## CHARACTERIZATION OF A COMPOSITE-CROSS POPULATION IN COTTON (<u>GOSSYPIUM HIRSUTUM</u> L.) THROUGH THE FIRST TEN GENERATIONS

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iii

## TABLE OF CONTENTS

| Chapter | Pag  | e              |
|---------|--|----------------|
| I.      | INTRODUCTION   | 1              |
| п.      | LITERATURE REVIEW  | 3              |
|         | Natural Selection in Bulk Hybrid Populations   | 3<br>5<br>7    |
| III.    | MATERIALS AND METHODS  | .2             |
|         | Experimental Procedures for Experiment II 1<br>Statistical Analyses for Experiment I 1 | .3<br>.4<br>.6 |
| IV.     | RESULTS AND DISCUSSION   | 3              |
|         | •  | 3              |
| V.      | SUMMARY AND CONCLUSIONS  | 4              |
| SELECTI | ED BIBLIOGRAPHY  | 7              |

## LIST OF TABLES

| Table |   | Page |
|-------|---|------|
| I.    | Cultural Information Relating to the Study of Possible<br>Changes Within the Composite-Cross Population                                   | 15   |
| II.   | Analyses of Variance for Entries (Populations) One Through<br>Six Over Three Locations and Two Years                                      | 17   |
| III.  | Least Squares Analyses for Entries (Populations) One<br>Through Six and Eight Over Seven Environments                                     | 18   |
| IV.   | Adjusted Means for Entries (Populations) One Through Six<br>and Eight Over Seven Environments   | 19   |
| V.    | Analyses of Variance for Entries (Populations) One Through<br>Six and Check Cultivars Over Three Locations and Two<br>Years               | 21   |
| VI.   | Comparisons Among the Means of the Three Check Cultivars<br>and the Mean of Entries One Through Six Over Three<br>Locations and Two Years | 26   |
| VII.  | Mean Performances and Heritabilities for Picked Lint<br>Percent and Four Fiber Characters Over Three Generations .                        | 29   |
| VIII. | Genotypic Correlations Between Parents and Offspring for<br>All Possible Pairs of Traits Over Three Generations                           | 31   |
| IX.   | Phenotypic Correlations Within Parents and Offspring for<br>All Possible Pairs of Traits Over Three Generations                           | 32   |

## LIST OF FIGURES

## Figure

Page

1. Regression of Mean 2.5% Span Length on Entry, i.e., Generation, Codes (Entry Seven Omitted. See Text.) . 25

## CHAPTER I

#### INTRODUCTION

No single system of breeding is used in cotton (<u>Gossypium hirsutum</u> L.) primarily because the crop is not strictly self- or cross-pollinated; cotton has some characteristics of both conditions (2, 11), though selfpollination predominates. Early work in cotton improvement was concerned mainly with mass and individual plant selections. Progeny-row selection was then widely adopted by breeders because of the desire for uniformity in addition to superior performance; but as the progeny-row method results in inbreeding, the genetic base in such populations is often narrowed to the point that area of adaptation is also restricted. To avoid possible declines in productivity because of inbreeding and to increase the probability of obtaining better cultivars, cotton breeders have attempted many different breeding systems especially those that create and maintain broad genetic bases in populations.

A breeding method which emphasizes the concept of a broad genetic base and which has been successful particularly in barley (<u>Hordeum</u> <u>vulgare</u> L.) is the composite-cross technique, wherein a set of parents is intercrossed in various combinations and then the crosses are bulked to form a population. The population is carried over a long period of time under the influence of natural selection and minimal or no artificial selection. In general, cultivars developed by this method have been more stable to fluctuations in environmental conditions

than have many of those based on single-plant selection.

The objectives of this series of experiments were to determine changes which had occurred over time in a composite-cross population of cotton and how the population performed relative to known cultivars and to determine the present status of the population in a genetic sense, i.e., how effective would selection be for specific traits within the population and how would selection for one trait influence other traits of economic importance.

## CHAPTER II

#### LITERATURE REVIEW

#### Survival in Cultivar Mixtures

A pure-line cultivar usually performs well in the particular environment under which it was developed; however, its yield can be drastically affected when conditions change from the "normal." A mixture of genotypes appears to possess an advantage over pure lines (31) in that various components of a composite could respond differently to variable environments. Even if strong genotype by environment interactions were present, a mixed population would (in spite of individual weaknesses in the components) be expected to have greater stability than would any single line (3). A mixture of pure lines usually does not produce the highest yield at any given time, although mean yield may be higher over a number of years.

Harlan and Martini (9) studied the effects of natural selection and competition in a mixture of eleven barley cultivars grown under ten sets of environmental conditions for periods of 4 to 12 years. They found marked variation in dominant cultivars from environment to environment. Well-adapted cultivars rapidly became dominant; other cultivars, dominant at some locations, did not survive in others. Few cultivars could grow well at all locations; while some increased for a period of time, then declined. The best adapted cultivar at some locations exhibited higher yield than did the commonly grown local cultivar.

Laude and Swanson (13) observed the rate of change in two cultivar mixtures of winter wheat, <u>Triticum aestivum</u> L. ('Kanred' with 'Harvest Queen' and Kanred with 'Currell'). They found the rates to be so rapid that the population shifted from an equal mixture to a nearly pure stand of Kanred in both mixtures in less than nine years. The change was attributed to the better adapted cultivar producing more seed each year.

Suneson and Wiebe (24) formulated two barley and one wheat cultivar mixtures and grew the three over a period of 5 to 9 years at Davis, California. They observed that a well adapted and high yielding cultivar of barley ('Vaughn') and of wheat ('Ramona') did not perform as well in the mixture as did other cultivars with slightly lower yield when grown in pure stands. They suggested that the bulk population method of breeding may have a limitation in that genotypes which show the best performance in mixtures do not necessarily perform the best in pure stands. Another study which supports their finding was done by Suneson (20) in which four barley cultivars were grown in a mixture for 16 years. His results indicated that Vaughn (which had a high yield and showed resistance to several leaf diseases when grown in pure stands during the same period) was virtually eliminated by the end of the experiment. 'Atlas' (which had the poorest leaf disease record and a mean yield in pure stands below the median for the component cultivars) dominated the mixture. Suneson concluded that the bulk population method of breeding may not necessarily perpetuate either the highest yielding or the most resistant genes. In other words, survival capacity is not directly related to agronomic fitness.

#### Natural Selection in Bulk Hybrid Populations

The idea that greater genetic variability and more vigorous cultivars could be developed from crossing pure lines brought about a new approach to bulk population breeding (8). Lines were crossed; and the crosses were then grown in bulk for a number of generations. The main features of such a breeding method are, as stated by Suneson (21, p. 190), "a broadly diversified germ plasm, and a prolonged subjection of the mass of the progeny to competitive natural selection in the area of contemplated use."

Harlan, Martini, and Stevens (10) compared a composite cross population of 379 barley crosses derived from 28 parent cultivars and grown for seven generations with the pedigree selection method. They found that hybrid progenies which had high yields also produced highyielding selections, whereas those which had low yields gave lowyielding selections. However, the mean yield of the selections from the composite was as high as that derived using the pedigree method. Suneson and Stevens (23) investigated the effect of natural selection in a bulk hybrid of six different composite crosses of barley grown 6 to 24 generations and compared them with a commercial cultivar, Atlas. The yield of Composite Cross II was less than Atlas until the  $F_{15}$  generation; whereupon, the bulk hybrid began to improve and yielded more than Atlas. Other composite crosses also showed improvement in yield when grown over long periods (21). This suggested that bulk hybrids be continued for some time after becoming relatively homozygous. With respect to scald [Rhynchosporium secalis (Oud.) J. J. Davis] resistance, only 17 resistant selections (4.8%) were found among 356 progenies

taken from the  $F_{12}$  of Composite Cross II. In the  $F_{23}$  generation, only seven percent of the plants in the population were highly resistant. In the Composite Cross II population, Suneson (21) conducted a study of the bulks and lines selected for resistance to yellow dwarf virus in the  $F_{25}$  and  $F_{26}$ ; and he found that as resistance to the disease increased, yield declined slightly. This supported previous findings that disease resistance is not necessarily an indication of better survival in bulk populations (20).

The trend in increasing yields of the composites with time suggested to Suneson (21) that the populations had a higher degree of adaptation than pure-line cultivars. This realization led to a further study of Composite Cross XVI which was derived by crossing 165 selections from the various composites in the  $F_{10}$  to  $F_{27}$  of the previous crosses. After this population had been subjected to 13 generations of natural selection, it was released for commercial production. The composite was very diverse, and it had higher mean yield than any cultivar derived from pedigree or back-cross selection released up to that time (22).

Adair and Jones (1) investigated the effect of natural selection on the characteristics of rice (<u>Oryza sativa</u> L.) in three bulk hybrid populations grown over eight years at three locations. They found heading date, plant height, and proportion of grain types varied markedly with location. In addition, the characters were associated with each other, i.e., date of heading with plant height and date of heading with grain type. They suggested that the bulk hybrid population is a valuable method in breeding especially where it is necessary to grow large populations to provide a better opportunity for desired

characters to combine with resistance to certain diseases.

Atkins (4) studied a bulk hybrid population of ten oat (<u>Avena</u> <u>sativa</u> L.) crosses grown for eight generations. Observations were made on the reaction of the bulk population to specific races of crown and stem rust and to <u>Helminthosporium Victoriae</u>, yield, and other characters of economic importance. He found the forces of natural selection to be effective in increasing the proportion of disease-resistant types but found no significant associations between heading date, maturity, or plant height of segregates from the bulk population.

From long-time records and additional studies on the performance and distribution of weedy rye (<u>Secale cereale</u> L. X <u>S. montanum</u> L.), Suneson, Rachie, and Khush (25) reported the spread and natural establishment of weedy rye populations in California's northern mountain counties. They concluded that the abundance of weedy rye could be ascribed to a favorable climate, soil, and opportunity for continued introgression with many different cultivars of rye (<u>Secale cereale</u> L.) which resulted in increased genetic diversity and adaptability of the population.

## Performance of Cotton in Mixed Populations

In two series of experiments, Richmond and Lewis (18) compared the performance of stocks grown from seed mixtures of cotton cultivars with that of the components grown as pure stocks. In Series I, the results showed no consistent differences in yield between the mixtures and the components. For Series II, the yield of the mixtures exhibited no significant differences from the pure stocks. However, analyses of the agronomically important characters showed that the mixtures differed

significantly in boll size, seed index, and fiber strength but not in fiber length and lint index. Pure stocks also differed for the same characteristics. When the mixtures were compared with the pure stocks, only boll size and seed index were not significantly different. Fiber strength (in four of the nine mixtures) was significantly higher, although all the mixtures had greater fiber strength than the corresponding pure-stock means. They concluded that there was no yield advantage in growing a mixture of cultivars, but it is possible that mixture will produce fiber properties not obtainable from single commercial pure lines.

Ramiah and Panse [quoted by Richmond and Lewis (18)] conducted a series of tests of pure and mixed cultivars, and reported that certain mixtures had approximately equal or better yields than the pure lines and produced lint of superior spinning quality. Sawhney and Narayanayya [also quoted by Richmond and Lewis (18)] concluded that the sole justification for adopting the practice of growing mixtures of pure lines is their ability to give uniformly good yields year after year.

Riggs (19) studied four cotton cultivars grown in mixtures at three ratios for two seasons. His results demonstrated that not all mixtures had yields greater than the best cultivar when grown in pure stands. In general, the results indicated that the mixtures (when combined over all cultivars) gave, on the average, yields equal to or less than the best cultivar when grown alone. Similarly, the fiber properties of the mixtures used did not show an improvement over the best cultivar.

Duncan, Pate, and Porter (6) utilized Empire-derivative strains of

cotton to produce eight synthetic cultivars at two locations (four per location) during 1954-1957. Lint yield of their synthetics was significantly lower than the check cultivar, but the fiber of the synthetics was longer. Only two of the four synthetics produced at Knoxville (high natural crossing) were superior in yield to the Empire-derived original mixtures. Moreover, the synthetics produced at Knoxville gave higher yield than those from Greenville (low natural crossing). The differences between the synthetics from the two locations was attributed to greater heterosis in those from Knoxville due to the greater amount of natural crossing. A similar study was carried out using a mixture of eight Acala-Hopi-Acala stocks (7). Five synthetics were produced during a five-year period and tested for either one or two The three top-yielding synthetics were not significantly difyears. ferent from the best check cultivar. The synthetics grown at Knoxville had higher yield and were earlier in maturity but weaker in fiber strength than those grown at Shafter, California, under low natural crossing. The differences in performance were attributed partly to the effect of natural selection and partly to heterosis.

Kohel and Richmond (12) compared the performances of four parental homozygous strains, a parental mixture, an  $F_1$  mixture, and eight synthetic cultivars (various products of three years open- and selfpollination at two levels of natural crossing). Their tests showed that the  $F_1$  mixture was significantly higher in yield than the other entries except for the synthetic produced by open-pollination each generation in the area of high natural crossing. The  $F_1$  mixture also had higher mean values for all agronomic characters than the parental mixture except fiber length and strength, but the  $F_1$  mixture had lower

mean values in fiber strength and elongation than did the parental strains.

Linkage is known to hinder character recombination in early generations of segregation and thus limit the rate of crop improvement. It has been hypothesized that intermating for several generations would tend to break up such linkages and increase genetic recombination in breeding populations.

Miller and Rawlings (15), working with populations derived from a cross of 'Empire 10' with 'TH 131-5', demonstrated that after six generations of mixed selfing (approximately 50% selfing) and random mating, almost all of the genotypic correlations for all possible pairs among six traits, excluding fiber length, decreased in magnitude (ignoring sign). The correlations involving fiber length increased in the intermated population. These results suggested that intermating does tend to break up initial linkage disequilibrium, but it may also lead to closer linkages.

A similar study was conducted by Meredith and Bridge (14) who worked with populations derived from a cross between 'Stoneville 7A' and 'Pee Dee 165'. They found that most traits had higher genotypic correlations in the original population (an  $F_2$  selfed population) and that the correlations declined in the intermated population after two generations of random mating. The study indicated that linkage was still a hindrance to improving both yield and strength of cotton. They suggested that some modifications of the conventional method of cotton breeding would be necessary to improve both traits simultaneously.

The influence of selection for fiber length and fineness on other agronomic characters in cotton was studied under nonirrigated conditions

by Quisenberry, Ray, and Jones (17). From a composite-cross population, they developed four groups of lines based on selection for those two characters. Correlation coefficients between the parental and selected lines indicated that the associations between fiber length and both lint yield and lint percent did not alter and that the associations between fiber fineness and both fiber strength and lint index remained unchanged during the selection process. However, the correlations of fiber length and fineness with other characters changed in intensity or direction. In their study, linkage relationships between some traits were not broken.

#### CHAPTER III

#### MATERIALS AND METHODS

The parental material used in the present study included five cottons which were either stormproof or storm-resistant and five which were open-boll. The stormproof or storm-resistant parents were 'Paymaster 101', 'Gregg', 'Western Stormproof', 'Lankart 57', and '6-77'; the open-boll cultivars were 'Deltapine 45', 'Coker 100A WR', 'Acala 44', 'Stoneville 7', and 'Auburn M'. Except for 6-77, all the above were at one time commercial cultivars of cotton. Strain 6-77 was a bacterial blight-resistant [Xanthomonas malvacearum (E.F.Sm.) Dows.] selection from the cultivars 'Stormproof No. 1'.

The 45 possible crosses among these ten parents (ignoring reciprocals) were made in Iguala, Mexico, in the winter of 1964, and the  $F_1$ seed were grown at Perkins, Oklahoma, in 1965. Individual  $F_1$  combinations were selfed to produce  $F_2$  seed. Diallel analyses of the ten parents and 45  $F_1$ 's in 1965 and 1966 (plus  $F_2$ 's in the latter year) were conducted to study the inheritance of agronomic and fiber property traits, and those results have been reported previously (27, 28, 30).

An equal amount of the remnant  $F_2$  seed by weight (50 g apiece) from each of the 25 crosses between stormproof or storm-resistant and open-boll parents was mixed thoroughly to form a composite-cross population. The composite was grown in a block approximately 0.25 ha (0.62 acres) in isolation from other cotton at Perkins on dryland in 1966.

Rows were 1.02 m (40 inches) apart; seed was planted thinly, but plants were not thinned after emergence. After frost, bolls were picked by hand. One boll was taken from the central part of each stormproof or storm-resistant plant until two large onion bags were packed full of seed cotton. After ginning, approximately nine kg (20 pounds) of seed were obtained. The bolls were collected from the central portion of the greater part of the block each year. A portion of the harvested seed was used for planting the generation the following year, and the remainder was put in cold storage. This procedure was repeated each year and is continuing at the present time.

#### Experimental Procedures for Experiment I

This series of experiments were conducted to study the changes, if any, which had occurred in the population over time, such changes being the effect of natural selection, unintentional artificial selection, or both. Another objective was to determine the performance of the population relative to known cultivars. A replicated experiment was conducted on dryland at Perkins in 1972. The material in this test included remnant seed of the populations harvested each year from 1966  $(F_3)$  through 1971  $(F_8)$ , inclusive. In addition, three commercial cultivars ['Lockett 4789-A', 'Westburn 70' (29), and 'Paymaster 202'] were included as reference points in comparisons. The experimental design used was a randomized complete-block with six replications. In 1973 and 1974, the same type experiments were carried out on dryland at Perkins, Mangum, and Chickasha, Oklahoma. The seed in these six experiments include (in addition to the entries in 1972) remnant seed from the population harvested in 1972  $(F_9)$ , and the 1974 experiments

also had an entry derived from the remnant seed harvested from the population the previous year  $(F_{10})$ .

All plots were single rows 1.02 m (40 inches) apart. Other details of the above experiments as to soil types, fertilizer applications, plot lengths, etc., may be found in Table I.

Traits measured in this experiment included lint yield (kg/ha), pulled lint percent [(lint/snapped cotton) X 100]; picked lint percent [(lint/seed cotton) X 100], 2.5 percent span length (2.5% SL) (inches); uniformity index (UNIF) [(50%/2.5% span length) X 100]; micronaire (MIC) [Mg/inch]; 0-inch gauge stelometer, T<sub>0</sub> (grams-force/tex); and 1/8-inch gauge stelometer, T<sub>1</sub> (grams-force/tex).

#### Experimental Procedures for Experiment II

This series of experiments was conducted to determine the genetic status of the population by estimating heritability for and genotypic and phenotypic correlations among selected traits. In the bulk populations at Perkins in 1971, 1972, and 1973, after the bolls were harvested to perpetuate the population, approximately 250 plants were selected based on their apparent yield and boll-type (open-boll plants were discriminated against). A seed-cotton sample was harvested from each individual plant selected; ginned; and picked lint percent, 2.5 percent span length, uniformity index, micronaire, and 1/8-inch gauge stelometer was estimated for each plant (measured as described under Experiment I). Seed from each plant was grown as a separate progeny row on dryland at Chickasha, Oklahoma, the following year. Rows were 9.1 m long and 1.02 m apart, and there were no border rows between plots. After frost, the seed-cotton from one mature boll was taken from the central portion

## TABLE I

# CULTURAL INFORMATION RELATING TO THE STUDY OF POSSIBLE CHANGES WITHIN THE COMPOSITE-CROSS POPULATION

|             | and the second | Plot*   |   | Date of  |   |
|-------------|--|---|---|--|---|
| Year        | Fertilizer   | Length, m   | Planting  | Thinning   | Harvesting  |
| 1972        | 80 lbs N**   | 6.6   | June 1  | June 16  | October 5   |
| • • • • • • |  |   |   |  | December 28   |
| 1973        | 66-30-54   | 6.6   | June 12   | July 13  | December 27   |
| 1974        | 200 lbs 18-46-0  | 9.1   | June 14   | July 2   | December 21   |
| 1973        | 33-0-40  | 7.6   | June 14   | <u>†</u><br>†  | December 8  |
| 1974        | 175 lbs 20-20-10   | 9.1   | June 1  | June 17  | January 23  |
| 1973        | None   | 9.1   | June 14   | July 5   | December 6  |
| 1974        | None   | 9.1   | May 29  | June 26  | December 13   |
|             | 1972<br>1973<br>1974<br>1973<br>1974<br>1973   | 1972 80 lbs N**   1973 66-30-54   1974 200 lbs 18-46-0   1973 33-0-40   1974 175 lbs 20-20-10   1973 None | Year   Fertilizer   Length, m     1972   80 lbs N**   6.6     1973   66-30-54   6.6     1974   200 lbs 18-46-0   9.1     1973   33-0-40   7.6     1974   175 lbs 20-20-10   9.1     1973   None   9.1 | Year   Fertilizer   Length, m   Planting     1972   80 lbs N**   6.6   June l     1973   66-30-54   6.6   June l2     1974   200 lbs 18-46-0   9.1   June l4     1973   33-0-40   7.6   June l4     1974   175 lbs 20-20-10   9.1   June l     1973   None   9.1   June l4 | Year   Fertilizer   Length, m   Planting   Thinning     1972   80 lbs N**   6.6   June 1   June 16     1973   66-30-54   6.6   June 12   July 13     1974   200 lbs 18-46-0   9.1   June 14   July 2     1973   33-0-40   7.6   June 14   i     1974   175 lbs 20-20-10   9.1   June 1   June 17     1973   None   9.1   June 14   July 5 |

\*All plots were single rows 1.02 m apart.

\*\*Pounds per acre multiplied by 1.12 equals kilograms per hectare.

Not thinned.

of each of the first 15 plants per plot (ignoring plants bordering alleys and skips). The progeny row samples were measured for the same characters measured on the original plants. The parent- (Perkins plants) offspring (Chickasha rows) data were then used to estimate heritability of and correlations among the above traits.

## Statistical Analyses for Experiment I

In the initial analyses of variance, the check cultivars were not included to permit the tests of significance to indicate clearly whether or not there were differences among generations for the traits measured. Preliminary analyses demonstrated that the population harvested in 1972 (entry number seven) had a mean unusually low for a number of traits including yield when compared to the generation before <u>and after</u> it. Therefore, that entry was also deleted in the analyses of variance. Leaving out this population can be rationalized on the basis of poor seed quality. The fall of 1972 was extremely wet, and this population was not actually harvested until well into the following year (March 12).

Data for the first six entries over the three locations and last two years were analyzed to derive estimates of entry by year, entry by location, and entry by year by location interactions (6). Since the test detected no significant interactions (Table II), data including the last entry (number eight, the  $F_{10}$  generation) was reassessed using the least squares analysis technique. The results of those analyses are shown in Table III; the means adjusted for environments and replicates (in environments) are shown in Table IV. It was also desirable to know whether there were linear relationships between characters and

## TABLE II

## ANALYSES OF VARIANCES FOR ENTRIES (POPULATIONS) ONE THROUGH SIX OVER THREE LOCATIONS AND TWO YEARS<sup>+</sup>

|                 |     |                         |                     | Nalassa and a strangerige - Sectional Astro |                     |                               |        |         |  |
|-----------------|-----|-------------------------|---------------------|---|---------------------|-------------------------------|--------|---------|--|
|                 |     |                         |                     |   | Mean Squ            | ares                          |        |         | ·<br>· · · · · · · · · · · · · · · · · · · |
| Source          | df  | Lint<br>Yield,<br>kg/ha | Pulled<br>Lint<br>% | Picked<br>Lint<br>%                         | 2.5% SL<br>(X 10-4) | UNIF                          | MIC    | To      | T  |
| Years (Y)       | 1   | 1974369                 | 7.44                | 60.80                                       | 537.39              | 528 <b>.</b> 59 <del>**</del> | 2.14   | 251.12  | 92.70                                      |
| Locations (L)   | 2   | 86837                   | 121.39              | 12.08                                       | 108.77              | 27.11*                        | 4.50   | 41.05   | 37.84                                      |
| YXL             | 2   | 1289986**               | 134.72**            | 66.67**                                     | 271.54**            | 4.67                          | 6.04** | 62.97** | 19.29**                                    |
| Reps in Y and L | 30  | 42901                   | 1.71                | 1.40  | 17.31               | 7.83                          | 0.15   | 7.21    | 4.03                                       |
| Entries (E)     | 5   | 13844                   | 2.56                | 1.31  | 21.15*              | 3.50                          | 0.03   | 2.64    | 0.65                                       |
| YXE             | 5   | 23318                   | 0.42                | 0.36  | 5.09                | 1.81                          | 0.08   | 1.20    | 0.87                                       |
| LXE             | 10  | 22224                   | 1.34                | 0.57  | 5.84                | 1.26                          | 0.09   | 1.84    | 0.66                                       |
| YXLXE           | .10 | 8228                    | 1.12                | 0.71  | 4.59                | 1.89                          | 0.05   | 0.89    | 1.22                                       |
| Error           | 150 | 14669                   | 1.81                | 1.38  | 8.19                | 2.15                          | 0.09   | 2.88    | 1.07                                       |

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

+Analyses did not include the check cultivars nor entries seven and eight.

## TABLE III

## LEAST SQUARES ANALYSES FOR ENTRIES (POPULATIONS) ONE THROUGH SIX AND EIGHT OVER SEVEN ENVIRONMENTS<sup>+</sup>

|                  |     |                 | · · · · · · · · · · · · · · · · · · · |                     | Mean Squa           | ares     | - <u> </u> |         |                |
|------------------|-----|-----------------|---------------------------------------|---------------------|---------------------|----------|------------|---------|----------------|
|                  |     | Lint            | Pulled                                | Picked              |                     |          |            |         |                |
| Source           | df  | Yield,<br>kg/ha | Lint<br>%                             | Lint<br>%           | 2.5% SL<br>(X 10-4) | UNIF     | MIC        | TO      | T <sub>l</sub> |
| Environments (E) | 6   | 2821526**       | 140.32**                              | 50.22 <del>**</del> | 280.10**            | 120.24** | 6.41**     | 96.57** | 37.03**        |
| Reps in E        | 35  | 58899           | 1.58                                  | 1.35                | 16.24               | 6.96     | 0.14       | 6.68    | 3.62           |
| Entries          | 6   | 17412           | 2.14                                  | 1.13                | 22.82**             | 2.68     | 0.02       | 1.81    | 0.25           |
| Error            | 222 | 17234           | 1.50                                  | 1.15                | 7.31                | 1.92     | 0.07       | 2.69    | 1.08           |

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

<sup>1</sup>Analyses did not include the check cultivars nor entry seven.

## TABLE IV

## ADJUSTED MEANS FOR ENTRIES (POPULATIONS) ONE THROUGH SIX AND EIGHT OVER SEVEN ENVIRONMENTS

| Entry               | Genera-<br>tion | N  | Lint<br>Yield,<br>kg/ha | Pulled<br>Lint<br>% | Picked<br>Lint<br>% | 2.5% SL<br>(X 10 <sup>-4</sup> ) | UNIF   | MIC   | т <sub>о</sub> | Т <u>1</u> |
|---------------------|-----------------|----|-------------------------|---------------------|---------------------|----------------------------------|--------|-------|----------------|------------|
| 1                   | F <sub>3</sub>  | 42 | 638. a*                 | 26.4 a              | 36.2 a              | 1.053 a                          | 47.7 a | 4.3 a | 39.9 a         | 19.1 a     |
| 2                   | F <sub>4</sub>  | 42 | 677 a                   | 26.4 a              | 36.2 a              | 1.051 a                          | 48.3 a | 4.3 a | 40.1 a         | 19.4 a     |
| 3                   | F <sub>5</sub>  | 42 | 641 a                   | 26.6 a              | 36 <b>.</b> 3 a     | 1.053 a                          | 48.5 a | 4.3 a | 39.9 a         | 19.3 a     |
| 4                   | F <sub>6</sub>  | 42 | 695 a                   | 27.0 a              | 36.6 a              | 1.037 b                          | 48.2 a | 4.3 a | 40.1 a         | 19.3 a     |
| 5                   | F <sub>7</sub>  | 42 | 652 a                   | 26.8 a              | 36.3 a              | 1.037 b                          | 48.1 a | 4.3 a | 40.2 a         | 19.3 a     |
| 6                   | Fg              | 42 | 660 a                   | 26.5 a              | 36.1 a              | 1.044 ab                         | 48.0 a | 4.2 a | 39.7 a         | 19.3 a     |
| 81                  | <sup>F</sup> 10 | 18 | 675 a                   | 26.4 a              | 36.2 a              | 1.036 b                          | 48.3 a | 4.3 a | 39.5 a         | 19.3 a     |
| Overal              | l Means         |    | 663                     | 26.6                | 36.3                | 1.044                            | 48.2   | 4.3   | 39.9           | 19.3       |
| ISD <sub>0.</sub> ( | 05              |    |                         |                     |                     | 0.012                            |        |       |                |            |

\*Entries followed by the same letter were not significantly different at the 0.05 probability level. \*Entry number seven was not included for reasons discussed earlier. generations. To obtain regression coefficients to test such relationships, entries (generations), replicates (in environments) and environments were considered as independent variables. Each character (the dependent variable) was regressed on generations (the independent variable). Regression lines were plotted for those characters which demonstrated significant differences among generations.

A second series of analyses of variance was performed including the three check cultivars (Table V) to test whether there were significant differences between the bulk population and the check cultivars and to show how the population related to the checks in performance.

#### Statistical Analyses for Experiment II

The effect of artificial selection on the improvement of the five selected characters was studied by estimating heritabilities and phenotypic and genotypic correlations.

Narrow-sense heritability,  $h_{ns}^2$ , was estimated by the regression coefficient of offspring on parent, i.e., <u>b</u>. Tests for the significance of the heritability estimates were made using the standard errors of the regression coefficient. If the estimate exceeded the standard error by two or three times, it was considered equivalent to sigificance at the 0.05 and 0.01 probability levels, respectively.

The phenotypic correlations,  $r_p$ , between parent and offspring were calculated as:

$$r_{p} = \delta_{ij} / (\delta_{i}^{2} \delta_{j}^{2})^{\frac{1}{2}}$$

where  $\delta_{ij}$  is the phenotypic covariance between traits  $\underline{i}$  and  $\underline{j}$  and  $\delta_{i}^{2}$ and  $\delta_{j}^{2}$  are the phenotypic variances for those traits, respectively.

## TABLE V

## ANALYSES OF VARIANCE FOR ENTRIES (POPULATIONS) ONE THROUGH SIX AND CHECK CULTIVARS OVER THREE LOCATIONS AND TWO YEARS+

| <del> </del>    |     |                         |                     |                     | Mean Squa                        | ares    |         |                     | ,      |
|-----------------|-----|-------------------------|---------------------|---------------------|----------------------------------|---------|---------|---------------------|--------|
| Source          | df  | Lint<br>Yield,<br>kg/ha | Pulled<br>Lint<br>% | Picked<br>Lint<br>% | 2.5% SL<br>(X 10 <sup>-4</sup> ) | UNIF    | MIC     | т <sub>о</sub>      | Tl     |
| Years (Y)       | l   | 2655270                 | 10.96               | 64.18               | 742.26                           | 676.58  | 3.91    | 350.73              | 135.98 |
| Locations (L)   | 2   | 160451                  | 216.39              | 19.20               | 130.60                           | 34.48   | 7.78    | 46.78               | 60.88  |
| YXL             | 2   | 2339239**               | 216.69**            | 104.74**            | 406.94**                         | 4.85    | 10.66** | 82.11**             | 21.80* |
| Reps in Y and L | 30  | 62203                   | 3.32                | 2.27                | 20.78                            | 11.75   | 0.19    | 11.57               | 5.10   |
| Entries (E)     | 8   | 79932**                 | 9.99**              | 8.25                | 278.94**                         | 36.24** | 1.66**  | 45.14 <del>**</del> | 7.17** |
| YXE             | 8   | 17962                   | 1.02                | 3.31*               | 3.96                             | 2.68    | 0.14    | 6.59*               | 1.60   |
| LXE             | 16  | 20860                   | 1.99                | 1.29                | 9.33                             | 1.37    | 0.10    | 3.33                | 0.65   |
| YXLXE           | 16  | 12432                   | 1.64                | 0.90                | 8.83                             | 2.31    | 0.10    | 0.94                | 1.46   |
| Error           | 240 | 12913                   | 1.93                | 1.66                | 7.90                             | 2.04    | 0.08    | 2.67                | 1.08   |

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

Analyses did not include entries seven and eight.

The estimates of genotypic correlations,  $r_g$ , were calculated based on the formula provided by VanVleck and Henderson (26) which may be written as follows:

$$r_{g} = \ell_{ij}^{2} / (\ell_{i}^{2} \ell_{j}^{2})^{\frac{1}{2}}$$

where  $\epsilon_{ij}$ ,  $\epsilon_{i}^{2}$ , and  $\epsilon_{j}^{2}$  are covariance and variances, for traits <u>i</u> and <u>j</u>. The estimate of  $r_{g}$  was obtained as:

$$\mathbf{r}_{g} = \left[ (\mathbf{S}_{p_{i}o_{j}} + \mathbf{S}_{p_{j}o_{i}})/2 \right] / (\mathbf{S}_{p_{i}o_{i}} + \mathbf{S}_{p_{j}o_{j}})^{\overline{z}}$$

where  $S_{p_i o_j}$ ,  $S_{p_j o_i}$ ,  $S_{p_i o_i}$ , and  $S_{p_j o_j}$  are the genetic covariances and variances between parent and offspring for traits <u>i</u> and <u>j</u>.

The variance estimate for  $r_g$  given by VanVleck and Henderson (26) may be generalized as:

$$\begin{split} \widehat{V(\mathbf{r}_{g})} &= \frac{\mathbf{r}_{g}^{2}}{\mu f} \Biggl[ \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} + \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} + \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} + \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} + \frac{2 \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} + \frac{2 \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} + \frac{2 \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}o_{1}}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}}}^{2} s_{p_{1}o_{1}}^{2}}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}}{(s_{p_{1}o_{1}})^{2}} + \frac{2 \frac{s_{p_{1}o_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}}^{2} s_{p_{1}o_{1}}^{2}}}{(s_{p_{1}o_{1}})^{2}} - \frac{2 \frac{s_{p_{1}o_{1}o_{1}}^{2}}$$

where f is the degrees of freedom associated with each variance and covariance estimated.  $S_{p_i}^2$ ,  $S_{p_j}^2$ ,  $S_{o_i}^2$ , and  $S_{o_j}^2$  are the phenotypic variances of parent and offspring for traits <u>i</u> and <u>j</u>, respectively.

#### CHAPTER IV

RESULTS AND DISCUSSIONS

## Experiment I

To obtain some indication of genotype by environment interactions, an analysis of variance (5) was conducted among the first six populations over 1973 and 1974 at the three locations. These analyses omitted the first test in 1972 to permit a balanced design, the seventh population (which was available in those years at those locations) for the reason described earlier, and the eighth population (available only in 1974) again to permit a balanced design. Since the great majority of the data were included in these rather straightforward analyses, it is doubtful whether the complicated inclusion of the 1972 test or of the eighth population in 1974 would have altered the conclusions significantly. Since none of the entries by environment interactions for these traits were significant (Table  $\Pi$ ), least squares analyses could be conducted for populations one through six in the seven experiments in 1972 through 1974 plus population eight in the three experiments in 1974. Each individual test was treated as a separate environment in these analyses. There were no significant differences (Table III) among entries for any character except 2.5 percent span length. This suggests that the population has been more-or-less stable genetically since the  $F_3$  generation, except for fiber length. Table IV shows the

adjusted mean performances of entries one through six and eight. The  $\mathrm{ISD}_{0.05}$  is given for fiber length to provide a test for differences between generations since the analysis of variance for that trait was significant at the 0.05 level of probability or higher (Table III). It should be noted that fiber length declined significantly after the F<sub>5</sub> generation and remained fairly constant thereafter. A regression analysis depicts the decline as a linear trend (Figure 1) and the rate of length loss as about 0.0027 inch per generation. Assuming this trend will be maintained, the fiber length in this population would be reduced over the next four to five generations to the extent that it would be of economic importance, i.e., 1/32 of an inch (since the F<sub>3</sub>).

In analyses of variance including the three check cultivars and entries one through six over two years and three locations, highly significant differences among entries were exhibited for all traits except picked lint percent (Table V). Since Table  $\Pi$  indicates that the first six entries were not significantly different for any character except 2.5 percent span length, these results imply that there were differences among the check cultivars or between at least one of the check cultivars and the population, or both. Table VI compares the means of the check cultivars with the mean of entries one through six. There were no significant differences in yield among the check cultivars, but there were between the checks and the bulk population. The superior yield performance of this genetically complex population to the check cultivars in the study agrees with a large number of reports in crops (1, 3, 10, 21, 23) including cotton (12). Suneson (21) attributes the yield superiority to the heterogeneous germplasm in the population which implies diversity of adaptation factors. The consistent high

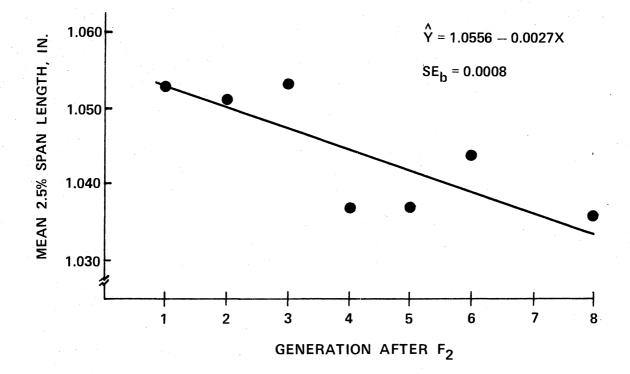


Figure 1. Regression of Mean 2.5% Span Length on Entry, i.e., Generation, Codes (Entry Seven Omitted. See Text.)

## TABLE VI

## COMPARISONS AMONG THE MEANS OF THE THREE CHECK CULTIVARS AND THE MEAN OF ENTRIES ONE THROUGH SIX OVER THREE LOCATIONS AND TWO YEARS

| Entry  | N   | Lint<br>Yield,<br>kg/ha | Pulled<br>Lint<br>% | Picked<br>Lint<br>%   | 2.5%<br>SL | UNIF            | MIC   | т <sub>о</sub> | Tl     |
|--|-----|-------------------------|---------------------|---|------------|-----------------|-------|----------------|--------|
| $\overline{x}_{1-6}^{\dagger}$                                 | 216 | 572 <b>a</b> *          | 26.2 a              | 36.1 a  | 1.043 b*   | 48.4 b          | 4.2 b | 39.7 c         | 19.2 c |
| Lockett 4789-A   | 36  | 481 b                   | 24.9 Ъ              | 34.7 a  | 1.066 a    | 47 <b>.</b> 2 c | 3.9 c | 40.7 b         | 19.6 b |
| Westburn 70  | 36  | 500 Ъ                   | 26.6 a              | 36.0 a  | 1.030 c    | 47.0 c          | 3.9 c | 38.0 d         | 18.5 d |
| Paymaster 202  | 36  | 471 b                   | 26.2 a              | 36.2 a  | 0.967 d    | 50.4 a          | 4.6 a | 42.2 a         | 20.2 a |
| $ISD_{0.05}(\overline{X}_{36} \text{ vs } \overline{X}_{36})$  |     | 52                      | 0.64                | anna da Mara da angenda | 0.013      | 0.66            | 0.13  | 0.75           | 0.48   |
| $LSD_{0.05}(\overline{x}_{36} \text{ vs } \overline{x}_{216})$ | ·   | 40                      | 0.49                | . Envirónmen  | 0.010      | 0.50            | 0.10  | 0.58           | 0.37   |

\*Entries followed by the same letter were not significantly different at the 0.05 probability level.

<sup>1</sup>Means of entries one through six.

\*Mean is not truly representative of group because this character shows a trend over generations. (See Table IV.)

yield performance of this composite-cross population from generation to generation and from environment to environment implies the presence of considerable genetic diversity in the material. The lack of inbreeding depression for yield beyond the  $F_3$  (the character in which such effects would be most likely to occur and to the largest degree) suggests that cross-pollination is sufficient to maintain a certain level of heterozygosity in the population. The lack of trends (except for the small decline in fiber length) suggests that effective selection pressure (artificial or natural) in this population has been slight to date. This can probably be attributed in large part to the way in which the population was sampled each fall to provide seed to plant the following spring (plus a remnant to save in cold storage for testing purposes). By taking a single boll from every plant that was stormproof or storm resistant regardless of the number of bolls per plant and by sampling a large number of plants, any tendencies for increased numbers of bolls per plant (i.e., increased yield) and any tendencies for genetic drift would have been opposed by the sampling process followed. This explanation is subject to experimental verification; and beginning in the fall of 1975, the population will be sampled using two different techniques.

Suneson (21) reported that natural selection was effective in improving yield in composite-crosses of barley, but most of those composites showed improvement only after the  $F_{10}$  generation. Therefore, it may be too soon to expect substantial yield improvement in this material.

Other traits in the population except picked lint percent also exhibited significant differences from the check cultivars (Table VI).

The population had an acceptable fiber fineness (i.e., between 3.5 and  $4.9\,\mu$ g/inch inclusive); pulled lint percent was not significantly different from the better check cultivars. Its uniformity index was less than that of only Paymaster 202. Fiber strength was not as high as the better check cultivars, but it was higher than that of Westburn 70. The fiber length of the population is declining at a slow rate, but it is significantly shorter than that of only Lockett 4789-A. All fiber traits considered, the population appears to have equal or better fiber than any of the cultivars used herein as checks.

#### Experiment II

Heritabilities estimated by the regression of offspring progenyrow performance on that of parental plant selections was significantly different from zero except for fiber fineness and strength in 1971/72 and 1973/74, respectively (Table VII). Fiber fineness showed rather inconsistent heritabilities from year to year; thus, its overall mean heritability would not be reliable in predicting expected gain. Selection for fineness would not be consistently effective from environment to environment. For the other characters, fiber length and uniformity exhibited moderate heritabilities; and selection for those traits should be more effective than for lint percent and fiber strength which had low heritabilities.

These estimates of heritability were obtained by calculating the regression of offspring on parent and should approximate narrow-sense estimates, i.e., the ratio of additive genetic variance to phenotypic variance. The estimates were unbiased by genotype by year, genotype by location, and genotype by year by location interactions because they

## TABLE VII

## MEAN PERFORMANCES AND HERITABILITIES FOR PICKED LINT PERCENT AND FOUR FIBER CHARACTERS OVER THREE GENERATIONS

| Years     | Means and<br>Heritabilities | Picked<br>Lint<br>% | 2.5%<br>SL         | UNIF               | MIC                | T1          |
|-----------|-----------------------------|---------------------|--------------------|--------------------|--------------------|-------------|
| 1971/72   | ₹<br>₹                      | 38.1                | 0.979              | 46.2               | 3.9                | 18.1        |
|           | -<br>X <sub>2</sub>         | 35.9                | 0.964              | 45•4               | 4.2                | 20.1        |
|           | $h^2 \pm SE$                | 0.17 <u>+</u> 0.04  | 0.36 <u>+</u> 0.05 | 0.19 ± 0.04        | 0.05 <u>+</u> 0.04 | 0.18 ± 0.07 |
| 1972/73   | $\overline{\mathbf{x}}_{1}$ | 38.4                | 1.041              | 48.3               | 4.6                | 19.5        |
|           | $\overline{\mathbf{x}}_{2}$ | 36.7                | 1.081              | 48.5               | 4.3                | 19.7        |
|           | h <sup>2</sup> ± SE         | 0.30 + 0.04         | 0.31 <u>+</u> 0.04 | 0.32 <u>+</u> 0.05 | 0.25 <u>+</u> 0.04 | 0.29 ± 0.04 |
| 1973/74   | $\overline{x}_{1}$          | 37.1                | 1.020              | 47.9               | 4.3                | 19.1        |
| ****      | $\overline{x}_2$            | 37.3                | 1.004              | 47.7               | 4.6                | 19.6        |
|           | $h^2 \pm SE$                | 0.20 ± 0.06         | 0.24 + 0.06        | 0.36 + 0.05        | 0.32 ± 0.05        | 0.13 ± 0.07 |
| Mean Heri | tabilities                  | 0.21                | 0.30               | 0.28               | 0.16               | 0.20        |

\*  $\overline{X}_1$  = parental means,  $\overline{X}_2$  = offspring means.

were computed from parent and offspring data obtained at different locations in different years (16).

Estimates of genotypic and phenotypic correlations for all posible pairs of the traits measured are presented in Tables VIII and IX, respectively. In the genotypic correlations, 2.5 percent span length is consistently and significantly negatively correlated with lint percent and uniformity index. The negative relationships would make it difficult to improve fiber length without a reduction in lint percent and fiber uniformity. However, since neither correlation was a perfect -1.00, those associations need not be irreversible for all selections. The phenotypic correlations of these two pairs of traits showed agreement in the direction and significance of correlation in both parents and offspring. Most genotypic and phenotypic correlations between 2.5 percent span length and micronaire were negative, and most were significantly different from zero. The inconsistencies (the one estimate not significantly different from zero and the one with a positive sign) were associated with the population-environment combination in which the heritability for fiber fineness was not significantly different from zero.

As could be surmised from their similar negative relations to fiber length, uniformity index and micronaire were positively related. Selection for coarse fiber would tend to increase fiber uniformity in this composite and vice versa. Fiber strength exhibited no significant genotypic or phenotypic correlations with length, uniformity or fineness though it was negatively associated with lint percent. Six of the nine correlations between those two characters were significant. Genotypic correlations between fiber fineness and lint percent were not

## TABLE VIII

## GENOTYPIC CORRELATIONS BETWEEN PARENTS AND OFFSPRING FOR ALL POSSIBLE PAIRS OF TRAITS OVER THREE GENERATIONS

|                  |                    | Genotypic            | Correlations (r      | $(r_g) \pm SE'$    |
|------------------|--------------------|----------------------|----------------------|--------------------|
| Combina          | tions of Traits    | 1971/72              | 1972/73              | 1973/74            |
| Picked<br>Lint % | vs. 2.5% SL        | -0.53 + 0.16**       | -0.32 + 0.14*        | -0.56 + 0.17**     |
| 70 11110         | vs. UNIF           | -0.20 ± 0.18         | -0.02 <u>+</u> 0.01  | 0.12 ± 0.23        |
|                  | vs. MIC            | -0.20 ± 0.18         | -0.06 + 0.13         | 0.09 ± 0.22        |
|                  | vs. T <sub>l</sub> | -1.15 + 0.28**       | -0.65 + 0.11**       | -0.75 + 0.36*      |
| 2.5% SL          | vs. UNIF           | -0.52 <u>+</u> 0.18* | -0.71 ± 0.11**       | -0.63 ± 0.12**     |
|                  | vs. MIC            | -0.58 + 0.41         | -0.50 + 0.19*        | -0.57 ± 0.14**     |
|                  | vs. T <sub>l</sub> | 0.31 ± 0.16          | 0.22 + 0.22          | 0.15 + 0.13        |
| UNIF             | vs. MIC            | 0.51 + 0.23*         | 0.52 <u>+</u> 0.11** | 0.66 + 0.10**      |
|                  | vs. T <sub>l</sub> | 0.36 + 0.22          | 0.31 + 0.21          | 0.53 <u>+</u> 0.29 |
| MIC              | vs. T <sub>l</sub> | -1.11 <u>+</u> 0.65  | 0.06 + 0.08          | 0.06 ± 0.04        |

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

<sup>1</sup>Number of observations, n, equaled 249, 260, and 255 for 1971/72, 1972/73, and 1973/74, respectively.

## TABLE IX

## PHENOTYPIC CORRELATIONS WITHIN PARENTS AND OFFSPRING FOR ALL POSSIBLE PAIRS OF TRAITS OVER THREE GENERATIONS

|                  |                    | Parental Phe | enotypic Corre | elations $(r_p)^{\dagger}$ | Offspring Ph | enotypic Corr | relations $(r_{p})$ |
|------------------|--------------------|--------------|----------------|----------------------------|--------------|---------------|---------------------|
| Combina          | tions of Traits    | 1971/72      | 1972/73        | 1973/74                    | 1971/72      | 1972/73       | 1973/74             |
| Picked<br>Lint % | vs. 2.5% SL        | -0.44**      | -0.36**        | -0.41**                    | -0.18**      | -0.39**       | -0.16**             |
| -<br>            | vs. UNIF           | 0.13*        | 0.00           | -0.03                      | 0.03         | 0.08          | 0.04                |
|                  | vs. MIC            | 0.51**       | 0.06           | 0.27**                     | 0.25**       | 0.34**        | 0.34**              |
|                  | vs. T <sub>1</sub> | -0.24**      | -0.37**        | -0.10                      | -0.12        | -0.24**       | -0.08               |
| 2.5% SL          | vs. UNIF           | -0.44**      | -0.38**        | -0.41**                    | -0.13*       | -0.32**       | -0.29**             |
|                  | vs. MIC            | -0.42**      | -0.42**        | -0.52**                    | 0.19**       | -0.41**       | -0.28**             |
|                  | vs. T <sub>1</sub> | 0.27**       | 0.24**         | -0.01                      | 0.25**       | 0.06          | 0.14*               |
| UNIF             | vs. MIC            | 0.54**       | 0.37**         | 0.37**                     | 0.32**       | 0.36**        | 0.40**              |
|                  | vs. T <sub>1</sub> | 0.27**       | -0.08          | 0.32**                     | 0.11         | 0.25**        | 0.16**              |
| MIC              | vs. T <sub>1</sub> | 0.02         | -0.14*         | 0.10                       | 0.02         | 0.08          | -0.09               |

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

<sup>+</sup>Number of observations, n, equaled 249, 260, and 255 for 1971/72, 1972/73, and 1973/74, respectively.

- 32

significant; the phenotypic correlations between the two traits were all positive, and all six were significant except one. Selection for fine fiber in this material would not change lint percent.

Miller and Rawlings (15) and Meredith and Bridge (14) reported that linkage blocks in cotton could be broken by allowing an intercrossed population to intermate for several generations before selections were made. They found that high genotypic correlations were reduced in intermated populations for most traits. In this material, linkages between some traits may have been broken before 1971 when the first plant selections were made. However, trends, if any, in the genotypic correlations calculated from the 1971 versus 1972 versus 1973 selections were inconclusive at best.

#### CHAPTER V

#### SUMMARY AND CONCLUSIONS

Five stormproof or storm-resistant and five open-boll cultivars were crossed between boll-type categories in the 25 possible combinations. Equal amounts of  $F_2$  seed were bulked, thoroughly mixed, and grown at Perkins, Oklahoma, in 1966. A portion of the harvested seed was used for planting the next generation, and this procedure has been repeated through the  $F_{10}$  generation.

Two types of experiments were initiated in 1971 to characterize this material. In Experiment I, a fraction of the remnant seed from each generation (previously maintained in cold storage) and three check cultivars were included in replicated field trials to study trends, if any, in the population for eight traits. In 1971, 1972, and 1973, the experiments were conducted at one, three, and three locations, respectively. In Experiment II, approximately 250 plants were selected from the bulk population on the basis of boll type and apparent yield in three consecutive years. The fiber was analyzed, and the seed from each plant was grown as a progeny row at Chickasha, Oklahoma, the following year. Five of the eight characters measured in Experiment I were also studied in Experiment II.

In Experiment I, only fiber length showed a significant difference from generation to generation. The trait exhibited a downward trend of about 0.0027 inches per generation. Assuming this trend is maintained,

an additional four to five generations would be required before the fiber length loss from the  $F_3$  would be sufficient to be of economic importance, i.e., 1/32 inch. There were no significant entry by environment interactions for any character. These results suggest that effective selection pressure (artificial or natural) was slight in this population on the eight traits measured. The lack of trends from generation to generation can probably be attributed in some degree to the sampling procedures used. All traits of the bulk population except picked lint percent showed significant differences from at least one of the check cultivars. The composite-cross population demonstrated yield superiority to the highest yielding check cultivar used, i.e., Westburn 70. For the other traits, it was significantly higher than at least one of the check cultivars. The population appeared to have equal or better fiber (all traits considered) than did any of the checks.

In Experiment II, fiber length and uniformity exhibited moderate heritability estimates while estimates for lint percent and fiber strength were low. Fiber fineness heritability estimates were erratic from year to year indicating that selection for that trait would not be consistently effective.

Fiber length was negatively correlated with lint percent, uniformity index, and fiber fineness, but not with fiber strength. Micronaire was positively correlated with fiber uniformity, but not with lint percent or fiber strength. Negative correlations were noted between fiber strength and lint percent, but not between fiber strength and any other character. Lint percent and uniformity index were unrelated. As a number of significant correlations were present in this material, selection for one trait may influence another trait in a general,

perhaps undesirable, direction; but as none of those correlations were perfect (i.e., 1.00 or -1.00), more desirable combinations of traits are possible in this material. If more undesirable linkage blocks previously existed in this population, they were partially broken before the last three generations as trends in the genotypic correlations, if any, in those three generations were inconclusive.

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