A GENETIC STUDY OF EARLINESS IN COTTON USING

THE DIALLEL CROSS ANALYSIS AND A BREEDING

STUDY TO DETERMINE THE POSSIBILITY OF

DEVELOPING AN EARLY, LONG-FIBERED

STRAIN OF COTTON

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ii

ACKNOWLEDGMENTS

TABLE OF CONTENTS

LIST OF TABLES

CHAPTER I

INTRODUCTION

Earliness and fiber length are among the more important criteria
used for determining the relative merits of different strains and vari-
eties of cotton (Gossypium hirsutum L.).

Early maturing varieties are of particular importance in the north-
ern regions of the Cotton Belt where planting is frequently delayed by
adverse weather conditions, where there is a shortage of moisture in
the mid and late part of the growing season, where the growing season is
often severely shortened by an early frost, and where insect and disease
damage late in the season is fairly extensive.

Varieties having long fiber are desirable because staple length
accounts for approximately 75 percent of the spinning value of cotton
fiber, while all known fiber properties (including fiber length)
account for only 86 percent of the spinning value (38). Increasing the
spinning value of cotton has been necessary to meet the increasing
economic competition from synthetic fibers.

Certainly, if one of these traits is desirable in a variety, both
in the same variety would be even more advantageous. The ultimate aim
of this research is to determine if this goal is feasible and, if so, to
determine the best breeding method to use to accomplish that end.

To efficiently breed for any trait, information concerning the
types and relative amounts of gene action is needed. A diallel

1

experiment involving 10 varieties of upland cotton was conducted in 1965 and 1966 at Perkins, Oklahoma. The fiber data, including fiber length, has been analyzed and published (56,57) prior to this time. However, several characters, including earliness, from that experiment have not been analyzed or published. With the consent of the persons who conducted the diallel, the earliness data from that experiment was analyzed by the author as part of this thesis.

The second part of the thesis involves a selection experiment designed to explore the possibility of developing an early, long staple variety and if it is possible, to determine the most efficient and effective breeding system which should be used in its development.

CHAPTER II

REVIEW OF LITERATURE

Methods of Estimating Earliness

Brown (9) defined "true earliness" as the period of time from sow-
ing to first flower since it was easy to measure and responded to selec-
tion. Other good measures he thought acceptable were the date of peak
flowering and the rate of bolling curve. He considered the most pract-
ical measure of earliness to be the weight of the first harvest of seed
cotton expressed as a percentage of the total seed cotton yield.

Ter-Avenesjan (55) felt that the only true criterion for measuring
earliness should be the yield of raw cotton harvested and that a really
early variety should produce no less than 90 percent of its yield before
frost.

In a detailed study of seven methods for measuring the earliness of
individual plants in early generation material, Richmond and Radwan (46)
found all the measurements they used were positively correlated. This
suggested that any of the seven could be used with confidence to esti-
mate earliness. The seven methods studied were: (1) E_1--number of days
from planting to appearance of first observable square; (2) E_2--number
of days from planting to appearance of first bloom; (3) E_3--number of
days from planting to opening of first boll; (4) E_4--ratio of number of
open bolls at the first harvest to the total number of bolls produced

expressed as a percentage; (5) E_5--ratio of number of open bolls in the combined first and second harvest to the total number of bolls produced expressed as a percentage; (6) E_6--ratio of weight seed cotton harvested at the first harvest to the total weight of seed cotton harvested expressed as a percentage; and (7) E_7--ratio of weight of seed cotton harvested in combined first and second harvest to the total yield expressed as percentage.

Based on the number of vegetative branches, the percentage of bolls on vegetative branches, and the node of first fruiting branch, Ray and Richmond (44) found that the measures were significantly correlated at the 0.01 level of probability and concluded that such measurements of earliness were valid. In another study Richmond and Ray (47) suggested that "mean maturity date" was a better estimate of earliness than the amount of crop harvested or the percentage of crop harvested because it was the most discriminating and reliable of the three methods.

In a study of earliness in cotton based on the percent of open bolls, the percent of open flowers, the weight of first harvest, and the percent of first harvest of seedcotton, Murray (36) concluded that the latter two measures were more reliable than those made at earlier stages in the growing season.

Genetics of Earliness

In the study of three varieties ('Lankart 57', 'Oklahoma Special', and 'Stormproof #1'), their F_1's, F_2's, and backcrosses, Hintz and Green (25) indicated that boll period as a mean for measuring earliness was controlled largely by genes having additive effects. The

narrow-sense heritability of boll period in the Lankart 57 X Stormproof #1 cross was 50.6 percent.

In an investigation involving the estimation of broad-sense heritabilities of three measures of earliness [amount of crop harvested (ACH), the percentage of crop harvested (PCH), and the mean maturity date (MMD)] using three stocks of American upland cotton designated as 'C.B. 3051', 'Z-106', and 'Contextum' and the F_2's of some of their corresponding crosses, Richmond and Ray (47) found estimates based on ACH using C.B. 3051 X Z-106 and C.B. 3051 X Contextum were greater than zero only after the fourth harvest or when approximately 30 percent of the crop was open. Heritabilities of PCH of the C.B. 3051 X Z-106 and Z-106 X Contextum croeses were .14 and .03, respectively, at the sixth harvest date. They exceeded .20 at the sixth, seventh, and eighth harvest dates based on the C.B. 3051 X Contextum cross. A broad-sense heritability estimate of .41 for MMD based on boll number rather than seedcotton yield was obtained in the C.B. 3051 X Contextum cross.

Ray and Richmond (44) in a study of morphological measurements of earliness in the stocks C.B. 3051, Z-106, and Contextum indicated that earliness was a quantitatively inherited character. Broad-sense heritability estimate on a plant basis of the node of first fruiting branch were .60 and .43 for the C.B. 3051 X Z-106 and C.B. 3051 X Contextum crosses, respectively.

In a diallel cross study of five different parental stocks of cotton ('MU 86', a Cambodia selection; 'Texas 468', a punctatum collected in Mexico; 'CB3150', a Russian upland cotton; Texas 63, a latifolium collected in Mexico; and '2-8-7-6', the F_4 of a cross between

'DPL-14' and 'Texas 324') White and Richmond (58) found that general
combining ability for earliness based on the percentage of the first
two harvests to the total of harvests of lint cotton, was large and sig-
nificantly different from zero at the 0.025 level of probability. No
significant specific combining ability was detected. These results were
in agreement with the findings of Miller and Marani (34) in a diallel
study of eight lines representing the eight varieties ('Deltapine 14',
'Cook 144', 'Stoneville 2B', 'Coker 100', 'Rowden 80', 'Acala 1517',
'Mexiczn Big Boll 128', and 'Florida Green Seed'). They observed that
in general F_1,s were significantly earlier than the average of their
corresponding parents at the 0.01 level of probability and that inbreed-
ing depression was statistically insignificant at the 0.05 level of
probability. General combining ability variance for earliness was large
in magnitude and significantly different from zero at the 0.01 level of
probability. The specific combining ability variance was relatively
small and statistically insignificant at the 0.05 level of probability.
Since general and specific combining ability are related to the nature
of gene action (33), the two papers cited above suggest that the gene
action for earliness is primarily additive and/or additive by additive
while there is no significant amount of dominance and/or epistatic gene
action. Dominance was in general toward earlier maturity. White and
Kohel's diallel analysis (59) supported this premise by showing the
additive nature of the genetic variance for earliness coupled with the
presence of partial dominance in the five parental stocks studied pre-
viously by White and Richmond (58).

Environment and Earliness

Spooner et al.(49) pointed out that irrigation affects earliness by delaying the opening of the bolls and that more time was also required from boll set to maturity which resulted in a lower yield of the first harvest. Conversely, shortage of water during the maturation period of the bolls contributed to their opening earlier. Eaton (14) also concluded that earliness in non-irrigated cotton was the result of drouth which in turn caused a reduction of the boll maturation period.

Tabrah (54) in a study conducted on three varieties and six strains of different genetic makeup('Acala 44', 'Verden', 'Kemp', '31A097', '31A109', '31A112', 31A132', '31A134',and 31A139)concluded that percent first harvest based on seedcotton decreased with irrigation. However, the weight of the first harvest increased for all varieties and strains included in the study. Perkins and Douglas(40)showed that earliness was not influenced by fertilization with different rates of nitrogen.

Methods of Estimating Fiber Length

There are several different, yet acceptable, ways to measure fiber length in cotton. However, the most commonly used are described as follows (6):

(1) Mean length - the average length of all fibers in the sample,

(2) Upper-Half Mean length (UHM) - the mean length of the longer one half of the fibers, by weight in the sample,

(3) Fifty percent span length - the fiber length measured on a fiber beard to a point beyond which only 50 percent of the fibers extend, and

(4) Two and one-half percent span length - the fiber length measured on a fiber beard to a point beyond which only 2.5 percent of the fibers extend.

Genetics of Fiber Length

Brown and Ware (10) state that under any given set of conditions staple length in cotton is a species and varietal characteristic which in turn suggests that it is largely inherited character. Baker (8) stated that "all" fiber properties of cotton are essentially genetically controlled. However, this statement is debatable, especially for fiber coarseness (56).

Green (17) in a study of staple length variability in the varieties 'Bobshaw 1', 'Coker 100 (Str. 9)','Delfos 9169', 'Deltapine 15', and Stoneville 2B, found enough phenotypic variability in UHM for effective selection to be possible.

White and Richmond (58) in the diallel cross study mentioned previously showed significant variance for UHM among varieties by using Duncan's Multiple Range Test. Miller and Marani (34), in the diallel cross study also cited previously, observed that staple length of F_1's was in general larger than the average of their corresponding parental lines. Inbreeding depression for length in the F_2 was significant and proceeded in a linear manner. General combining ability variance for length was significant at the 0.01 level of probability while the variance for specific combining ability was not significant at the 0.05 level of probability.

Ramey and Miller (43) in a study of the population from a cross between 'Empire 10' and the line 'TH 131-5' which was derived from the

sixth backcross to upland cotton of the trispecies hybrid of

G. hirsutum, G. thurberi, and G. arboreum, were able to detect a sub-

stantial amount of additive and dominance genetic variance components

for UHM.

In a diallel analysis of 10 varieties ('Paymaster 101', 'Gregg',

'Western Stormproof', 'Lankart 57', '6-77', 'Deltapine 45', 'Coker 100A

WR', 'Acala 44', 'Stoneville 7', and 'Auburn M') Verhalen and Murray

(56) found narrow-sense heritability estimates on a plot basis for 2.5

percent span length in the F_1 of .49 and .61 in two different consec-

utive years, and an estimate of .49 in the F_2 in the second year. Par-

tial dominance for longer fiber was also detected.

Marani (30) in diallel studies conducted within the varieties 'Acala

42', 'Coker 100W', 'Empire 7', 'Acala 1517C', and 'Coker 100A' of

G. hirsutum, and within the varieties 'Pima 32', 'Pima S-1', 'Ashmuni',

'Karnak', 'Malaki', and 'Giza 7' of G. barbadense, found the components

of variance for UHM and mean fiber length were mostly additive with

small amounts of dominance. In a study of interspecific crosses between

the varieties of G. hirsutum and G. barbadense mentioned above, Marani

(29) indicated that additive , dominance, and additive X additive epi-

static effects were operating in the inheritance of both UHM and mean

fiber length. The effects of general combining ability were significant

in both species, and it was concluded that additive gene action plays a

major part in the fiber length genetics of G. hirsutum and

G. barbadense.

In a biometrical analysis of parents, F_1's and F_2's of the cross

between 'Half and Half' and 'Delfos 9252', Ramey (42) suggested the

possibility that allelic and non-allelic gene interactions were

operative in the inheritance of fiber length because of the deviation

of the F_1 from the midparent value and because the inbreeding depression

of the F_2 was to a point other than midway between the F_1 and midparen-

tal means. In a cross between 'Acala' and 'Hopi' and through the sub-

sequent study of F_2 and F_3 generations, Stith (51) concluded that fi-

ber length is partially dominant over shortness. Broad-sense herita-

bility estimates were .22 and .70 based on F_2 and F_3 data, respect-

ively.

Young and Murray (60) conducted a study on four inbred lines ('M-

11', 'Z-104', Z-106, and 'M-8') which originated through haploid doub-

ling of G. hirsutum and found that heterosis for fiber length was stat-

istically significant at the 0.01 level of probability in the crosses

Z-106 X Z-104 and M-11 X Z -106 in 1961 and 1962, respectively, while

heterosis was statistically significant at 0.05 level of probability

for the cross Z-106 X M-8 in year 1962. Some inconsistency of heter-

otic effects for fiber length over years were observed for each cross.

Environment and Fiber Length

Reynolds and Killough (45) concluded that staple length was posi-

tively correlated with the amount of rainfall during the time of boll

development. Hanson et al. (19) found staple length in Deltapine 15

negatively correlated with the difference between the maximum and min-

imum temperature of the period between July 6 to August 23 and signifi-

cant at 0.01 level of probability ($r = -0.773$) while it was positively

and significantly correlated ($r = +0.774$) at 0.01 level of probability

with the amount of rainfall for the period of July 6 to

August 23. Hancock (18) demonstrated that in dry years cotton fiber was shorter while in the years of uniform rainfall the fiber tended to be longer.

Sturkie (52) concluded that available moisture in the soil was the prime factor in the development of lint and that favorable moisture produced heavier bolls with longer staple. In another study he (53) showed that adequate soil moisture was a factor in producing a longer cotton fiber than that grown in moisture-deficient soil.

Spooner et al. (48), Tabrah (54), Adams et al. (1), and Eaton and Ergle (15) also concluded that adequate moisture significantly increased fiber length above that produced under non-irrigated conditions. Losses in staple length from inadequate moisture usually are about 1/32 of an inch (1).

Pope and Ware (41) noticed a substantial decrease in staple length under marked to moderate drouth conditions and under relatively high temperatures. These results were supported by the findings of Hanson and Knisel (20) who noticed that under irrigation on finer soils staple length varied proportionally to the amount of water.

Hesketh and Low (24) showed the staple length of two short staple varieties ('CA 491' and 'Paymaster 54B') was negatively and significantly correlated at the 0.01 level of probability with high temperature (r = -0.71) while the length of 'Acala 1517 BRZ' and 'Albar-SATU 66' did not change with temperature in any consistent manner.

Sturkie (53) and Spooner et al. (48) concluded that various levels of nitrogen application had no significant effect on fiber length. Armstrong and Bennett (7) found that cotton plants suffering from malnutrition produced lint of practically the same length as that produced

by heavily fertilized plants. Perkins and Douglas (40) discovered that
the UHM of fiber increased with the first increment of nitrogen fertil-
izer added but remained constant with additional applications.

In a study of the effect of nitrogen, phosphorus, and potassium on
fiber quality Murray, Reed, and Oswalt (37) concluded that fertilizer
treatments exert their influence primarily on yield components and not
on lint quality (including staple length). While Reynolds and Killough
(45) found no significant correlation between staple length and fertil-
izer treatments (nitrogen, phosphorus, potassium and their various com-
binations) though staple length was slightly negatively correlated with
potassium.

Matthews et al. (32) in a study of the effect of Carbaryl, D.D.T.
and Dimethoate on fiber quality characters of the variety 'Albar' found
no significant differences between sprayed and unsprayed cotton in
spite of large yield increases in the sprayed plots and fairly heavy
jassid attack at one location.

Intermating and Cotton Breeding

Al-Jibouri et al. (2) conducted a population study of 92 randomly
chosen F_3 progenies from a cross between the high fiber strength, low-
yielding strain 'TH131-5' extracted from the trispecies hybrid,
(G. arboreum X G. thurberi) X G. hirsutum, and 'Empire 10' which is
characterized by high yield and lint percent in order to investigate
the possibility of combining the desirable qualities of each into a
single strain. Though inconclusive, their results suggested that link-
age rather than pleiotropism prevented them from attaining their objec-
tive and that an intercrossing program among the segregates of the F_1

should be considered to maximize the opportunity for breaking up those linkage blocks.

To study the effect of intermating on genetic recombination among seven quantitative characters Miller and Rawlings (35) intermated Al-Jibouri et al.'s (2) F_2 population through the F_6 in an isolated block. A decrease of genetic variance for six traits and an increase for the seventh was observed. These observations were attributed to a predominance of the coupling and repulsion phases of linkage for the six traits and the seventh trait, respectively. A change in the genetic correlation between yield and fiber strength and between yield and fiber length was observed from (-0.69) to (0.35) and from (0.02) to (-0.37), respectively.

CHAPTER III

MATERIALS AND METHODS

EXPERIMENT I

Description of the Population

The 10 parents used in the diallel cross were all varieties or
strains of upland cotton. Five were stormproof, i.e., 'Paymaster 101',
'Gregg', 'Western Stormproof', 'Lankart 57', and '6-77'. The other five
were the open-boll varieties 'Deltapine 45', 'Coker 100A WR', 'Acala 44',
'Stoneville 7', and Auburn M'. All are commercial varieties except
6-77 which is a bacterial blight-resistant selection from the variety,
Stormproof #1. The 10 varieties do not constitute a random sample from
any particular population. Therefore, inferences are strictly applic-
able only to them and the crosses between them. The extent to which the
inferences apply to the species as a whole is uncertain.

Experimental Procedure

The parents were crossed in all 45 possible combinations at Iguala,
Mexico, in the winter of 1964-65. Reciprocal crosses were not made. The
45 F_1's and 10 parents were planted in 1965 in a 7 X 8 rectangular lattice
design with three replications. A dummy entry, '8948', was also inclu-
ded since 56 entries are required by the design. In 1966 the 10 par-
ents, 45 F_1 crosses, and 45 F_2 progenies were planted in 10 X 10 triple

lattice design with three replications.

The experiment was conducted on the Agronomy Research Station Farm at Perkins, Oklahoma, on a Vanoss loam soil. Plots were single rows 25 feet long while plants within the plots were spaced 1 1/2 feet apart. The variety, Kemp, was planted in a single border row between plot rows to minimize border effects as much as possible. Due to considerable seedling disease loss in both years, 'De Ridder Red', a variety with the dominant marker gene, R_1, was planted in the missing hills to par- tially compensate for the differential spacing within plots which did occur.

Laboratory and Statistical Procedure

Earliness was estimated by percent first harvest, i.e., the lint yield from the first harvest expressed as a percentage of the total lint yield from both harvests. Six plants were chosen within each plot using random number tables. In the few cases where there were six plants or less, all were harvested. The procedures described by Hayman and Jinks (21,26,27) were employed in the analysis of the data. These procedures will be described in detail in the results and discussion.

EXPERIMENT II

Description of the Populations

The four populations used in this study are described as follows:

Population No. 1 was derived by selecting for fiber length in a highly heterozygous base population of Upland Cotton. The original cross which produced this base population was between 'Acala 44' and 'OK 86', an early Yugoslavian strain.

Population No 2 was derived by selecting for earliness in the base population mentioned above.

Population No. 3 was the first generation of crosses between two selection groups from the base population after one cycle of mass selection had been completed in each and it was derived by selecting for both fiber length and earliness.

Population No. 4 was used as a check population. It was a part of the base population mentioned above in which selection had not been practiced.

Experimental Procedure

This experiment was conducted over a three-year period on the Agronomy Research Station Farm at Perkins, Oklahoma, on a Vanoss loam. All rows in this experiment were 50 feet long. Rows were spaced 40 inches apart, and plants within rows were spaced approximately one foot apart.

In 1966, populations one and two were planted in a randomized complete block design with three replications. Population three was planted in an isolated block consisting of ten rows.

Population four was grown in 1967 and 1968. The population in 1968 was constructed from equal quantities of seeds by weight from all plants in the population in 1967.

Earliness was estimated on an individual plant basis by the weight of seedcotton from the first harvest expressed as a percent of the total seedcotton yield, while staple length was measured on the digital fibrograph as 2.5 percent span length in inches. Mass selection was conducted in populations one and two. In population one the upper five percent were selected for fiber length for two generations (1966 and 1967) to obtain the first and the second cycle mass selection progenies. In population two the earliest five percent were also selected for two generations to obtain the two progenies. First cycle progenies were grown in 1967. Second cycle progenies were grown in 1968.

In population three, the upper five percent of the population was selected for earliness and the upper five percent were selected for fiber length in 1966. The following summer the progenies of these two selection groups were intermated. Sixty maternal families were chosen at random. These families were planted separately and selfed in the winter of 1967-1968 at Iguala, Mexico. Earliness was estimated visually and staple length was measured on the fibrograph for each individual plant in each family. In 1968 the five earliest and five latest families and the five longest and five shortest fibered families were selected. These twenty entries were planted in a completely randomized block design with two replications in single row plots 12.5 feet long. Also individual plants characterized by high staple length and early maturity were selected from the groups as a whole, bulked, and planted in a block of ten rows in 1968.

Laboratory and Statistical Procedure

Due to the extremely large number of plants in population one and two in 1966 and to the shortage of technical help to measure staple length, the "Systematic Sampling" procedure described by Cochran (11) was used to choose no more than 300 plants from each population. However, this method was not required in 1967 and 1968 since the number of plants in those populations did not exceed 500. In all populations other than one and two in 1966, all plants were taken.

The methods described by Steel and Torrie (50) were used to calculate the means and variances of length and earliness and linear correlation coefficients between the two traits.

Means between populations were compared by using the formula:

$$t_{(cal)} = (\bar{x}_1 - \bar{x}_2)/(s_{\bar{x}_1} - \bar{x}_2) = \bar{d}/s_{\bar{d}}$$

where $s_{\bar{d}} = [s^2_1/n_1) + (s^2 2/n_2)]^{\frac{1}{2}}$

Variances between populations were compared using the formula:

$$F_{(cal)} = \text{(The larger } s^2\text{)}/\text{(The smaller } s^2\text{)}.$$

Ninety-five percent confidence limits were placed on the correlation coefficients using the table (Table A.11A) in Steel and Torrie (50) provided for that purpose.

CHAPTER IV

RESULTS AND DISCUSSION

EXPERIMENT I

Analysis of Variance

Analyses of variance were conducted on a plot mean basis in each
year. Analyses on a plot mean rather than on a plant basis were neces-
sitated since a computer program for the 7 x 8 rectangular lattice
design with unequal number of subsamples was not available. Means used
in subsequent analyses were uncorrected for the block effect associated
with the lattice design. These analyses for 1965 and 1966 are shown in
Tables I and II, respectively. Highly significant variation was found
among entries in 1965 and 1966. Since entries were significantly dif-
ferent from one another for earliness, a diallel analysis could be con-
ducted in each year. The results of these analyses are described in
the remainder of this section. Highly significant differences among
replications were also encountered, which justified the earlier decis-
ion to use a randomized complete block design rather than a completely
randomized one.

Assumptions of the Diallel Analysis

Crumpacker and Allard (13) summarized the assumptions of the
diallel analysis as follows:

19

TABLE I

ANALYSIS OF VARIANCE OF EARLINESS IN 1965

Source	d.f.	Sum of Squares	Mean Squares
Replications	2	7,189.0	3,594.5**
Entries	55	27,275.5	495.9**
Error	110	18,864.6	171.5

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

TABLE II

ANALYSIS OF VARIANCE OF EARLINESS IN 1966

Source	d.f.	Sum of Squares	Mean Squares
Replications	2	766.6	383.3**
Entries	99	13,867.4	140.1**
Error	198	15,996.0	80.8

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

(1) No genotype-environment interaction within locations and
    years (except within certain prescribed limits)

(2) Homozygous parents

(3) Diploid segregation

(4) No reciprocal differences

(5) No epistasis (that is, no nonallelic gene interaction)

(6) No multiple alleles

(7) Uncorrelated gene distributions

General Tests of the Assumptions

The correctness of the conclusions obtained from the analysis of
any diallel experiment is dependent upon the validity of the above
assumptions. Therefore, should earliness fail to comply with any of
those assumptions, the analysis would be invalidated to some extent.
The degree of invalidation is in turn dependent upon the degree of non-
compliance.

To determine whether earliness fulfills the assumptions of the
analysis, the following broad, general test (56,57) were employed:

A. Analysis of Variance of the Quantity $(W_r - V_r)$,

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

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

W_r is an estimate of the covariance of the members of an array
with their non-recurrent parents, W_r' is the convariance of the members
of an array with the array means of their non-recurrent parents, and
V_r is the variance of the members of an array. An array includes a
parent as well as all the crosses derived from it.

A. Analysis of Variance of the Quantity $(W_r - V_r)$

The quantity $(W_r - V_r)$ is expected to be constant over arrays. Heterogeneity is an indication that the trait in question does not comply with one or more of the assumptions of the analysis. (27)

The quantity $(W_r - V_r)$ was calculated for each of the ten arrays in each of the three replications, and an analysis of variance was conducted on the 30 values obtained. Results of this analysis for the F_1 population in 1965 and for the F_1 and F_2 populations in 1966 are summarized in Table III. Lack of significance for the arrays mean square in all of the analysis suggests that the assumptions according to this test are valid for earliness.

TABLE III

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

Source	d.f.	Mean Squares for Earliness		
		F_1 (1965)	F_1 (1966)	F_2 (1966)
Arrays	9	7,214.05	1,440.59	575.09
Replications	2	4,889.55	1,871.05	5,426.39*
Error	18	9,503.95	1.026.02	1,366.61

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

B. Analysis of the (W_r, W_r') Regression

In the (W_r, W_r') analysis, regression coefficients are expected to be significantly different from zero but not significantly different from 0.5 if the assumptions are valid (3). Regression coefficients from each population along with the 95 percent confidence limits about the regressions were calculated (50) and are presented in Table IV. The calculated coefficients of the F_1 populations were significantly different from zero, while that of the F_2 population was not. Only the F_1 in 1966 was not significantly different from 0.5. Therefore, according to this test, two of the three populations showed some failure of the assumptions.

TABLE IV

(W_r, W_r') REGRESSION COEFFICIENTS

Populations	Coefficients	95% Confidence Limits
F_1 (1965)	.3430	.4392 - .2468
F_1 (1966)	.3934	.5713 - .2155
F_2 (1966)	.1185	.3327 -(-.0857)

C. Analysis of the (V_r, W_r) Regression

In this test the regression coefficient for earliness should be

significantly different from zero but not significantly different from
1.0 (27).

Regression coefficients and their 95 percent confidence limits (50)
are summarized in Table V. The coefficient for the F_1 population in
1966 was not significantly different from zero. The F_2 coefficient was
significantly different from 1.0. According to this test, the F_1 and
F_2 populations in 1966 failed to comply with the expectations had earli-
ness fulfilled all assumptions of the analyses.

TABLE V

(V_r, W_r) REGRESSION COEFFICIENTS

Populations	Coefficients	95% Confidence Limits
F_1 (1965)	0.634	1.161 – .107
F_1 (1966)	0.361	1.316 – (–.594)
F_2 (1966)	0.640	.973 – .307

In summary, three general tests were conducted on three populations
(the F_1 in 1965 and 1966 and the F_2 in 1966) to check the compliance of
earliness in cotton with the assumptions of the diallel analysis.
Therefore, in a sense, nine tests were conducted on this trait. Four of
these nine tests were failed; and, as a result, earliness in cotton
does not appear to fulfill all assumptions of the analysis.

Specific Tests of the Assumptions

The tests conducted above are broad, general tests which confirm
or deny the compliance of a trait with the assumptions of the analysis
as a whole. They are not capable of pinpointing which assumptions have
failed. However, some assumptions based on past experience may be con-
sidered valid. Others should be tested.

A. Assumptions Not Tested

The assumption of diploid segregation was not tested because
Kimber (28) and Endrizzi (16) concluded from cytological studies that
the chromosomes of G. hirsutum form bivalents at meiosis and that there
is a genetic system of diploidization (similar to that of wheat) which
is responsible for organizing the meiotic behavior so that only homo-
logous chromosomes can pair.

In general, reciprocal crosses in G. hirsutum have not been sig-
nificantly different. In a recent study among primitive, foreign, and
cultivated American upland cottons, White and Richmond (58) found no
significant differences between reciprocals for earliness in cotton.

The parents in this study were varieties of upland cotton. Since
cotton is known to be predominately self-pollinated and since the vari-
eties were selfed for one generation prior to crossing and testing, it
is assumed that parents were relatively homozygous. However,
heterozygosity my exist even after selfing for many generations, as
Allard (5) and Brown and Ware (10) have indicated. The assumption of
homozygous parents may not be strictly true and may account for at
least part of the noncompliance found earlier in this study.

The assumptions of no multiple alleles and of uncorrelated gene distributions were not tested because no test for those assumptions is known at present to the author. Either or both could be involved in the failure of earliness to fulfill the assumptions.

B. Assumptions Tested

The assumption of no epistasis may be tested using the chi-square test devised by Hayman (22). For this test F_1 and F_2 data are needed. Therefore, only the 1966 data could be used to make this test. From the two populations Hayman (22) devised the construction of a so-called $(2L_2-L_1)$ table which is independent of dominance so that the sum of squares tests epistasis. A diallel table containing F_1 and parental means is defined as an L_1 table, while a diallel table containing F_2 and parental means is defined as an L_2 table. A $(2L_2-L_1)$ table is constructed by subtracting each term in the L_1 table from twice the term in the identical position of the L_2 table. From the $(2L_2-L_1)$ table the statistics V_{0L0}, V_{0LX}, V_{1LX}, and W_{0L0X} can be estimated where V_{0L0} is the variance of the parents, V_{0LX} is the variance of array means, V_{1LX} is the mean variance of arrays, and W_{0L0X} is the mean covariance of arrays. In other words, these symbols are calculated in the same manner as $V_{0L0'}$, V_{0L1}, V_{1L1}, and W_{0L01} from the F_1 diallel table. Calculations of these quantities is described later in this paper. The calculated chi-square value is estimated using the following formula:

$$\text{Chi-square}_{(cal)} = k_2 \, [(n-1)(V_{1LX} - V_{0LX}) + n(\bar{p} - \bar{x})^2/(1 + k)$$

$$+ (n - 1) (V_{0L0} - 4W_{0L0X} + 4V_{0LX})/(2 + k)]$$

This chi-square$_{(cal)}$ is then compared with chi-square$_{(tab)}$ with
$1/2\ n(n-1)$ degrees of freedom. Both k and k_2 are constants and are
estimated by the following equations:

$$k = \frac{nE_0}{8E_2 + 2E_1 - E_0}$$

$$k_2 = \frac{n}{8E_2 + 2E_1}$$

E_0, E_1, and E_2 are estimates of the parental, F_1, and F_2 environ-
mental variances, respectively; n is the number of parents in the
diallel cross; $\bar{p}$ is the mean of the parents; and $\bar{x}$ is equal to the
overall mean of the entries in the experiment.

The chi-square$_{(cal)}$ was 22.07 which at 45 degrees of freedom is
not significant at the 0.05 probability level. Therefore, epistasis
is either absent in or made a negligible contribution to the expres-
sion of earliness in 1966.

The assumption of no genotype-environment interaction within
locations and years could partially be tested using the procedure of
Allard (4). Since this experiment was tested at one location over two
years, a location effect is confounded in the results rendering them
less sensitive than they would have been had another location been in-
cluded.

This test for the additive components of variation is based on
the fact that heritable differences between homozygous parents in the
absence of non-allelic interaction result from the additive effects of
genes controlling that trait. Thus, parental lines differing signifi-
cantly from each other must carry genes with different additive effects

while the constancy of the additive components over environments can be detected by testing the parents x years interaction mean square. In each year an estimate of earliness was obtained for each parent in each replication. The test consists of an analysis of variance among the resulting 60 means. The results of this analysis are listed in Table VI.

TABLE VI

GENOTYPE BY ENVIRONMENT ANALYSIS OF THE
ADDITIVE COMPONENT OF VARIATION

Source	d.f.	Sum of Squares	Mean Squares
Reps in Years	4	1,114.64	--
Years	1	449.64	449.64
Parents	9	4,845.31	538.37**
Parents x Years	9	1,295.80	143.98
Error	36	5,098.34	141.62

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

The significant parents mean square suggests that these parents do carry genes with different additive effects for earliness. Lack of significance of the parents x years interaction term indicates that these additive effects were constant over years.

A combined analysis of variance of the 60 W_r and 60 V_r estimates from the three L_1 tables in 1965 and three in 1966 provides information about any dominance and/or dominance by environment interactions that earliness may show. Prior to conducting the analysis of variance the individual W_r and V_r estimates in each replication were divided by the V_{OLO} estimate in that replication to minimize the additive component of variation in the test and to improve the test's sensitivity in regard to dominance interaction terms. This rescaling also is necessary to minimize the fluctuation of basic variability in different environments which also tends to confuse between-environment comparisons of genetic systems. The results of this analysis are given in Table VII.

The years mean square was significant, which suggests that the rescaling of the data was not entirely successful, i.e., differences in dominance between years were still apparent. The significance of the dominance mean square indicates that the mean degree of dominance is either partial dominance or overdominance. From this test the alternative determation between these two degrees of dominance cannot be made. However, they can be differentiated at a later stage in the analysis.

The dominance x years interaction mean square tests the stability of the average degree of dominance. Since this mean square was not significant at the 0.05 probability level, the average degree of dominance for earliness was considered to be consistent over years.

The arrays mean square was significant. This suggests that there were differences in dominance among parents.

The arrays x years mean square was also significant providing evidence that the relative dominance among parents changes with the

season. This must then be at least one of the reasons for the failure

of earliness to correspond to expectations in the general tests of the

assumptions.

TABLE VII

GENOTYPE BY ENVIRONMENT ANALYSIS OF THE
DOMINANCE COMPONENT OF VARIATION

Source	d.f.	Sum of Squares	Mean Squares
Years	1	339,267.13	339,267.13**
Dominance	1	225,870.98	225,870.98**
Years x Dominance	1	6,541.64	6,541.64
Reps Within Years	4	21,430.57	---
Arrays	9	101,751.64	11,305.74*
Arrays x Years	9	91,527.73	10,169.75*
Arrays x Dominance	9	22,950.30	2,550.03
Arrays x Years x Dominance	9	15,828.18	1,758.69
Error	76	373,454.35	4,913.87

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

The non-significance of the dominance x arrays and dominance x

arrays x years mean squares provides additional evidence for the lack of

epistasis in this trait.

Estimates of Population Parameters

Even though earliness exhibited a partial failure of the assumptions, estimates of the population parameters for that trait could still be made (21). However, it should be recognized that these estimates are somewhat less reliable than they would have been had all the assumptions been fulfilled.

Nelder (39) suggested that each replication be treated as a separate experiment with its own estimate of environmental variation. Each parameter could then be estimated in each replication independently. The variation of the block means around the overall mean could be used to calculate the standard error of the mean used in tests of significance.

The parameters estimated are E_0, E_1, E_2, D, H_1, H_2, and F. E_0, E_1, and E_2 are the estimates of the parental, F_1 and F_2 environmental variation, respectively. E_0 was estimated from between plot-within plot analyses of variance of the parental entries within each replication. E_1 and E_2 were estimated in the same manner using the F_1 and F_2 entries, respectively.

The additive genetic variance is estimated by D while H_1 and H_2 are dominance genetic variances. D may include additive x additive epistatic effects while H_1 and H_2 may include additive x additive, additive x dominance, and dominance x dominance epistatic effects (12). D, H_1, and H_2 as variances are expected to be positive. F serves as indicator of the relative frequency of dominant as opposed to recessive alleles in the parents. If F equals to zero, the dominant and recessive alleles in the parents are equally distributed or there is no dominance. With an excess of dominant alleles F will be positive. An

excess of recessive alleles results in a negative F.

The above parameters were estimated by the equations of Hayman (21,23). Those equations are as follows for the F_1 and parental data where n equals the number of parents:

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

[2] Mean covariance of arrays = W_{OL1} = $1/2\ D - 1/4\ F + E_{0/n}$.

[3] Mean variance of the arrays = V_{1L1} = $1/4\ D + 1/4\ H_1$

$$- 1/4\ F + [E_0 + (n-1)\ E_1]/n$$

[4] Variance of array means = V_{OL1} = $1/4\ D + 1/4\ H_1 - 1/4\ H_2$

$$- 1/4\ F + [E_0 + (n-2)\ E_1]/n^2.$$

Estimates of F, H_1 and H_2 in the F_2 were obtained using the following equations on the F_2 and parental data where n again equals the number of parents.

[5] Mean covariance of arrays = W_{OLO2} = $1/2\ D - 1/8\ F + E_{0/n}$.

[6] Mean variance of array = V_{2L2} = $1/4\ D + 1/16\ H_1 - 1/8\ F$

$$+ [E_0 + (n-1)\ E_2]/n.$$

[7] Variance of array means = V_{OL2} = $1/4\ D + 1/16\ H_1 - 1/16\ H_2$

$$- 1/8\ F + [E_0 + (n-2)\ E_2]/n^2.$$

The parameter estimates are summarized in Table VIII.

All estimates of environmental variance were significantly different from zero in each year. The mean of E_0 exceeded that of E_1 in both years. These results reinforce the assertion of Hyman (23) that E_0 is not equal to E_1 in cotton. These findings are also in agreement with those of Verhalen and Murray (56,57). However, E_2 was larger than E_0 or E_1 in 1966. These results contrast to those of Verhalen and Murray (56,57) where E_2 for fiber properties was generally intermediate between E_0 and E_1.

TABLE VIII

MEAN PARAMETER ESTIMATES OF EARLINESS

Parameter Estimate	F_1 (1965)	F_1 (1966)	F_2 (1966)
E_0	58.61**	48.47*	--
E_1	55.17**	47.15*	--
E_2	--	--	52.55**
D	259.51**	49.71*	--
F	52.59	- 4.63	130.85*
H_1	467.17*	167.97*	576.96
H_2	445.64**	161.09*	441.80

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

The estimates of D were significantly different from zero in both years.

The F values were not significantly different from zero at the 0.05 probability level for the F_1's in either year. However, the F value estimated from the F_2 populations in 1966 was significantly different from zero and positive. Since dominance does exist in this population for earliness as either partial or overdominance (see Table VII), it appears that the frequency of dominant alleles versus recessive alleles in F_1's is about the same while dominant alleles appear to predominate in the F_2. A ready explanation for these results other than segregation is not apparent.

H_2 was smaller than H_1 in each of the three populations. These results typically occur when the frequencies of the dominant and recessive alleles are not equal in the parents (21). The H_1 and H_2 values from the F_1 populations were significantly different from zero, while they were not in the F_2. H_1 and H_2 exceeded D in all populations, suggesting that dominant gene action is more important for this trait than is additive gene action. H_1 and H_2 were also larger than F in every case.

Investigation of the Genetic System

A number of genetic estimators may be derived from the diallel cross parameters, variances, and covariances. All were calculated in each replicate. Then overall means and standard errors of the means were calculated for each estimator as was done for the parameters. These estimators described below are found in Table IX.

Degree of dominance was estimated in the F_1 by dominance ratios one, two, and three by H_1/D, $(H_1/D)^{1/2}$, and $(V_{1L1} - E)/(W_{0L01} - E/n)$, respectively. The same estimates based on F_2 data were calculated by $1/4\ H_1/D$, $(1/4\ H_1/D)^{1/2}$, and $(V_{2L2} - E)/(W_{0L02} - E/n)$, respectively. All are weighted overall measures of the degree of dominance. With no dominance, the estimates are equal to zero. With partial dominance, they take any value between zero and one. In the case of complete dominance, estimates are equal to one. A value greater than one indicates overdominance. All estimates of the degree of dominance were greater than one, suggesting overdominance for this trait. The large estimate for dominance estimator three in the F_2 was due to a very large estimate in the first replication. The other two replications

TABLE IX

MEAN ESTIMATOR RATIOS OF EARLINESS

Estimator Ratios	F_1 (1965)	95 Percent Confidence Limits	F_1 (1966)	95 Percent Confidence Limits	F_2 (1966)	95 Percent Confidence Limits
Dominance #1	1.85	3.16 - .53	3.68	8.53 - (-1.16)	3.00	9.24 - (- 3.23)
Dominance #2	1.35	1.83 - .87	1.86	3.28 - .45	1.63	3.45 - (- .19)
Dominance #3	1.45	2.12 - .77	2.81	6.55 - (- .93)	25.25	272.01 - (-221.51)
$\overline{F_1} - \overline{P}$	12.60	18.53 - 6.66	6.87	14.44 - (- .70)	3.50	9.38 - (- 2.38)
$(1/4\ H_2)/H_1$	.24	.29 - .19	.25	.51 - (- .01)	.30	.71 - (- .12)
K	1.35	2.57 - .32	1.34	3.67 - (- .99)	2.69	13.68 - (- 8.30)
Heritability	.29	.42 - .15	.12	.16 - .07	.16	.25 - .06

had estimates of 2.29 and 1.41, which were of the same order of magnitudes as estimates obtained for estimator three in the other populations and for estimators one and two over all populations.

Before discussing the ratios of K and heritability in Table IX, the author elected to study the direction of dominance more fully. From a comparison of the $(\bar{F}_2 - \bar{P})$ and $(\bar{F}_1 - \bar{P})$ results in 1966 it is obvious that some of the hybrid vigor observed in the F_1 was lost in the F_2. Another estimate of the direction of dominance discussed by Crumpacker and Allard (13) is obtained through a correlation coefficient of the mean values of $(W_r + V_r)$ of each array averaged over replications with the corresponding parental means averaged over replications. When the correlation is high, it indicates that most of the dominant alleles act in one direction and most of the recessive alleles act in the opposite direction. If the correlation is low, some dominant and recessive alleles operate in one direction while other dominant and recessive alleles operate in the opposite direction.

The calculated correlation coefficients for the F_1 populations of 1965 and 1966 and the F_2 population were -.81, -.36, and -.45, respectively. All were negative in sign, but only the coefficient for the 1965 F_1 population was significantly different from zero at the 0.05 and/or 0.01 probability level. Since the parents having a larger number of dominant alleles are expected to have smaller variances and covariances than those parents with more recessives, the negative signs on the coefficients would suggest that the dominant genes were operating in the direction of increased earliness.

The quantity $(1/4\ H_2)/(H_1)$ is an estimator of the average frequency of the nagative versus the positive alleles in the parents. It is

expected to be 1/4 when distribution is equal and to be less than 1/4 when distribution is unequal. None of the estimates obtained were significantly different from 1/4. Therefore, the lower estimate of H_2 as compared to H_1 noted earlier, though they may be real, were not of sufficient magnitude to be significantly different.

K is an estimator of the number of effective factors controlling a trait where an effective factor is defined as the smallest unit 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 (31). Jinks (26) and Mather (31) have stated that the number of effective factors is always underestimated when dominance effects are different in size and/or direction and the distribution of the genes is correlated.

K is estimated in the F_1 and F_2 by the formulas which follow:

$$K \text{ (in the } F_1) = \frac{(\text{overall progeny mean} - \text{parental mean})^2}{1/4 \ H_2}$$

$$K \text{ (in the } F_2) = \frac{(\text{overall progeny mean} - \text{parental mean})^2}{1/16 \ H_2}$$

The estimates of K for the F_1 in 1965 and 1966 were very close, while that for the F_2 was somewhat higher. The higher value in the F_2 was probably due to segregation and recombination in that generation. However, none of these results were significantly different from zero at the 0.05 probability level.

Narrow-sense heritabilities were estimated according to Crumpacker and Allard (13) on a plot basis in the F_1 by the formula which follows:

$$h^2 \text{ (in the } F_1) = \frac{1/4 \ D}{1/4 \ D + 1/4 \ H_1 - 1/4 \ F + E}$$

The modified heritability formula given below (56) was used in the F_2.

$$h^2 \text{ (in the } F_2) = \frac{1/4\ D}{1/4\ D + 1/16\ H_1 - 1/8\ F + E}$$

The heritabilities were relatively low for this trait compared to those obtained for fiber length, strength, and coarseness (56,57) but each estimate was significantly different from zero. Based on these heritabilities, mass selection for this trait in early generation material probably would not be very effective as a breeding method. Pedigrees, sib tests, and/or progeny tests would probably be very helpful in choosing plants genetically superior for this trait.

EXPERIMENT II

Performance data of populations one, two, and four are presented
in Table X. Table XI contains the data of population three. Means and
phenotypic variances of earliness and fiber length, linear correlation
coefficients between the two traits, and 95 percent confidence limits
on those correlations are included in the tables.

Effectiveness of Two Cycles of Mass Selection for Fiber Length

In population one, the mean fiber lengths of the progenies which
resulted from the first and second cycles of mass selection for length
exceeded that of the check population, population four. The first
cycle progeny's fiber was .073 longer than the check while the second
cycle progeny's was .091 longer. Separate t-tests revealed that those
mean differences were significant at 0.01 level of probability. The
second cycle of selection increased length only .018 or about one-
fourth as much as did the first cycle. Therefore, selection was still
effective in the second cycle, but the rate of effectiveness was
rapidly decreased. Narrow-sense heritabilities calculated from actual
selection gains on an individual plant basis using the formula given by
Allard (5) for genetic progress were .78 and .23 for the first and
second cycles of selection, respectively. This decrease in herita-
bility would explain at least a portion of the decrease in the rate of
effectiveness of selection. Earliness did not show a trend in this
population relative to that of the check.

Selection apparently reduced the fiber length phenotypic variation
of the selected populations since separate F-tests showed that the
variances of the selected populations were significantly smaller than

TABLE X

POPULATIONS ONE, TWO, AND FOUR

Population	Number of Plants	Earliness		Fiber Length		Correlation Coefficients	95 Percent Confidence Limits
		Mean	Variance	Mean	Variance		
One							
First Cycle	401	61.0	999.50	1.126	.001955	-.12	(-.20) - (-.02)
Second Cycle	421	79.0	413.89	1.142	.002107	.26	(.18) - (.35)
Two							
First Cycle	361	53.8	677.85	1.080	.001154	.10	(-.01) - (.22)
Second Cycle	416	79.6	403.11	1.052	.002037	.21	(.12) - (.30)
Four							
In 1967	388	39.3	675.13	1.053	.002410	-.05	(-.15) - (.05)
In 1968	362	82.0	366.16	1.051	.003166	.13	(.03) - (.22)

TABLE XI

POPULATION THREE

Selection Groups	Number of Plants	Earliness		Fiber Length		Correlation Coefficients	95 Percent Confidence Limits
		Mean	Variance	Mean	Variance		
For earliness and fiber length (a)	434	78.9	409.75 a*	1.107	.007072 a*	.26	(.19) - (.36)
For earliness (b)	105	78.8	252.67 bc	1.072	.003151 bc	.06	(-.14) - (+.22)
For lateness (c)	95	79.8	242.54 bc	1.091	.002773 bc	.06	(-.14) - (+.22)
For long fiber (d)	120	83.5	213.12 c	1.091	.002324 c	-.20	(-.38) - (-.04)
For short fiber (e)	91	83.5	335.88 ab	1.048	.003612 b	-.21	(-.42) - (-.03)

* Variances followed by the same letter are not significantly different at the .05 level of probability.

of the check populations. The phenotypic variance for earliness was significantly larger at the 0.01 probability level than the check in the first-cycle progeny, but was not even significant at the 0.05 level in the second-cycle progeny. The calculated phenotypic correlation coefficients were inconsistent in direction in populations one and four from first to second cycle and from 1967 to 1968, respectively. However, the coefficients were negative for both populations in 1967 and were positive for both population in 1968, suggesting a possible year effect rather than actual linkage or pleiotropism of genes.

Effectiveness of Two Cycles of Mass Selection for Earliness

In population two, the mean earliness of the progeny which resulted from the first cycle of mass selection for earliness exceeded that of the check population in 1967. A t-test showed this difference to be significant at the 0.01 probability level. However, the mean earliness of the check population exceeded that of the second cycle progeny in 1968; and the t-test detected no significant difference between them at the 0.05 level. These results are rather puzzling. They indicate that the apparent increase in earliness from the first cycle was spurious or that the second cycle selection negated the gains obtained in the first cycle or that 1968 was such a year that genetic differences in earliness were obscured. Considering the unusually early onset of cool temperatures in the fall and the fairly early frost in 1968, the last explanation appears the most likely. If so, one cycle of selection increased earliness by 14.5 percent. The further genetic increase, if any, by the second cycle of selection cannot be estimated at the present time. A narrow-sense heritability value of

.35 for earliness in the first cycle on a single plant basis was cal-
culated, again using Allard's (5) method. A value was not calculated
for the second cycle. The fiber length did not show a trend in this
population relative to that of the check.

The phenotypic variances for earliness in the first and second
cycle progenies were not significantly different at the 0.05 probability
level from the variances exhibited by the check population. The fiber
length variances were significantly reduced at the 0.01 probability
level below that of the check population. The reason for this reduc-
tion is not clear. Correlation coefficients between the two traits in
this population were positive in both cycles of selection. However,
only the coefficient in the second cycle was significantly different
from zero.

Effectiveness of One Cycle of Mass Selection for Fiber Length and Earliness After Intermating

The data from the five groups in population three are summarized
in Table XI. Those groups were selected for (a) earliness and fiber
length (b) earliness (c) lateness (d) long fiber (e) short fiber.

A t-test of the fiber length means between groups (d) and (e)
revealed a significant difference at the 0.10 level but not at 0.05
level. A narrow-sense heritability estimate (h^2) on an individual
plant basis of .37 for fiber length was obtained by assuming genetic
progress (ΔG) from selection for this trait to be one-half the dif-
ference between the means of groups d and e and inserting the proper
values into the formula given by Allard (5). Selection for fiber
length or shortness apparently had no effect on earliness, but here

again the year could have masked what genetic differences there were present, if any. The selection group for longer fiber had significantly smaller phenotypic variances for length and earliness than did the group for shorter fiber.

The earliness means for selection groups (b) and (c) were not significantly different at the 0.05 probability level. Three possible explanations are: (1) genetic variability was relatively too low compared to environmental variation to permit effective selection, (2) visual selection was ineffective as a selection method, and/or (3) the year masked the genetic differences which ordinarily would have been exhibited in the progeny. Probably (2) and/or (3) are the most logical explanations of these results. Fiber length differences between these two groups were not significant. No significant trends in reduction of phenotypic variance for earliness or length were noted between groups (b) and (c).

Because of the supposed masking effect of 1968 on earliness values, it is impossible to determine how selection group (a) genetically relates to the other groups for that trait or how much less effective it is to select for two rather than one trait. Its fiber length was significantly greater than the other group (e's) at the 0.05 level but not significantly greater than the other groups. Phenotypic variabilities for earliness in this group were significantly larger than all other groups except (e).

Phenotypic correlation coefficients for groups (b) and (c) were not significantly different from zero. The significant negative correlation in groups (d) and (e) suggests that selection for long fiber decreases earliness and that selection for short fiber increases earliness. However, the means for earliness in those two groups do not

bear that conclusion out as the means are exactly equal. The positive and significant correlation in selection group (a) presents exactly the opposite conclusion as did the one above. This one suggests that as you increase one of these traits you increase the other and vice versa. The reason for the discrepancy is not readily apparent.

CHAPTER V

SUMMARY AND CONCLUSIONS

EXPERIMENT I

A diallel study among 10 varieties of upland cotton was conducted
at Perkins, Oklahoma in 1965 and 1966. Parental and F_1 populations
were grown in replicated tests in both years. F_2 populations were in-
cluded in the test.

The objective of this experiment was to obtain some information on
the inheritance of earliness in cotton. Analyses of variance in each
year showed significant differences among entries. A diallel analysis
was then conducted. The diallel cross is based on a genetic model with
seven recognized assumptions. Three broad, general tests of those
assumptions were conducted on three populations (the F_1 in 1965 and
1966 and the F_2 in 1966) to determine whether earliness fulfilled the
assumptions or not. In a sense, nine tests were conducted on earliness.
Earliness failed four of the nine. Specific tests of the assumptions
were conducted in order to pinpoint the offending assumptions, if pos-
sible. Five assumptions were not tested because of the lack of ade-
quate tests or because tests for those assumptions were considered un-
necessary. Those assumptions were diploid segregation, homozygous
parents, no reciprocal differences, no multiple alleles, and uncorre-
lated gene distribution.

46

Because of the nature of the test the assumption of no epistasis could be tested only on the F_1 and F_2 data from 1966. Epistasis was absent in or made negligible contribution to the expression of earliness in that year.

The assumption of no genotype-environment interaction could only be tested over years since a single location was used in the experiment. Differences in the additive effects among parents for this trait were significant but constant over years. Significant differences in dominance among parents were also found, but these effects were not constant from year to year as shown by a significant arrays by years interaction term.

The environmental variance population parameters, E_0, E_1, and E_2, for parents, F_1's, and F_2's, respectively, were significantly different from zero. E_0 estimates exceeded E_1 estimates in each year. E_2 was larger than E_0 and E_1 in 1966.

The estimates of D in 1965 were significantly different from zero and exceeded the corresponding F values.

F values were inconsistent in sign from year to year in the same population and between populations in the same year. Only the F_2 estimate was significantly different from zero.

H_1 and H_2 exceeded D and F in each population. They were significantly different from zero for the F_1 populations in 1965 and 1966 but not for the F_2. H_1 was larger than H_2 in each population.

In the investigation of the genetic system for earliness, overdominance appeared to be the degree of dominance involved. The direction of dominance was toward earlier maturity, with the majority of the dominant alleles operating in that direction.

In the estimation of effective factor number (K), the estimated number was low for all populations, varying from 1.34 to 2.69.

Narrow-sense heritabilities on a plot basis were fairly low. Therefore, mass selection would be highly ineffective as a breeding method for earliness. Other methods which should be considered are pedigrees, sib tests, and/or progeny tests.

EXPERIMENT II

In this experiment four populations of upland cotton were derived from a highly heterozygous base population. Two cycles of mass selection for fiber length and two for earliness were employed in populations one and two, respectively. Five selection groups were obtained in population three after intermating. Population four was maintained for two years without selection as a check population.

The objective of this experiment was to explore the possibility of developing a strain early in maturity and having a long fiber.

In population one, significant increases in fiber length were gained in each cycle of selection, but the narrow-sense heritability and rate of progress was less in the second cycle. Selection apparently decreased the phenotypic variance for fiber length as well.

The correlation coefficients between length and earliness were inconsistent in direction in this population and in population four from first to second cycle and from 1967 to 1968, respectively.

In population two, the mean for earliness of the first cycle exceeded that of the check population in 1967 by 14.5 percent while the mean for earliness in the second cycle was not significantly different from the check population in 1968. The 1968 results could logically be attributed to that particular year being such a year that obscured what genetic differences in earliness that were actually present. Selection for earliness did not appear to reduce the phenotypic variance for that trait in the succeeding generations. The correlation coefficients between fiber length and earliness were positive after both cycles of selection. However, the one obtained after the first cycle was not significantly different from zero.

In population three, selection in opposite directions for fiber length in groups (d) and (e) was effective while selection for earliness in groups (b) and (c) was not. Apparently, the year obscured genetic differences here, also, or visual selection for this trait is ineffective or both. Selection for longer fiber seemed to have significantly reduced phenotypic variance for length and earliness more so than did selection for shorter fiber. No significant trends were noticed in this regard when selection was made for earliness. Phenotypic variabilities for length and earliness in group (a) were significantly larger than all other groups, except one. The correlation for groups (b) and (c) were nonsignificant, while correlations for groups (a), (d), and (e) were contradictory.

Due to the masking effect on earliness of the year 1968, definitive statements cannot be made, but it appears likely that maximum progress per unit of time can be made by selecting for both earliness and length and not one or the other. The breeding of an early variety with long fiber appears feasible, though difficult.

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