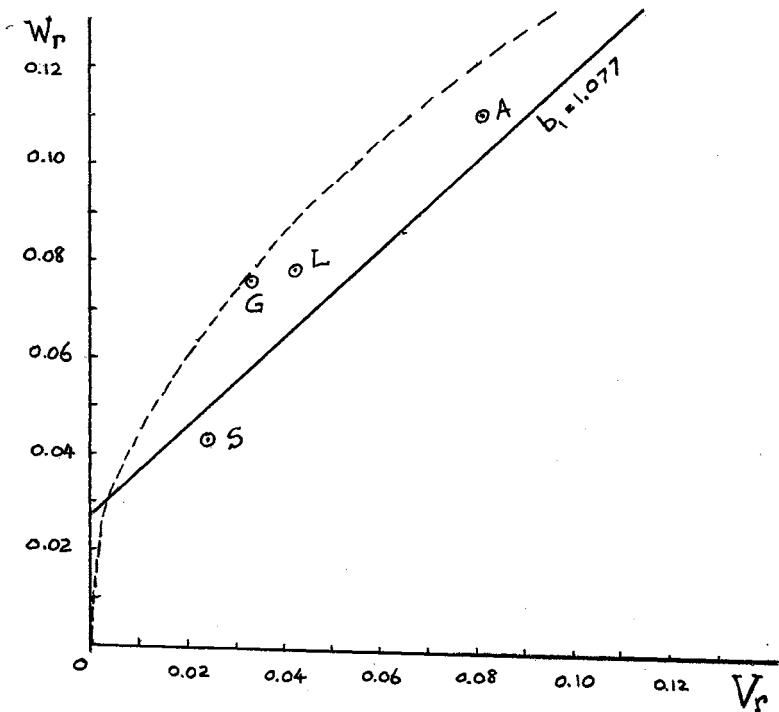
Fig. 3. The (Vr, Wr) graph of the F₂ family.

(42, 45, 48).

The positions of the arrays along the regression line in figure 2, suggest that Lankart 57 and Stoneville 62 are parents with a preponderance of dominant alleles, and Acala 4-42 and Gregg are highly recessive parents. However, in figure 3 Gregg, Lankart 57, and Stoneville 62 do not maintain their positions. The downwards shifting of Gregg and Stoneville 62, suggests that these two parent probably contribute non-allelic interactions (7, 13, 23). The positions of Acala 4-42 and Lankart 57 shift upwards and to the right; an indication that these two parents are probably not quite homozygous. The position of Acala 4-42 in the F_1 and F_2 generations are always on the top of all arrays, farthest from the origin. Therefore Acala 4-42 is the parent that has the least dominant effects.

Test of Non-allelic Interactions

Due to the evidence of the presence of non-allelic interactions, as shown from Figure 2 and Figure 3, it is necessary to test the significance of these interations. The method given by Hayman (12) was used here. Table VII is the $2L_2 - L_1$ table.

TABLE VII

THE $2L_2 - L_1$ TABLE*

Parent	A	G	L	S
A	4.00	4.06	3.60	3.36
G		4.10	3.81	3.83
L			3.23	3.65
S				3.47

*See text for explanation.

The calculated Chi-square value for 6 degrees of freedom is 0.94. The tabulated value at 5% probability level for 6 degrees of freedom is 12.6. Thus, non-allelic interactions exhibited by Gregg and Stoneville 62 arrays are not significant at the 5% probability level. This is also supported by the results of the regression analysis that the slopes of the regression lines in both generations do not deviate significantly from one. Since there are no significant non-allelic interactions, no further test was conducted to find the type of interactions.

Diallel Cross Analysis

Evidence from the regression analysis of Wr on Vr, in both F_1 and F_2 generations and the result of the Chi-square test for non-allelic interactions suggests that the basic assumptions are, to a certain extent, valid. Hence, the estimation of the diallel cross parameters can be justified.

As suggested by Nelder (38), by Crumpacker and Allard (6), and by Hayman (17), each replicate was treated as separate experiment, and the estimates of D, H_1, H_2, and F from each replicate are regarded as samples of the true parameters. In addition, the estimates of these parameters calculated from the F_2 and backcross generations were also regarded as such samples, since these estimates are also estimates of the true parameters in the parents.

The sets of parent and F_1 generation means, of the parent and F_2 generation means, and the parent and the average of reciprocal backcross means for each replicate are presented in Table VIII, Table IX, and Table X. In most cases, the differences between the means of any generation in the two replicates are not apparent. This was expected,

TABLE VIII

MEANS OF PARENTS AND F_1 IN REPLICATE 2*
AND REPLICATE 4, IN GRAMS/GREX

Parent	A	G	L	S
A	3.90	4.01	3.54	3.69
	4.10	4.02	3.54	3.59
G		4.12	3.54	3.84
		4.08	3.67	3.70
L			3.22	3.35
			3.24	3.34
S				3.46
				3.47

*Upper figures are the means in replicate 2.

TABLE IX

MEANS OF PARENTS AND F_2 IN REPLICATE 2*
AND REPLICATE 4, IN GRAMS/GREX

Parent	A	G	L	S
A	3.90	3.88	3.60	3.50
	4.10	4.20	3.54	3.49
G		4.12	3.62	3.83
		4.08	3.81	3.76
L			3.22	3.52
			3.24	3.48
S				3.46
				3.47

*Upper figures are the means in replicate 2.

TABLE X

MEANS OF PARENTS AND B_1^* IN REPLICATE 2**

AND REPLICATE 4, IN GRAMS/GREX

Parent	A	G	L	S
A	3.90	4.09	3.39	3.72
	4.10	4.07	3.42	3.56
G		4.12	3.55	3.89
		4.08	3.78	3.88
L			3.22	3.44
			3.24	3.43
S				3.46
				3.47

*The average of reciprocal backcrosses

**Upper figures are the means in replicate 2.

since there were no significant differences between replicates, as indi-
cated from the analysis of variance.

Estimates of variances and covariances needed to estimate the dial-
lel cross parameters, calculated from each replicate for each generation,
do not differ markedly. The low figures of the estimates are probably
due to the scale of measurement used in this study.

Estimates of environmental variances for the parents, F_1, and F_2
generations, namely, E_0, E_1, and E_2, were calculated as the within group
variance of each generation in each replicate. These estimates and each
of their averages can be found in Table XII.

It appears that the estimates in both replicates are homogeneous,
but no statistical test is conducted, since the estimates of each repli-
cate will be used separately in the estimation of the diallel cross

TABLE XI

ESTIMATES OF THE SECOND DEGREE STATISTICS, USED FOR THE ESTIMATION OF THE DIALLEL CROSS PARAMETERS, OF F_1, F_2, and B_1 GENERATIONS

Statistics	F_1		F_2		B_1	
	Rep. 2	Rep. 4	Rep. 2	Rep. 4	Rep. 2	Rep. 4
V_{0L0}	0.1673	0.1923				
V_{0L1}	0.0454	0.0475				
V_{1L1}	0.0329	0.0416				
W_{0L01}	0.0845	0.0895				
V_{0L2}			0.0364	0.0722	0.0588	0.0589
V_{1L2}			0.0263	0.0462	0.0473	0.0459
V_{2L2}			0.0426	0.1276	0.1241	0.1153
W_{0L02}			0.0662	0.0899	0.0962	0.0881

TABLE XII

ESTIMATES OF ENVIRONMENTAL VARIANCES

Statistics	Rep. 2	Rep. 4	Mean
E_0	0.0441	0.0291	0.0366
E_1	0.0251	0.0536	0.0396
E_2	0.0342	0.0422	0.0382

parameters. The averages seem to be more uniform, and were used to
determine the values of k and k_2 for the test of non-allelic interactions.
In general, the estimates of environmental variances are rather large, in
comparison to some of the estimates of the second degree statistics given
in Table XI.

By substituting the value of environmental variances into the equa-
tions given in the previous chapter, the estimates of D, H_1, H_2, and F
were solved. These estimates, each of their means, and their standard
errors are presented in Table XIII. Each of their standard errors were
estimated from the variation of each estimate in each replicate in each
generation, around their respective means.

Of all the estimates, only those of D that are consistently posi-
tive throughout the replicates and generations, and the mean of these
estimates is significantly different from zero at the 5% probability
level. The mean of the estimates of F is also positive, but its stan-
dard error is comparatively big. The mean of the estimates of F is signi-
ficantly different from zero at approximately 20% probability level.
Only by disregarding the estimates from the F_1 generation in the calcula-
tion is the mean of F significantly different from zero at 5% probability
level. The negative estimates of H_1 and H_2 are rather puzzling, since
their true values should be either zero or positive. Probably the true
values of each of these parameters, are very small. It may also be
due to the large value of the estimates of environmental variances.
As is observed from Table XI and Table XII, some of the estimates of
variances that contain these two parameters, are even smaller than the
environmental variances.

TABLE XIII

ESTIMATES OF THE DIALLEL CROSS PARAMETERS,

THEIR MEANS AND STANDARD ERRORS

Parameter	F_1		F_2		B_1		Mean	Standard Error
	Rep. 2	Rep. 4	Rep. 2	Rep. 4	Rep. 2	Rep. 4		
D	0.1232	0.1632	0.1864	0.3144	0.3212	0.2938	0.2337	0.0787
F	-0.0476	-0.0024	0.3040	0.5968	0.6032	0.5288	0.3305	0.2705
H_1	-0.1600	-0.1892	-0.3056	0.0544	0.0768	-0.0027	-0.0877	0.1399
H_2	-0.1468	-0.1796	-0.6368	-0.9216	-0.6214	-0.7136	-0.5371	0.2438

33

It can be concluded that the estimate of D is bigger than that of H_1, or presumably the genetic variance of the parents are primarily additive and/or additive by additive components. The component of variance due to the dominant effects, H_1, is either zero or very small. If it were zero, most probably the dominant effects of each locus cancel each other.

The positive value of the mean of F suggests that the frequency of positive alleles, in this case the high tensile strength, in the parents is higher than its negative counterparts. It was rather expected, because from the history of these four varieties, they had been selected for their agronomic characteristics, probably including their tensile strength.

Due to the negative estimates of H_1 and H_2, (and they are also not significantly different from zero) some of the estimators that contain any or both of these parameters were not estimated. The average degree of dominance, that can be estimated as H_1/D, was estimated by $(V_{1L1} - E)/(W_{0L01} - E/n)$, where E is the average of E_0 plus E_1 over all replicates. Since there are only two estimates of V_{1L1} and W_{0L01}, their means were used in the calculation. The estimate calculated thusly is 0.09. Therefore, on the average the dominant effect among the parents is not complete. No statistical test was conducted on this estimates. This value supports the evidence shown from the (Vr, Wr) graph of partial dominance of the character.

Estimates of heritability were calculated as the additive and/or additive by additive genetic portion of the variance of parents (V_{0L0}), and as that of the mean variance of arrays (V_{1L1}). These estimates are 79% and 94%, respectively. In both cases, the heritability estimates

are high.

Discussion

Cotton breeder, as many other breeders of self-pollinated crop plants, realize slow progress has been achieved in breeding quantitative characteristics. This slow progress, in part, may be due to a slow development of the breeding principles for the complexly inherited character.

Two important problems are faced by the breeders of self-pollinated plants. First, to choose the best parents for hybridization, and second, the selection of the best lines from hybrid progenies. The efficiency of breeding self-pollinated plants, thus depends on accurate identification of the hybrid combinations that have a good potential of producing maximum improvement, and on identifying in early generations superior lines among the progeny of the promising hybrids.

Diallel cross analysis is probably the most popular design for assessing quantitative variability in self-pollinated crops, because it may be used to characterize crossing relationships among a group of varieties or lines (30). In a way, this study was aimed towards the assessment of the progress that could possibly be obtained from the diallel cross study.

In choosing the best parents for hybridization, naturally, the first thing to see is whether any of the F_1 crosses show some significant heterotic effect in the desirable character. In this study, none of the crosses showed significant heterotic effects, as indicated from the comparison of the F_1 of individual crosses and their mid-parents value. By comparing the array points along the regression line, Acala

4-42 seems to be constantly the variety most removed from the origin.
This suggests that the crosses with Acala 4-42 might be the promising
hybrids, at least among the crosses in this study. Although the Gregg
array in the F_1 generation is almost in the same position as Acala 4-42,
it shifts downwards in the F_2 generation, an indication of the instability
of this array, which is probably due to non-allelic interactions.
Thus, based on this study, although Gregg in itself has tensile strength
as high as Acala 4-42, its hybrids are less promising than those of Acala
4-42.

The (Vr, Wr) graph can also be used to identify which of the parents,
if any, contribute to the significant deviation due to non-allelic inter-
actions. It can be done visually from the graph, or probably more accura-
tely by conducting the regression analysis, using all possible combina-
tions of all arrays but one. The results of the regression analysis in
this study do not indicate that such a test should be conducted, since
in the F_1 and the F_2 generations, the slope of the regression line do
not significantly differ from one, and non-allelic interactions are not
significant in the materials under study.

In the presence of significant non-allelic interactions, further
tests can be conducted to determine in which generation these inter-
actions are manifested, and whether the interactions are complementary
or duplicative (14).

The second use of diallel cross is concerning information of the
base population, from which the parents is a sample. Due to the small
number of parents included in this study, none of the components of
variation, either statistical or genetical, can be significant estimates
of the population parameters (17). However, based on Eisenhart's (8)

suggestion, Hayman (17) stated that the estimates be interpreted, for the particular set of parents, as if it would have been interpreted for a population when derived from a sufficiently large sample of parents. Thus, as it has been summarized in the conclusion, presumably the additive and/or the additive by additive components composed primarily the genetic variance in the parents.

Large estimates of heritability of the trait suggest that improvement can be efficiently made by mass selection within the promising hybrids. Thus, mass selection applied to Acala 4-42 array, in particular to the best cross among this array, is expected to be effective for improving tensile strength.

One of the important problems in using Hayman's method is to see that the basic assumptions can be fulfilled for the analysis to be valid. It was indicated that certain of these assumptions are not strictly valid for these materials. One of these was that of no non-allelic interactions, as indicated from the unstabile position of the array points, and that of no linkage. The latter is presumably present because the materials are selected varieties. Nevertheless, since these partial failures of the assumptions seemed unlikely to produce gross biases in the genetic analysis, it was concluded that the application of the dialel analysis to the data is justified.

Another problem involves practical difficulty. By accepting the assumptions of Crumpacker and Allard (6) that block values be treated as samples, which is also justified by Hayman (17) for small diallel crosses, ample number of blocks should be provided. This means more seeds are needed, and more crosses should be made. Thus, creating a practical problem of tedious hand pollinations, which will increase with

increasing number of parents.

In general, providing that these problems can be overcome, diallel cross analysis is a valuable tool, that can guide the breeders in improving quantitative characters in self-pollinated crop plants. To test the stability of the estimates of the parameters and the interaction of any of the parameters with environment, the experiment should be repeated in time and space. The inclusion of the backcross generations is not quite necessary in this analysis; the F_1 and F_2 generations can provide ample information.

CHAPTER V

SUMMARY AND CONCLUSIONS

A diallel cross analysis of fiber strength was conducted among four commercial varieties of upland cotton. The study included the parents, F_1, F_2, and backcross generations.

The objectives of the study were to characterize the crosses among these varieties, and to obtain information on the genetic system of the parents, with respect to fiber strength.

The analysis of variance showed that there were differences among the populations. Comparisons of the means of F_1 and the mid-parents values indicated that heterotic effects were not present in any of the F_1 crosses. Inbreeding depression, as shown from the differences of the F_1 and F_2, was not apparent.

Regression analysis of Wr on Vr indicated that the basic assumptions of the diallel cross analysis were valid, to a certain extent; thus, estimations of the diallel cross parameters were justified. The (Vr, Wr) graphs revealed, however, that certain of these assumptions are not strictly valid for these materials, as indicated by the instability of the positions of some array points along the regression lines.

Low tensile strength was a partially dominant character as indicated by the positive Wr intercept of the regression line. This is supported by an estimate of 0.09 for the average degree of dominance.

The positive, recessive alleles among the parents were more frequent than their negative, dominant counterparts. Due to the negative estimates of H_1 and H_2, the estimator of the average frequencies of the positive versus negative alleles in the parents were not estimated.

Presumably the genetic variance of the parents was primarily additive and/or additive by additive in nature; the dominance component was probably very small comparatively.

The heritability estimates were high, suggesting that mass selection should be effective in improving fiber strength in the materials being studied.

Acala 4-42 seemed to be a promising parent. The position of this array along the regression line in the F_1 and F_2 generations were constantly on the top of the rest of the arrays. This indicates that Acala 4-42 has the least dominant effects. The position of Gregg along the regression line were unstable, suggesting that it was one of the parents that contributed to non-allelic interactions. Thus, based on this study, although Gregg has virtually the same high tensile strength as Acala 4-42, its progeny is not as promising as that of Acala 4-42. Mass selection of the best among Acala 4-42 hybrids should be an effective method in improving fiber strength, at least among the hybrids included in this study.

The conclusions given above cannot be regarded as decisive, not only due to the small number of replicates, but also due to the relatively large estimates of environmental variances. The experiment should be repeated over years and locations to see that the estimates of the parameters are stable, and to be able to test the magnitudes of the genotype-environment interactions (2).

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THE REGRESSION ANALYSIS OF Wr ON Vr OF THE F_1 FAMILY

Array	Vr	Wr
A	0.0605	0.1023
G	0.0510	0.0941
L	0.0303	0.0725
S	0.0342	0.0758
Total	0.1760	0.3447
Mean	0.0440	0.0862

$\Sigma\ x^2 = 0.00060498$ $\Sigma\ xy = 0.00061056$ $\Sigma\ y^2 = 0.00061747$

$b_1 = 0.00061056/0.00060498 = 1.009$

$b_0 = 0.0862 - 1.009 \times 0.0440 = 0.0418$

Analysis of Variance

Source of variation	d.f.	Sums of Squares	Mean Squares
Total	4	0.03032199	
Due to b_0	1	0.02970452	0.02970452
Due to b_1/b_0	1	0.00061619	0.00061619
Residual	2	0.00000128	0.00000064

$s^2_{b_1} = 0.00000064/0.00060498 = 0.00105788$ $s_{b_1} = 0.0325$

$s^2_{b_0} = 0.00000064\ (0.25 + 0.00208724/0.00060498)\ = 0.000023$

$s_{b_0} = 0.000023$

$b_0;\ t = (0.0418 - 0)/0.00023 = 18.1 \times 10^2;\ {}^t(0.05,\ 2) = 4.303$

$b_1;\ t = (1.009 - 1)/0.0325 = 0.0028$

THE REGRESSION ANALYSIS OF Wr ON Vr OF THE F_2 FAMILY

Array	Vr	Wr
A	0.0795	0.1110
G	0.0337	0.0765
L	0.0420	0.0785
S	0.0242	0.0423
Total	0.1794	0.3083
Mean	0.0449	0.0771

$\sum x^2 = 0.00175949$ $\sum xy = 0.00189596$ $\sum y^2 = 0.00236257$

$b_1 = 0.000189596/0.00175949 = 1.077$

$b_0 = 0.0771 - 1.077 \times 0.049 = 0.0287$

Analysis of Variance

Source of variation	d.f.	Sums of Squares	Mean Squares
Total	4	0.02612479	
Due to b_0	1	0.02376222	0.02376222
Due to b_1	1	0.00204195	0.00204195
Residual	2	0.00032063	0.00016032

$s^2_{b_1} = 0.00016032/0.00175949 = 0.0911737$ $s_{b_1} = 0.3018$

$s^2_{b_0} = 0.00016032 (0.25 + 0.00245139/0.00175949) = 0.00026344$

$s_{b_0} = 0.0162$

b_0; $t = (0.0287 - 0)/0.0162 = 1.770$; $t_{(0.05, 2)} = 4.303$

b_1; $t = (1.077 - 1)/0.3018 = 0.255$

VITA

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Doctor of Philosophy

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