# A Diallel Analysis of Several Fiber Property Traits in Upland Cotton (Gossypium birsutum L.) II.

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#### ABSTRACT

Diallel analyses of upper 2.5% span length, micronaire, 1/8-inch gauge stelometer, and 0-inch gauge stelometer were conducted on 10 selected varieties of upland cotton, Gossypium hirsutum L., the 45 possible F1 crosses among them, and their 45  $\mathbf{f}_2$  progenies using the procedure of Jinks and Hayman. A partial failure of the basic assumptions of the analysis was noted for each trait though the stelometer measurements more nearly fulfilled the assumptions than did length or micronaire.

Fiber length and strength appeared to be governed by a weighted overall degree of dominance that was partial in nature. The degree of dominance for micronaire ap-

peared to be in the overdominance range.

Based on the relative size of their heritability estimates, mass selection should be an effective breeding method for improving fiber length and strength in this material though it should be slightly more effective for strength than for length. Pedigrees, sib tests, and/or progeny tests may be necessary to improve micronaire.

The reliability of diallel estimates made on  $\mathbf{F}_1$  popula-

tions from one year to the next at the same location was studied. Comparisons between F1 and F2 estimates were also made. Specific similarities and differences are dis-

cussed in the body of this paper.

Additional index words: Fiber length, Fiber strength, Micronaire.

DIALLEL analyses of several fiber traits in upland cotton, Gossypium hirsutum L., recently published (13). These analyses were based on parental and F1 data from a randomized, replicated experiment conducted at a single location in a single year. Since that time, data including parental, F<sub>1</sub>, and F<sub>2</sub> populations from tests conducted the following year have been analyzed. These additional results substantiate many of the conclusions derived the previous year but modify others. They also demonstrate the degree of reliability of the various diallel estimates made from one year to the next at the same location in the  $F_1$ as well as from the  $F_1$  to the  $F_2$ .

### MATERIALS AND METHODS

'Paymaster 101,' 'Gregg,' 'Western Stormproof,' 'Lankart 57,' '6-77,' 'Deltapine 45,' 'Coker 100A WR,' 'Acala 44,' 'Stoneville 7,' and 'Auburn\_M' were the parental varieties included in the experiment. These varieties were specifically chosen and do not represent a random sample of all upland cotton varieties. Therefore, inferences derived from the data apply only to the varieties and crosses studied. The extent to which they apply to the species as a whole is uncertain.

In 1966 the 10 varieties, the 45 possible F<sub>1</sub> crosses among them, and their 45  $F_2$  progenies were planted in a  $10 \times 10$  triple lattice design. Reciprocal crosses were not included. The location of the test, soil type, number of replications, plot size, and plant spacing within plots were the same as used previously (13). Single border rows of the variety 'Kemp' were planted between adjacent plots to equalize border effects between plots. Seedling diseases were not as severe as in 1965, but to compensate for

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the differential spacing between plants which did occur, 'De Ridder Red,' a variety with the dominant marker gene, R<sub>1</sub>, was planted in the blank hills as soon as they developed.

Two harvests were made on the material with six random plants from each plot being chosen for laboratory analysis. However, 10 plots had only three to six plants, and within those plots all plants were taken. In the laboratory fiber length was measured by the digital fibrograph as upper 2.5% span length, fiber coarseness by micronaire in micronaire units, and fiber strength by 1/8-inch gauge stelometer and 0-inch gauge stelometer in grams per grex. Fiber samples from each plant from each harvest were analyzed separately, and then a weighted average of each fiber measurement over the two harvests was calculated for each plant based on percentage of total lint yield per harvest. All subsequent calculations were made from these weighted averages. The analysis of the data followed the diallel procedure of Jinks and Hayman (4, 8, 9).

#### RESULTS AND DISCUSSION

Analyses of variance were conducted on a plot mean basis for each trait. Plants within plots were weighted equally in the determination of those plot means. These analyses, as did those in the previous year (13), revealed highly significant differences among entries for each fiber trait. Variety means of the characters studied are listed in Table 1 to give the reader some feel for the characteristics of the parents used. Diallel analyses on values unadjusted for block effects were then conducted on the  $\dot{F}_1$  and parental data and on the  $F_2$  and parental data. The results of these analyses were then compared to those obtained in 1965 (13) and to each other.

## General Tests of the Assumption

Assumptions of the analysis are diploid segregation, no reciprocal differences, homozygous parents, no multiple alleles, uncorrelated gene distribution, no genotype-environment interaction within locations and years, and no epistasis (3). Failure of any one or any combination of these assumptions invalidates to some degree the conclusions obtained by means of the analysis. Therefore, the three general tests of the assumptions used previously (13) were employed to test for failures.

In the discussion which follows, V<sub>r</sub> is the variance of the members of the rth array; W<sub>r</sub> is the covariance

Table 1. Mean performance of parental varieties over 1965 and

Variety	2,5% span	Micro	naire*	1/8-inch gauge	0-inch gauge stelometer	
	length	1965	1966	stelometer		
Paymaster 101	0,990	4,9	4.1	2,09	4.07	
Gregg	1,036	4.1	3, 9	2, 11	4.11	
Western Stormproof	1,008	4.2	3.4	1.84	3,77	
Lankart 57	1.076	4.9	4.0	1, 77	3.33	
6-77	1,079	4.2	3.6	1.99	4.01	
Deltapine 45	1,130	4,6	3.9	2, 13	3.88	
Coker 100A WR	1.124	4.6	3.8	2,00	3.90	
Acala 44	1, 116	3.9	3.3	2,30	4.10	
Stoneville 7	1.123	4.8	3.7	2.04	3, 88	
Auburn M	1.097	4.6	3.6	2,00	3,81	

<sup>\*</sup> Since the parents exhibited a significant years × parents interaction for this trait (see Table 5), the means for each year are listed separately.

of the members of the rth array with their nonrecurrent parents; and  $W_{\mathbf{r}'}$  is the covariance of the members of the rth array with the array means of their nonrecurrent parents. The rth array includes the rth parent as well as all of the crosses in which that parent is involved.

The first general test of the assumptions is an analysis of variance of the quantity  $(W_r - V_r)$ . This quantity should be constant over arrays if all assumptions of the analysis are fulfilled (7, 9). The quantity was calculated for each of the 10 arrays in each of the three replications, and then analyses of variance were conducted separately upon the 30 values obtained from the F<sub>1</sub> data and upon those from the F<sub>2</sub>. Results of this test are summarized in Table 2. The mean squares obtained in the F<sub>1</sub> were similar to those obtained in 1965 (13) in that the variation of  $(W_r-V_r)$  attributable to arrays was not significant at the 0.05 probability level for any of the fiber measurements. The only array mean square significant at that level was for fiber length in the F<sub>2</sub>. This would suggest a partial failure of the assumptions for length in that generation. Results of this test in the F<sub>1</sub> appear to be comparable from one year to the next. The performance between the  $F_1$  in either year and the  $F_2$  was generally the same, but the results obtained here imply that each generation should be tested to be certain that they respond to this test in a similar manner.

The second general test of the assumptions is an analysis of the (W<sub>r</sub>, W<sub>r</sub>') regression. Estimates of W<sub>r</sub>', like V<sub>r</sub> and W<sub>r</sub>, were calculated in each replication. In this test the regression coefficient is expected to be significantly different from zero but not from 0.5 if all of the assumptions are valid (1). Ninety-five percent confidence limits about the regressions were calculated (12). The results presented in Table 3 show that the coefficients were significantly different from zero for all four traits as they were previously (13). However, fiber length and 1/8-inch gauge stelometer in the F<sub>1</sub> and 0-inch gauge stelometer in the F<sub>2</sub> were significantly different from 0.5 in contrast to 1965 (13) where only micronaire was significantly different from 0.5. Consequently, the results of this second test over the two years suggest that none of the traits strictly complied with the assumptions. Results of this test were not consistent in the  $\overline{F}_1$  from year to year nor in the  $F_1$  versus  $F_2$  comparisons. If this test is to be used, every generation for each trait must be tested every year.

The third and last general test of the assumptions is an analysis of the  $(V_r, W_r)$  regression. In this test the regression coefficient is expected to be significantly different from zero but not from 1.0 if the assumptions are valid (9). Ninety-five percent confidence limits about the regressions were again calculated (12). These estimates are presented in Table 4. All  $F_1$  coefficients in 1966 conformed to expectations in contrast to the previous year when length and micronaire did not (13). The  $F_2$  results were more similar to the  $F_1$  results of 1965 than to those of 1966. In the  $F_1$  in 1965 and the  $F_2$  micronaire was not significantly different from zero, and length was significantly different from 1.0. Thus, this test indicates a partial failure of the assumptions for those two traits. This test, like the second one, does not give consistent results from year to year or from population to population.

Table 2. Analyses of variance of (W, -V,) values.

			Mean squares							
		2.5% spa	n length	Micro	naire	1/8- gau stelor	ıge	0-in gau stelon	ge	
Source	df	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	
Total	29	(× 1	0-6)	(× 1	0-2)	(× 1	10-4)	(× 10	)- <b>3</b> )	
Arrays Replica -	9	. 0814	.4088**	. 0172	.0900	. 0305	. 0375	.0141	. 0790	
tions	2	.5388**	.6040**	. 0905	. 1342	. 1234	. 1379	. 3528**	.0008	
Error	18	. 0569	. 0444	. 0325	.0752	. 0389	. 0545	. 0258	. 0520	

Table 3. (Wr, Wr') regression coefficients.

Measurement	Generation	Coefficient	95% confidence limit	
2,5% span length	F,	.488	.402473	
	$\mathbf{F}_{2}$	. 558	. 389 686	
Micronaire	F,	. 4.14	. 078 750	
	F,	4.0	. 236-, 564	
1/8-inch gauge stelometer	F,	. 250	. 106 475	
	F,	.318	. 010 626	
0-inch gauge stelometer	F.	.450	.316584	
	F,	.338	. 197 479	

Table 4. (Vr, Wr) regression coefficients.

Measurement	Generation	Coefficient	95% confidence limits
2.5% span length	F,	1,017	. 724-1. 311
	F,	.472	.21 ~0.730
Mier <b>o</b> naire	F,	. 697	. 277-1, 117
	F <sub>2</sub>	.405	(-, 233)-1, 043
1/8-inch gauge stelometer	F <sub>1</sub>	. 821	. 369-1, 273
	F <sub>2</sub>	.701	. 124 - 1. 277
0-inch gauge stelometer	$\mathbf{F}_{1}^{-}$	. 969	603-1,335
	F <sub>2</sub>	. 930	.452-1,507

In summary, three general tests were conducted on three sets of data (the F<sub>1</sub> in 1965 and the F<sub>1</sub> and F<sub>2</sub> in 1966) for each fiber measurement. Therefore, in a sense, nine tests were conducted on each trait. Length failed four of those nine tests, micronaire three, ½-inch gauge stelometer one, and 0-inch stelometer one. As a result, one could not say that any of these traits completely fulfilled the assumptions of the analysis, but one could suggest that the strength measurements fulfilled those assumptions more nearly than did length or micronaire.

## Specific Tests of the Assumptions

The specific assumptions of diploid segregation, no reciprocal differences, and no multiple alleles were not tested for the reasons cited previously (13). The ratio,  $\frac{1}{4}$  (H<sub>2</sub>/H<sub>1</sub>), was used to test the assumption of uncorrelated gene distribution in our paper published earlier (13). Since that time, it has been pointed out to us that the ratio measures the average frequency of negative versus positive alleles in the parents (3), not the correlation of gene distribution. Therefore, the ratio was not used to test that assumption in this paper. The assumption of homozygous parents was not tested because an unambiguous test for that assumption is not available. However, failure of this assumption as well as of some of the others could have caused a portion of the difficulties encountered in the general tests of the assumptions.

The specific assumption of no epistasis could be tested, and the assumption of no genotype-environment interaction within locations and years could be partially tested.

Verification of the no-epistasis assumption may be accomplished using the chi-square test devised by Hayman (5). The definitions, formulas, and procedures are outlined in his paper so they need not be repeated here. The observed chi-square values with

45 degrees of freedom were 58.0, 47.1, 42.1, and 44.3 for 2.5% span length, micronaire, 1/8-inch gauge stelometer, and 0-inch gauge stelometer, respectively. None of the values were significant at the 0.05 probability level suggesting that epistasis did not make a significant contribution to the expression of those traits in 1966.

The assumption of no genotype-environment interaction within locations and years may be partially tested because only one location was involved. Therefore, a location effect is confounded in the results rendering them somewhat less sensitive than if an additional location had been used. The analysis proposed by Allard (2) was used to test this assumption for both the additive and dominance components of variation for each trait.

The test for the additive components of variation is based on the fact that heritable differences between homozygous parents, in the absence of epistasis, are caused by the additive effects of genes (2). Mean estimates for each trait were obtained for the 10 parents in three replications in two years. A test for the constancy of the additive components was possible from an analysis of variance among the resulting 60 means. Parental means from the replications within a single year were treated as subsamples for the purpose of error-term estimation. These test results are found in Table 5. Since there was no significant epistasis at the 0.05 level for any of these traits, Allard's (2) interpretations assuming no epistasis were followed. The significance of the mean squares for years has no specific genetical interpretation since any of a large number of environmental factors could have caused the observed differences over the two seasons for these traits. In contrast, the significance of the mean squares for parents indicates that for each of the fiber measurements certain parents carry alleles with different additive effects. In this test years were considered to be a random variable; and therefore the years by parents mean squares were used to test parents mean squares for significance. The lack of significance of the years by parents mean squares for fiber length and strength suggests that their additive effects were fairly constant relative to one another from one year to the next. This was not the case for micronaire.

The test for the dominance components of variation (2) was based on an analysis of variance of the 60 V<sub>r</sub> and 60 W<sub>r</sub> estimates for each trait from the 10 arrays, three replications, and two years in which the F<sub>1</sub> was grown. Before the analysis was run, however, the individual V<sub>r</sub> and W<sub>r</sub> terms were divided by the variance of the parents occurring within the same replication in order to minimize the additive component of variation in the test and, thereby, improve the test's sensitivity in regard to dominance interaction terms. This rescaling also minimizes the fluctuation of basic variability between environments which also tends to mask between-environment comparisons in genetic systems (2). Again, array estimates from the replications within à single year were treated as subsamples for error-term estimation. Results of this test are given in Table 6. As before, the interpretation of these results follows the reasoning of Allard (2), assuming no epistasis. Had epistasis been present, various effects would have been confounded, and the interpretation of results could not have been so straight forward. The lack

Table 5. Genotype by year analyses of the additive components of variation.

			Mean squares					
Source	df	2.5% span length	Micro- naire	1/8-inch gauge stelometer	0-inch gauge stelometer			
Years	1	.080008**	8,36**	. 1421**	6,2921**			
Reps within years	4	000251	.09*	.0087	.0694**			
Parents	9	015412**	.50**	. 1347**	. 3132**			
Years × Parents	9	000630	. 09*	.0068	.0239			
Error	36	.000334	. 03	.0071	.0125			

<sup>\* \*\*</sup> Significant at the 0.05 and 0.01 levels of probability, respectively.

Table 6. Genotype by year analyses of the dominance components of variation.

		squares			
Source	df	2.5% span length	Miero- naire	1/8-inch gauge stelometer	0-inch gauge stelometer
Years	1	, 0639	, 0546	.0378	. 0806
Reps within years	4	.3689**	.4818**	.0280	. 1025**
Dominance	1	. 0407	1.3525**	. 0677	.0170
Years × Dominance	1	0176	. 2084*	. 0055	. 0038
Arrays	9	. 1826**	. 1576**	.0571**	. 0250
Years × Arrays	9	. 0381	.0611	. 0342	. 0473
Dominance × Arrays	9	0059	. 0184	,0042	.0065
Years × Dominance ×					
Arrays	9	.0083	. 0355	.0021	.0016
Error	76	0222	. 0495	. 0183	. 0267

<sup>\*, \*\*</sup> Significant at the 0.05 and 0.01 levels of probability respectively.

Table 7. Mean parameter estimates of the fiber measurements.

2.5% s lengt					1/8-inch gauge stelometer		0-inch gauge stelometer	
Para- meter	F,	$\mathbf{F_2}$	$\mathbf{F}_{1}$	F <sub>2</sub>	$\mathbf{F}_1$	F <sub>2</sub>	$\mathbf{F}_{1}$	F <sub>2</sub>
E <sub>0</sub>	.000392		.0360		.0023*		.0073**	
E,	.000235**		.0222**		,0015**		0053**	
E <sub>2</sub>		.000300**		.0265**		.0021**		.0073**
D´	.002693		.0532	<b>-</b>	.0192*		.0512*	
F	.000347	000949	~,0033	.0053	. 0039	.0080	, 0063	, 0424
н,	.000915	,004779**	.0721*	.5003*	.0103*	.0357*	. 0205	. 1627
H <sub>2</sub>	.000837	.004613*	.0647*	.4523*	.0087*	,0288*	.0165	. 1056

<sup>\*, \*\*</sup> Significantly different from zero at the 0.05 and 0.01 levels of probability, respectively.

of significance of the mean squares for years shows that there were no differences in mean dominance between years for any of these traits. Significance of the dominance mean square for micronaire suggests that the mean degree of dominance for this trait is either partial dominance or overdominance. For the other traits dominance was either lacking or complete. Lack of significance of the years by dominance interaction terms for fiber length and strength shows that the degree of dominance, if any, was consistent over the two seasons. This was not true for micronaire. The significant array component for length, micronaire, and 1/g-inch gauge stelometer provides evidence that there were differences in dominance among the parents for those two traits. These differences were not apparent for 0-inch gauge stelometer. These relationships were also constant from year to year. The non-significance of the dominance by arrays interactions provides additional evidence for the lack of epistasis in these traits; and the lack of significance of the second-order interactions shows that these epistatic effects, or rather the lack of them, were constant over both years.

### Parameter Estimates

Even when a trait exhibits partial failure of the assumptions, estimates of the population parameters for that trait are still possible (4), though certainly the estimates for such a trait are less reliable than they would have been if all assumptions had been fulfilled. With this in mind the parameters were esti-

	2.5% spa	2.5% span length		Micronaire		ge stelometer	0-inch gauge stelometer	
Estimator	95% confidence F <sub>1</sub> limits	95% confidence F <sub>2</sub> limits						
Dominance 1	, 36 (-, 14)-0, 85	.50 (01)-1,01	1.69 (-1.35)-4.74	2,89 (-2,17)-7,95	.55 .06 -1.04	.48 .06 -0.89	.47 (44)-1.38	.77 .37 -1.16
Dominance 2	.58 .11 -1.05	.70 .36 -1.04	1, 25 , 14 -2, 36	1,63 ,12 -3,14	.74 .40 -1.08	.68 .34 -1.02	.64 (09)-1.37	.87 .65 -1.09
Dominance 3	.60 .18 -1.02	.75 .46 -1.04	. 95 . 25 -1.65	1.76 .29 -3.22	.71 .45 -0.98	. 73 . 53 -0.93	. 67 . 16 -1. 17	.90 .88 -0.92
K	5,54 2,01 -9,07	1.08 .56 -1.60	.64 (84)-2.11	. 17 ( 19)-0.54	. 19 (-, 20)-0, 58	.35 (47)-1.17	.40 (-, 82)-1.61	.06 (-, 18)-0,31
1/4(H,/H <sub>1</sub> )	. 26 . 08 -0, 45	24 . 09 -0.40	. 22 . 08 -0.36	. 23 . 16 -0.31	.22 .10 -0.34	. 21 . 14 -0. 27	.21 .15 -0.27	. 17 . 12 -0. 21
Heritability	.61 (-,09)-1,30	.49 (10)-1,08	.25 (-,11)-0,60	.19 (03)-0.41	.58 .41 -0.74	.62 ,47 -0,77	.57 .11 -1.04	,52 ,22 -0,82

\* The dominance estimators one, two, and three in the  $F_1$  are the estimators  $H_1/D$ ,  $(H_1/D)^{1/2}$ , and  $(V_{1L1}-E)/(W_{0L01}-E/n)$ , respectively. These formulas in the  $F_2$  were modified into 1/4  $(H_1/D)$ , [1/4  $(H_1/D)]^{1/2}$ , and  $(V_{2L2}-E)/(W_{0L02}-E/n)$ , respectively. The meaning of the symbols,  $V_{1L1}$ ,  $V_{2L2}$ ,  $W_{0L01}$ ,  $W_{0L02}$ , and  $H_{0L02}$ , and  $H_{0L02}$  and  $H_{0L02}$ . The meaning of the symbols  $W_{0L02}$ ,  $W_{0L02}$ ,

mated. To obtain them, each replication was treated as a separate experiment with its own estimate of environmental variation as suggested by Nelder (11). As a result, one estimate of each parameter for each trait was obtained in each replication. Means of those estimates are listed in Table 7. Standard errors of the mean, used in the tests of significance, were estimated by the variation of the block values around the overall mean. In the table  $E_0$ ,  $E_1$ , and  $E_2$  are estimates of parental, F<sub>1</sub>, and F<sub>2</sub> environmental variances, respectively.  $E_0$  and  $E_1$  were estimated by the same process used previously (13) while E<sub>2</sub> was estimated using F<sub>2</sub> entries rather than parental or F<sub>1</sub> entries. The remaining parameters (D, F, H<sub>1</sub>, and H<sub>2</sub>) are as defined by Jinks and Hayman (9) using the notation of Mather (10). These parameters were estimated by the same formulas used previously (13). In the F2 they were estimated using Hayman's (6) formulas on page 65 of his paper.

All estimates of environmental variation were significantly different from zero except E<sub>0</sub> for length and micronaire in 1966. As in 1965 (13), all estimates of E<sub>0</sub> were larger than their corresponding estimates of E<sub>1</sub>. The estimate of D for fiber length was not significantly different from zero whereas in the previous year it had been. D for micronaire was significant in neither year while D for the stelometers was significant in both. The exhibition of significant or non-significant differences from zero was consistent between the F<sub>1</sub> and F<sub>2</sub> populations for the remaining parameters in 1966 except for H<sub>1</sub> and H<sub>2</sub> for fiber length. Comparisons of F, H<sub>1</sub>, and H<sub>2</sub> between 1965 and 1966 were highly erratic in this regard.

Various ratios were calculated using the estimates obtained for Table 7 in order to provide further information about the genetic systems operating for each trait. An estimate of each ratio was calculated in each replication; and confidence intervals were placed on the mean of those estimates as was done previously (13). The means of these ratios and their 95% confidence limits are listed in Table 8.

As in 1965 (13), all of the estimates for length and the stelometers were within the partial dominance range, i.e., between zero and one. The estimates for micronaire in the F<sub>1</sub> were similar to those obtained in 1965 (13) in that two out of the three estimates were in the overdominance range, i.e., above one. All of the estimates for micronaire in the F<sub>2</sub> were well into the overdominance range. These results coupled those obtained from the genotype by year analysis of the dominance components for micronaire strongly suggest overdominance as being the weighted overall degree of dominance for micronaire in this material.

K is an estimate of the number of effective factors which are operating for a certain trait as defined by Mather (10), and it measures only those factors showing some degree of dominance. The formula (8) used in the  $F_1$  to obtain these estimates is as follows: K =(overall progeny mean – parental mean) $^2/(1/_4H_2)$ . The formula used in the F2 was modified into the following:  $K = (overall progeny mean - parental mean)^2$  $/(1/16 H_2)$ . K is underestimated if the dominance effects of all genes concerned are not equal in size and direction or if the distribution of the genes is correlated (8, 10). As in 1965 (13), the micronaire and stelometer estimates were small. The estimate for 0inch gauge stelometer was especially small in the  $F_2$ . Differences in direction of gene action probably was a factor in the low estimates obtained for micronaire and 0-inch gauge stelometer since, in a study of the individual crosses, each of these traits exhibited significant heterosis in the positive and negative directions. Dominance effects unequal in size could have played a part in the estimates for any of these traits. Fiber length gave the highest estimates of K among the traits in both years. The estimates of K for length were the only ones significantly different from zero in 1966 whereas in 1965 micronaire was the only trait to have that distinction (13).

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The ratio, 1/4 ( $H_2/H_1$ ), was used to estimate the average frequency of negative versus positive alleles in the parents (3). If distribution is equal among the parents, the ratio is expected to be 0.25. If not, the ratio will be less than 0.25. The calculated ratios for these traits did not differ significantly from the expected value of 0.25 in the  $F_1$  for any of the characters while 0-inch gauge stelometer had the only ratio in the  $F_2$  significantly less than that value. None of the values for this ratio from the 1965 data was significantly different from 0.25.

A narrow-sense heritability estimate,  $(1/4 D)/(1/4 D + 1/4 H_1 - 1/4 F + E)$ , was calculated for each trait in the  $F_1$  on a plot-mean basis (3). The formula was modified for use in the  $F_2$  as follows:  $(1/4 D)/(1/4 D + 1/16 H_1 - 1/8 F + E)$ . While the estimates obtained for fiber length and the stelometers were all fairly high, only those for strength were significantly different from zero at the 0.05 probability level. Where each "<" represents a narrow-sense heritability difference of about 0.10 units, the characters may be ranked on the basis of the 1966 data as follows: micronaire <<< (upper 2.5% span length, 0-inch gauge stelometer, and 1/8-inch gauge stelometer). Based on both year's data, they may be ranked: micronaire << upper 2.5% span length < (0-inch gauge stelometer, 1/8-inch gauge stelometer). A consideration of the aver-

age overall heritability estimates reveals that about one-fourth of the variance exhibited by micronaire, one-half of that by length, and about three-fifths of that by the stelometers is additive and/or additive by additive in nature. Therefore, mass selection should be most effective in improving strength, only slightly less effective in improving length, and relatively ineffective for micronaire. Some emphasis on pedigrees, sib tests, and/or progeny tests may be necessary to make satisfactory improvement in micronaire.

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