IDENTIFICATION OF GENETICALLY-SUPERIOR INDIVIDUALS FOR LINT LENGTH AND LINT FINENESS IN TWO STRAINS OF COTTON

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INTRODUCTION

The successful achievement of any beeeding program lies in the genetic nature of the breeding stock available and the methods used to exploit this genetic nature through selection. Therefore identification of genetically superior individuals can be considered as a major step in the improvement of the population. Furthermore, being able to identify these few superior individuals would add materially to the effectiveness of the breeding program.

The purpose of this study is to attempt to identify in two strains of cotton individuals which are genetically superior to the balance of their respective populations for lint length and lint fineness.

Prediction of genetic gains possible by selection of the identified-genetically-superior individuals are also made in order to evaluate the breeding value of the two populations and any further breeding program with these stocks.

REVIEW OF LITERATURE

The inheritance of lint length and lint fineness.

Despite the importance of cotton fiber, there have been few reports of actual experiments concerning the inheritance of fiber characteristics. However, the studies that have been made have shown that lint properties behave as quantitative characters, being governed by several pairs of genes and subject to considerable amount of environmental influence.

Ware (1929) found complete dominance of long lint over short in interspecific crosses between Pima cotton (*Gossypium barbadense*) x upland cotton (*G. hirsutum*). Segregation in the F_2 generation indicated that several pairs of genes were involved. Harland (1939) in interspecific crosses of *Gossypium purpurascens* (short) and *G. barbadense* (long) obtained an intermediate F_1, but somewhat nearer to the longer parent. On the basis of the data from other workers, he also stated that probably a large number of genes with independent minute effects are involved in the determination of lint length.

In a study of upland cotton Ware, Jenkins, and Harrell (1943) reported incomplete dominance of long fiber over short in a backcross of Florida Green Seed (short) to Rowden (long).

In a study of the inheritance of various economic characters in a cross of an upland variety and a strain of a three - species hydrid of *Gossypium arboreum*, *G. thurberii* and *G. hirsutum*, Nakornthap (1954) found that lint length and lint fineness were quantitatively inherited.

In upland cotton, Fortuno (1954) found that a large number of genes for length were segregating in an F_2 population, and he estimated the number of genes involved to be 9.38. He also found partial dominance of long fiber.

Very little information is available on the inheritance of the fineness of the fiber. However, Stafford (1953) found that perimeter also to be quantitatively inherited.

Lint length and lint fineness appear to be associated. Harland (1939) stated that length and fineness are correlated, long cottons are usually fine, while short cottons can be either fine or coarse.

In studies of upland cotton fiber, Moore (1941) found negative correlations between the average length and the average weight per inch and between average length and average diameter in 5 varieties. Hancock (1944) obtained results similar to those of Moore, but he stated that length and fineness are genetically independent. Negative correlations between length and weight per inch were also found by Barker and Pope (1948).

Fortuno (1954) found a significant correlation of -0.319 between length and perimeter. He also obtained a high negative correlation between length and wall thickness. Fortuno further found a highly significant multiple correlation between length, perimeter, and wall thickness, indicating a close relationship between these three characters.

Many authors have reported on the effects of environment on fiber properties. Ware and Harrell (1944) reported that seasonal variation affects some fiber characteristics. Hanson, Ewing, and Ewing Jr. (1956) found that dry, warm, and sunny years generally tend to produce shorter and stronger cotton than do cooler and wetter seasons.

Hancock (1947) stated that the length of maturity period causes significant differences in lint length, strength, and fineness. Especially long fruiting periods create environments in which ample opportunity is available to affect the development of the fiber.

Peebles, Den Hartog, and Pressley (1956) studied the effects of spacing within the rows on fiber length and fiber fineness. They found spacings from 2 to 16 inches had no effect on either fiber length or fiber fineness.

Spooner, Caviness, and Spurgeon (1958) found that irrigation significantly increased both micronaire reading and length.

Hessler, Lane, and Young (1959) found that temperature also plays an important role in the development of fiber to maturity. They reported that fiber development might be retarded from the start of the boll growth if temperature is the limiting factor.

In conclusion, the available information indicates that lint length and lint fineness behave as quantitative characters, governed by several pairs of genes. Presumably, there is some degree of partial dominance of long fiber over short. Lint length and lint fineness appear to be negatively correlated, with long fibers tending to be finer than short fibers. Several environmental factors also play an important role in fiber development.

The identification of genetically superior individuals.

The immediate genetic theory basic to the identification of genetically superior individuals is concerned with the partitioning of the variance into its various components.

Fisher (1918) was the first to provide a statistical method for partitioning the variance into its components. Fisher, Immer, and Tedin (1932) elaborated on this method and presented several formulas for the partitioning of the genetic variance. They stated that the mass effects of segregation of a large number of genes will closely simulate those of a cumulative system. In such a system, some quantities such as the mean and the variance possess the remarkable property that each is simply confounded with the contributions derived from several genes acting singly. So the observable variance may be regarded as the sum of variances due to the individual genes. They further stated that without recognizing any single gene the total contribution of each gene can be estimated. Leaf length of lettuce and the height of maize and barley plants were used to illustrate the application of the method.

Wright (1921, 1923) independently approached this problem by a rather different method which he called path coefficients. He explained the path coefficient as the ratio of standard deviation of one cause, when all other causes were kept constant, to the total standard deviation. This method gives a means of calculating the degree to which a given effect is determined in a complex system of correlated variables. He developed formulas which may be used in different mating systems and different kinds of genic relationship. Li (1955) presented illustrations of the applications of this theory on the relationship between parents and offspring. Wright's methods have been extended and applied by many research workers in animal and plant fields.

In animal breeding, Dickerson and Hazel (1944) studied the effectiveness of selection based on progeny tests which supplemented the earlier tests. Their criterion of the effectiveness of selection was the average genetic improvement expected yearly from selection alone as compared to that expected by the use of progeny tests. One of the two factors that determines annual improvement from selection is the average genetic superiority of those individuals selected to be parents over the group from which they were chosen. A formula to estimate the average genetic superiority was given with some examples on its applications.

Lush (1945) also presented formulas to estimate from selected parents the population mean. As an illustration, he gave an example of the increase in weight of fleece.

Using the method suggested by Dickerson and Hazel (1944) and Lush (1945), Lerner and Hazel (1947) predicted the egg production in a flock which had been recorded from 1933 to 1944. The predicted gains and the actual gains were remarkably close, namely 5.28 against 5.6 eggs per year respectively. Here the knowledge of selection intensity, heritability, and inter-generation span enabled the breeders to predict the improvement per year expected from selection.

Lerner (1950) developed further formulas and illustrated them with the inheritance of egg production in flocks studied at the University of California. He also listed formulas which may be used under different genetic conditions and different systems of mating. Under mass selection the genetic gains are the product of heritability and the selection differential expressed in actual units (Lerner, 1958).

While many reports have been made on the effectiveness of selection in animal breeding, relatively few have been reported in the plant fields. Hutchinson (1940), among others, studied the relative magnitude of genetic and environmental variances of several characters in Asiatic cotton. Panse (1940) used regression of the F_3 progenies on the F_2 parents of three strains of Indian cotton to estimate the genetic portion of the variance in the F_2.

Robinson, Comstock and Harvey (1949) applied the same method in studying the variability of corn.

Powers (1942, 1951, 1955, 1957) and Powers, Locke, and Garret(1950) developed methods and formulas in addition to the ones already presented. Since Powers' method is used in this study, it will be presented in more detail.

The identification of genetically superior individuals and the prediction of the genetic gains involve the analysis of the frequency distributions. One of the first steps in analyzing the frequency distributions is to partition the total variance into its components in order to estimate the genetic variance.

This is also important in determining which populations have genetic variability because only those populations which possess genetic variability are expected to contain genetically superior individuals. Powers used the total variance of an inbred line to estimate the environmental variance. The variance of an F_1 hybrid between two inbred lines was used to test the reliability of this estimate. The genetic variances of the other populations were estimated by subtracting the estimated environmental variance from their respective total variances (Powers, 1957).

In identifying genetically superior individuals, Powers (1957) assumes that the proportion of the individuals in each class can be estimated and the deviations from the estimates will not be greater than that expected by chance. The fitness of the obtained frequency distributions can be tested by the Chi-square method (Leonard, Mann, and Powers, 1957; Powers, Robertson, and Clark, 1958; Steel and Torrie, 1960). A detailed illustration of the method has been presented by Leonard, Mann, and Powers,(1957).

Limits are set for every population in such a way that only genetically superior individuals will be found beyond those limits. Hence, individuals falling beyond that limit are identified as the genetically superior individuals.

The genetic gains is predicted by subtracting the population mean from the estimated mean of the superior individuals.

By considering two characters simultaneously, it might be possible to identify individuals superior for both characters in question. However, individuals superior for two characters would probably not be found in small population. Furthermore, a negative correlation between the two characters under consideration might lessen the probability of finding an individual genetically superior for two characters simultaneously.

MATERIALS AND METHODS

Strains

Five strains of cotton were included in this study, namely Z-106, M-8948, an F_1 hybrid of these two strains, the commercial variety Parrott, and an F_2 hybrid of Lankart 57 x OK-86. Strain OK-86 is an extremely early, very short-stapled introduction from Yugoslavia. Strains Z-106 and M-8948 are double-haploid lines derived from a Stoneville type strain and from Deltapine 14 respectively.

The variety Parrott was released by the Oklahoma Agricultural Experiment Station in 1955. It is a short-stapled variety which yields well. Originally Parrott was selected from a field of Mebane 140, a variety selected and developed at the Texas Experimental Station at Chilicoth (Green and Oswalt, 1956).

Experimental Procedure

The plants were started in peat cups and kept in the greenhouse for 12 days. During the first week of June, 1962, the seedlings were transplanted into the nursery field near Perkins.

The design of the experiment was a Randomized Complete Block with 10 replicates. Each entry was transplanted into a one-row plot of 10 hills (cups), each hill containing 2 plants.

Irrigations were applied as needed, and the plants were sprayed several times for insect control. The plants were cultivated in the usual practice.

Shortly before the time of harvesting, there were 783 plants remaining in the experiment. In some rows less than 10 hills survived and in some hills only one plant. At the end of October, 1962, each plant with 5 or more bolls was harvested separately. After discarding those plants with less than 5 opened bolls at the time of harvest, 744 plants remained in the populations for study.

The cotton was ginned on a saw gin and samples of lint were taken to the laboratory for fiber analysis.

The staple length was measured with a digital fibrograph and the fineness of the lint was measured with a micronaire. Two measurements of each character for each plant (sample) were taken, and the averages of the two measurements were used in the statistical analysis.

Statistical Procedure.

Frequency distributions of each character from all entries were made. The classes of lint length were set at 0.031 inch intervals, which corresponds to 1/32 of an inch, and the classes of the micronaire reading differed by 0.25 microgram per inch. To facilitate the statistical analysis, the frequency distributions of lint length were expressed in 0.1 of an inch intervals.

The expected number of plants in each class was calculated according to the method used by Leonard, Mann, and Powers, (1957). First, Pearson's "x" value for each class was calculation. This is equal to the population mean minus the upper limit of the class expressed in the standard deviation of the populatinn. This "x" value corresponds to $\frac{1}{2}(1 \neq a)$ in Pearson's table of probability integral. If this value is positive, it must be subtracted from 1 and the difference multiplied by 100 to give the percentage of the population falling in that class. If the value of "x" is negative it is directly multiplied by 100 to get the theoretical percentage expected in that class. Since the percentage obtained is the cumulative one, the actual percentage of each class must be subtracted by the percentage of the previous class. The actual theoretical number of plants expected in each class can be obtained by multiplying the percentage by the total number of individuals in the population.

The test for fitness for the observed and expected number in each class was applied using the Chi-square method (Leonard, Mann, and Powers, 1957; Powers, Robertson, and Remmenga, 1958).

The means and the total variances of all populations studied were calculated on the basis of individual plant data. The standard error of the total variance was calculated according to the method and formula used by Fisher (1934).

The variances of the two inbred lines and the F_1 hybrid were tested for differences by using the Chi-square method. (Steel and Torrie, 1960). Since there were no significant differences between them, the pooled variance was used as the estimate of environomental variance.

The genetic variances of the Parrott and F_2 populations were estimated by subtracting the estimated environmental variance from their respective total variances. The standard error of the genetic variance was calculated by the conventional formula of the standard error of the difference. Comparison of the genetic variance with its standard error was made to detect any differences from zero.

To identify genetically superior individuals, a limit was set for each population beyond which only superior individuals could be found, using the method and formula given by Powers (1951, 1957) as follows:

$$z = \bar{x} + s_d x'$$

where: z = upper limit of class

$\bar{x}$ = population mean

s_d = standard error of environmental variance

x' = x value from Pearson's table for $\frac{1}{2}(1+a) = q$

$q = 1 - p$

p = a chosen value determined by the experimenter and depends on the number of individuals in the population and the intensity of selection.

By setting this limit in the frequency distributions, it should be possible to identify the superior individuals for each population.

The genetic gains, which is actually the selection differential expressed in actual units, were predicted by subtracting the population mean from the estimated mean of the superior individuals. The means of these sub-groups were calculated according to the method and formula given by Powers (1951, 1957) as follows:

$$y = z - s_d x'$$

where; y = the estimate of the mean of the sub-group

z = the upper class limit

s_d = the standard error of the environmental variance

x' = x value from Pearson's table for $\frac{1}{2}(1 + a) = q$

$q = 1 - p$

p = the proportion of genetically-superior individuals expressed in a decimal fraction.

In considering individuals which are superior in both characters, frequency distributions combined for both characters were made. From these combined frequency distributions, it can be determined whether there are any individuals which fulfill the requirements. The probability of finding these superior individuals is the product of the expected percentage of superior individuals in each character, if they are independent of each other.

Correlations between lint length and lint fineness for all populations were calculated. Their homogeneity was tested by using the Chi-square method (Steel and Torrie, 1960). The information obtained from the relationship of these two characters was useful in explaining the probability of detecting the superior individuals for both characters.

RESULTS AND DISCUSSION

Lint Length

The observed and the expected frequency distributions for all populations are presented in Table I. The Chi-square value obtained is smaller than needed to have a significant difference. In other words the observed frequency distributions for all populations followed the normal frequency curve.

This fitness indicates that the effects of the genes governing the length of the lint followed those of typical quantitative character. It is also an indication that any one of the two inbred lines can be used as an estimate of environmental variability

The test of homogeneity indicated no significant differences between the variances of Z-106, F_1 and M-8948 populations, (Appendix 1). Hence the pooled variance was used as an estimate of the environmental variance.

The means, total variances, and genetic variances of the populations studied are presented in Table II. The genetic variances of the F_2 and Parrott populations were estimated by subtracting the pooled variances from their respective total variances. Comparison of the genetic variances with the standard errors revealed that they were different from zero.

A class limit was calculated for the F_2 and Parrott populations using the p value of 0.004. For the F_2 population, the limit value was calculated as follows:

$$z = \bar{\bar{x}} + s_d\, x'$$

TABLE I

THE OBSERVED AND EXPECTED FREQUENCY DISTRIBUTIONS FOR LINT LENGTH (IN 0.1 INCH)

Population	Mean	Total	UPPER LIMIT OF CLASS															Chi-square
			7.67	7.98	8.29	8.60	8.91	9.22	9.53	9.84	10.15	10.46	10.77	11.08	11.39	11.70	12.01	
F_2																		
obs.	9.365	169		1	3	8	18	35	41	35	17	7	1	2	1			
exp.				1	3	9	20	33	37	33	20	9	3	1	0			4.21 n.s.
Parrott																		
obs.	9.259	156	1	0	6	7	18	44	37	26	9	4	3	1				
exp.			0	1	4	12	23	34	35	26	14	6	1	0				12.67 n.s.
Z-106																		
obs.	10.579	150					1	1	0	3	12	33	52	35	11	2	0	
exp.							0	0	1	5	17	34	38	36	14	4	1	11.13 n.s.
F_1																		
obs.	10.724	121					1	0	0	2	5	17	44	34	13	4	1	
exp.							0	0	1	2	8	22	35	31	17	4	1	6.79 n.s.
M-8948																		
obs.	10.544	148							0	3	17	46	47	24	8	2	1	
exp.									1	3	17	40	47	29	9	2	0	2.87 n.s.

TABLE II

THE MEANS, TOTAL VARIANCES AND GENETIC VARIANCES OF LINT LENGTH (IN 0.1 INCH)

Population	Means	Total variance	Genetic variance
F_2	9.365	0.2950 ± 0.0322	0.1292 ± 0.0360
Parrott	9.259	0.2806 ± 0.0319	0.1148 ± 0.0357
Z-106	10.579	0.1875 ± 0.0217	
F_1	10.724	0.1726 ± 0.0223	
M-8948	10.544	0.1381 ± 0.0161	
Pooled		0.1658 ± 0.0115	

where: z = upper limit

$\bar{x} = 9.365$

$s_d = 0.407$ (the square root of the pooled variance)

$p = 0.004$

$q = 0.996$

$x' = 2.66$

$$z = 9.365 + 0.407 \times 2.66$$

$$z = 10.445 \text{ (in 0.1 inch)}$$

Since this z value did not coincide with the upper limit of a class, the upper limit of the class into which the z value fell was taken as the upper limit. In this case, it fell into the class with the upper limit of 10.46.

Similar calculations were made for the Parrott population using its mean 9.259 while holding the other constants the same as those used in calculating the limits of the F_2 population. The calculated z value for Parrott was 10.341, which also fell in the class with the upper limit of 10.46. The falling of the limits of both populations in the same class value is not surprising because both have nearly the same population mean.

To facilitate further calculations, the frequency distributions of the F_2 and Parrott populations, expressed in percentage of individuals, are presented in Table III. From this table, the percentages of genetically superior individuals are easily detected, namely the sum of the percentages of the populations in classes beyond the 10.46 class limit. The percentage of superior individuals for lint length in the F_2 population was $0.6 + 1.2 + 0.6 = 2.4\%$ and in Parrott population $1.9 + 0.6 = 2.5\%$.

TABLE III

THE FREQUENCY DISTRIBUTIONS FOR LINT LENGTH OF F_2 AND PARROTT EXPRESSED IN PERCENTAGE OF PLANTS (IN 0.1 INCH)*

Population	Mean	S	UPPER LIMIT OF CLASS													
			7.67	7.98	8.29	8.60	8.91	9.22	9.53	9.84	10.15	10.46	10.77	11.08	11.39	11.70
F_2	9.365	0.5433		0.6	1.8	4.8	10.6	20.7	24.2	20.7	10.1	4.1	0.6	1.2	0.6	
Parrott	9.259	0.5297	0.6	0.0	3.8	4.5	11.5	28.2	23.7	16.7	5.8	2.6	1.9	0.6		

*) rounded figures

The odds are great that these individuals are genetically superior to the average population. Stated in another way, these individuals have greater value than those caused by chance fluctuation due to environmental influence.

The mean of this sub-group individuals was predicted using the formula:

$$y = z - s_d x'$$

For the F_2 population:

$z = 10.46$

$s_d = 0.407$

$p = 0.024$

$q = 0.976$

$x' = 1.98$

$$y = 10.46 - 0.407 \times 1.98$$

$$y = 9.654 \text{ (in 0.1 inch) or } 0.9654 \text{ inch}$$

Similar procedures were used to calculate the sub-group mean of the Parrott population. Since Parrott has the same z value as the F_2, the only difference is the value of p, which is equal to 0.025. The y value for Parrott is 9.663 (in 0.1 inch) or 0.9663 inch.

The predicted gains are 0.029 inch for the F_2 population and 0.040 inch for the Parrott population.

The upper limit of class, the percentage of superior individuals, the value of x', the population mean,the estimated mean of the sub-group and the predicted gains are listed in Table IV.

Lint Fineness

Similar procedures were applied as in analyzing the frequency distributions of lint length. The observed and expected frequency

TABLE IV

THE UPPER LIMIT OF CLASS, PERCENTAGE OF SUPERIOR INDIVIDUALS, VALUE OF X', POPULATION MEAN, ESTIMATED MEAN OF THE SUB-GROUP, AND PREDICTED GAINS, FOR LINT LENGTH OF THE F_2 AND PARROTT POPULATIONS (IN 0.1 INCH)

Population	Upper limit of class	% of superior individuals	Value of x'	Population Mean	Sub-Group Mean	Predicted Gains
F_2	10.46	2.4	1.98	9.365	9.654	0.289
Parrott	10.46	2.5	1.96	9.259	9.663	0.404

distributions of lint fineness for all populations are listed in Table V.

Based on the Chi-square value, the frequency distributions of both the F_2 and Parrott populations failed to fit the normal frequency distributions. Most probably this failure was caused by the failure of the genetic variability of this trait to follow a normal distribution due to genetic segregation. However, a rather odd phenomenon also occurred where the frequency distribution of Z-106 did not fit the normal frequency distribution, although the deviation was not highly significant. Since Z-106 is an inbred line, presumably it was an odd sample or there was some degree of inaccuracy in measuring the trait.

In identifying genetically superior individuals, it was assumed that we were dealing with a normally distributed population, therefore the same procedures were employed.

The means, total variances and the genetic variances for lint fineness are listed in Table VI. The test of homogeneity of the variances of Z-106, F_1, and M-8948 populations showed that there were no significant differences between them (Appendix 2). Based on the assumption that Z-106 followed the normal frequency distribution and the fact that there were no significant differences in the variances of the Z-106, F_1, and M-8948 populations, the pooled variance of these three variances was used as the estimate of environmental variance.

The genetic variances of the F_2 and Parrott populations were listed in Table VI. Comparisons with their respective standard errors showed that they were different from zero.

TABLE V

THE OBSERVED AND EXPECTED FREQUENCY DISTRIBUTIONS FOR LINT FINENESS (IN MCGRM/INCH)

Population	Mean	Total	UPPER LIMIT OF CLASS														Chi-square
			3.62	3.87	4.12	4.37	4.62	4.87	5.12	5.37	5.62	5.87	6.12	6.37	6.62	6.87	
F_2 obs	5.157	169	1	4	2	6	18	13	36	24	34	16	14	1	0		
exp			0	1	3	8	15	23	29	30	26	17	10	5	2		25.98**
Parrott obs	5.519	156			1	3	4	6	14	16	45	20	42	5	0	0	
exp					0	1	3	8	17	27	35	30	20	10	4	1	47.72**
Z-106 obs	4.736	150			0	10	53	42	35	6	2	1	1				
exp					2	13	36	50	35	12	2	0	0				15.00*
F_1 obs	4.979	121			2	1	16	22	42	24	12	2					
exp					1	3	12	28	37	27	11	2					6.05
M-8948 obs	4.990	148			1	0	13	31	59	31	12	0	1				
exp					0	2	11	35	52	35	11	2	0				6.29

* significant at 0.05

** significant at 0.01

TABLE VI

THE MEANS, TOTAL VARIANCES AND THE GENETIC VARIANCES OF LINT FINENESS (IN MCGRM/INCH)

Population	Means	Total variance	Genetic variance
F_2	5.157	0.3013 ± 0.0329	0.2126 ± 0.0340
Parrott	5.519	0.2054 ± 0.0233	0.1203 ± 0.0249
Z-106	4.736	0.0831 ± 0.0093	
F_1	4.979	0.0992 ± 0.0128	
M-8948	4.990	0.0755 ± 0.0088	
Pooled		0.0851 ± 0.059	

Limits of the upper class were calculated by the same procedure used to calculate the upper limit of class of lint length. In order to be able to combine the analysis of the two characters simultaneously, the same $p = 0.004$ was used in the calculations. For the F_2 population with its mean of 5.157, the standard error of the environmental variance of $s_d = 0.292$ (see footnote of Table VI), and the calculated z value of 5.933 coincide with the upper limit of the 6.12 class. Parrott has a calculated z value of 6.295, which falls in the class with upper limit of 6.37.

By setting these limits to the frequency distributions presented in Table VII, only 0.6% of the F_2 population was classified as being genetically superior individuals. No individual in the Parrott population was classified as superior. By looking at the observed and expected frequency distributions for the Parrott population, it can be seen that the observed frequency distribution for Parrott missed two extreme classes. Therefore, it is reasonable that no superior individuals would occur in the Parrott population.

The z value, the percentage of superior individuals, the value of x', the population mean, the estimated mean of the sub-group, and the predicted gains are listed in Table VIII.

By analyzing the data available and some assumptions on this method, the predicted gains for the F_2 population is 0.23 microgram per inch.

Lint Length and Lint Fineness.

So far the analysis in the data have dealt only with each character separately. However, since both characters are important in any breeding

TABLE VII

THE FREQUENCY DISTRIBUTIONS FOR LINT FINENESS OF F_2 AND PARROTT EXPRESSED IN PERCENTAGE OF PLANTS* (IN MICROGRAM PER INCH)

Population	Mean	S	UPPER LIMIT OF CLASS											
			3.62	3.87	4.12	4.37	4.62	4.87	5.12	5.37	5.62	5.87	6.12	6.37
F_2	5.157	0.5489	.6	2.4	1.2	3.5	10.6	7.7	21.3	14.2	20.1	9.5	8.3	0.6
Parrott	5.519	0.4532			0.6	1.9	2.6	3.8	9.0	10.3	28.8	12.8	26.9	3.2

*) rounded figures

TABLE VIII

THE UPPER LIMIT OF CLASS, PERCENTAGE OF SUPERIOR INDIVIDUALS, VALUE OF X', POPULATION MEAN, ESTIMATED MEAN OF THE SUB-GROUP, AND PREDICTED GAINS, FOR LINT FINENESS OF THE F_2 AND PARROTT POPULATIONS (IN MICROGRAM/INCH)

Population	Upper Limit of Class	% of Superior Individuals	Value of x'	Population Mean	Sub-Group Mean	Predicted Gains
F_2	6.12	0.6	2.52	5.157	5.384	0.227
Parrott	6.37	---	----	5.519	---	---

program, it is worth while to consider them simultaneously, or at least one character should be maintained while the other is being improved.

In analyzing two characters simultaneously, frequency distributions for both characters were made. Since there were no identified genetically superior individuals for lint fineness in the Parrott population, only the F_2 population was analyzed. The frequency distributions of the F_2 population for lint length and lint fineness are listed in Table IX.

From the previous information, the limit for lint length is 10.46 and for lint fineness is 6.12 in 0.1 of an inch and microgram per inch, respectively. The percentage of identified superior individuals for lint length is 2.4% and for lint fineness is 0.6%. Hence the proportion of the population which could be expected to be superior for both characters simultaneously is the product of the two separate probabilities, if both characters are considered to be independent. In this case, the probability of detecting superior individuals for both characters is $0.024 \times 0.006 = 0.00014$. On the basis of independent characters, we would expect to find about one plant genetically superior for both characters in 10,000 plants. Hence from 169 plants none would be expected to be found. None were found (see Table IX).

There were highly significant negative correlations between lint length and lint fineness in all populations studied. The test of homogeneity showed that there were no significant differences between these correlation coefficients. (Appendix 3). Whether

TABLE IX

THE COMBINED FREQUENCY DISTRIBUTIONS FOR LINT LENGTH AND LINT FINENESS OF THE F_2 POPULATION EXPRESSED IN PERCENTAGE OF PLANTS* (IN 0.1 INCH AND MCGRM/INCH)

Lint Length (in 0.1 inch) UPPER LIMIT OF CLASS / PERCENTAGE OF PLANT	Lint Fineness (in mcgrm/inch) UPPER LIMIT OF CLASS / PERCENTAGE OF PLANTS													
	3.62	3.87	4.12	4.37	4.62	4.87	5.12	5.37	5.62	5.87	6.12	6.37	Total	
7.67														
7.98											0.6		0.6	
8.29										1.2	0.6		1.8	
8.60							1.8		1.2	0.6	1.2		4.8	
8.91				1.1		1.7	1.2	1.8	3.0		1.2	0.6	10.6	
9.22				0.6	1.2	1.2	4.1	4.7	4.7	2.4	1.8		20.7	
9.53	0.6		0.6	0.6	1.8	1.2	5.9	3.5	5.9	2.9	1.2		24.2	1)
9.84		0.6	0.6	1.2	1.2	1.2	5.3	3.6	3.5	1.8	1.7		20.7	
10.15		0.6			3.5	0.6	2.4	0.6	1.8	0.6			10.1	
10.46		0.6			1.7	1.2	0.6						4.1	2)
10.77						0.6							0.6	
11.08		0.6			0.6								1.2	
11.39					0.6								0.6	
Total	0.6	2.4	1.2	3.5	10.6	7.7	21.3	14.2	20.1	9.5	8.3	0.6	100.0	
									1)			2)		

*) rounded figures

1) region for individuals which exceed the upper limit of the class into which the mean of the population falls, for both characters. (see text)

2) region for genetically superior individuals for both characters (see text)

this relationship affects the probability of detecting superior individuals for both characters can be tested by the following method,

Suppose as the z values the means of the population were taken and the portion of the population above the upper limits of class into which the means fall considered. For the F_2 population, the mean of the lint length is 9.365, which falls in the 9.53 upper class limit; and for lint fineness, the mean is 5.157, which corresponds to the upper class limit of 5.37. The percentage of individuals which exceed the limit for lint length is 37.3% and that for lint fineness is 38.5%. Hence, the expected proportion of the population that could be found beyond these two limits (delimited by solid lines in Table IX) is the product of 0.373 x 0.385 = 0.133 or 13.3%. The sum of the percentages of individuals falling within those limits is 9.4%. Among 169 individuals the expected number is 22 plants and the observed number is 16 plants. A Chi-square test of these proportions (22 : 147 and 16 : 153) indicated that they were from the same population. Stated in another way there was no significant difference between the expected and the observed proportions. It can be concluded that the correlation between these two traits does not affect the independence of the two characters; presumably the genes governing these two characters are independent, which is in accordance with the statement made by Hancock (1944). However, since this study comprised only a very small fraction of the population of the F_2 strain, this conclusion should not be regarded as a decisive one. Additional studies on the inheritance of these traits, the study of the physiological genetics on the formation and development of the fiber, and some other related knowledge should be considered before a decisive conclusion is reached.

Discussion.

Method and formulas by Powers (1957) were employed in identifying genetically-superior individuals for lint length and lint fineness in an F_2 and Parrott populations. This method involves the partition of the total variance into its genetic and environmental variances and the analysis of the frequency distributions of the populations for these traits.

The partitioning of the total variance into its components can be considered as the first and the important step in applying this method, since it is a means of detecting the presence of genetic variance in the population under study. The importante of partitioning the variance lies in the sense that only from a population which has genetic variability could genetically-superior individuals be expected to be found. However, the presence of the genetic variance in a certain population is not an assurance that genetically superior individuals can be found at any probability level. This detection is also dependent on the pattern of the frequency distributions of the character being studied, as it occured in Parrott population for lint fineness.

The data presented here indicate the presence of genetic variances for lint length and lint fineness in both populations. Using the value of $p = 0.004$, 2.4% or 4 plants and 2.5% or 4 plants were identified as being genetically superior for lint length in the F_2 and Parrott populations, respectively. There was 0.6% or 1 plant identified as being superior for lint fineness in the F_2 population. Despite the genetic variability of Parrott, no individuals were found that would be considered genetically superior. The lack of these genetically-superior individuals can be explained because the frequency distributions for lint fineness in Parrott does not follow the normal frequency distributions and more important because the frequency distributions for lint fineness of Parrott missed the two extreme classes, in comparison to the normal frequency distributions.

Identification of genetically-superior individuals in a certain population is not only useful in detecting the superior individuals, but it is also useful in determining which classes provide the superior individuals. As a result, the breeder can better understand from which range of the frequency distributions he should make selections. In the data presented, the upper limit of class for both populations was 1.046 inch for lint length and 6.12 microgram per inch for lint fineness for the F_2 population. These values show the characteristic of the populations, and individuals found beyond those limits are considered genetically-superior to their respective populations, unless the samples used in this study are unusual.

The genetic gains predicted for lint length were 0.029 inch and 0.040 inch for the F_2 and Parrott populations, respectively. The gains expected for lint fineness in the F_2 population was 0.23 microgram per inch. The reliability of these predictions is still subject to additional testing, since final evaluation must be based on performance in the field in subsequent generations.

Despite the uncertainity of this prediction, it is still useful in evaluating the value of the breeding stocks. From the values of the predicted gains for lint length, it can be seen clearly that Parrott has more possibilities for genetic gain from selection than does the F_2 population, which means that potentially Parrott is more promising than the F_2 as breeding material for lint length. However, if gains for coarser fiber are desired, the F_2 is more valuable as a breeding stock than Parrott.

By analyzing the combined frequency distributions for lint length and lint fineness, an attempt was made to detect genetically-superior individuals for both characters. On the basis of independence of the two characters, the probability of detecting superior individuals for both characters was 0.00014, or about 1 plant in 10,000 plants. As expected, no individuals were superior for both characters from the small sample studied. From this analysis it was also found that the negative correlation between lint length and lint fineness does not affect the probability of detecting superior individuals for both characters. Stated in other way, lint length and lint fineness are inherited independently. This is in accordance with the statement made by Hancock (1944), although with different basis of understanding. Additional studies on the inheritance of these traits, and studies on physiological genetics of the formation and development of the fiber should be conducted before a decisive conclusion is reached.

In conclusion, although there is some uncertainty on the reliability of the predicted gains, this method provides a useful tool in evaluating and selecting the breeding stocks of breeding programs.

SUMMARY AND CONCLUSION

A study of identification of genetically-superior individuals for lint length and lint fineness in an F_2 and Parrott populations was made, using the methods proposed by Powers.

The study involved the analysis of the frequency distributions and the partition of the variance into its genetic and environmental variance.

The data presented showed the presence of genetic variability in both populations. Using the probability $p = 0.004$, there were 2.4% or 4 plants and 2.5% or 4 plants in F_2 and Parrott populations respectively identified to be genetically superior to their respective populations. There was 0.6% or 1 plant from the F_2 population identified to be superior for lint fineness and none from Parrott population.

The predicted gains for lint length was 0.029 inch and 0.040 inch for F_2 and Parrott, respectively. The predicted gains for fineness for F_2 was 0.23 microgram per inch.

By considering both characters simultaneously, no genetically superior individuals were expected to be found and none were found. The probability of detecting them is 0.00014, or about 1 plant from 10,000 plants while the sample used was 169 plants.

There was a highly significant negative correlation for lint length and lint fineness, however presumably the genes affecting them are independent. More related knowledge should be considered before coming to a decisive conclusion.

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Appendix 1. Test of homogeneity of the variances for lint length of Z-106, F_1, and M-8948 (in 0.1 inch)

Population	df	x^2	s^2	log s^2	(n-1) log s^2
Z-106	149	27.1498	0.1875	-0.7270	-108.3230
F_1	120	20.7149	0.1726	-0.7630	- 91.5600
M-8948	147	20.3184	0.1381	-0.8598	-126.3906
Total	416	69.9751			-326.2736
Pooled			0.1658	-0.7804	-324.6464

$$\text{Chi-square} = 2.3026 \left\{ \left[\Sigma (n_i - 1) \log \bar{s}^2 \right] - \Sigma (n_i - 1) \log s^2 \right\}$$

$$= 2.3026 \quad \left[-324.6464 - (-326.2736) \right]$$

$$= 2.3026 \quad (1.6272)$$

$$= 3.7468 \quad \text{non-significant}$$

Chi-square 0.05 df 2 : 5.99

0.01 df 2 : 9.21

Appendix 2. Test of homogeneity of the variances for lint fineness of Z-106, F_1, and M-8948 (in mcgrm/inch)

Population	df	x^2	s^2	log s^2	(n-1) log s^2
Z-106	149	12.3883	0.08314	-1.0802	-160.9498
F_1	120	11.8983	0.09915	-1.0037	-120.4440
M-8948	147	11.0948	0.07548	-1.1222	-164.9634
Total	416	35.3814			-446.3572
Pooled			0.08505	-1.0703	-445.2448

$$\text{Chi-square} = 2.3026 \left\{\left[\textstyle\sum (n_i-1) \log \bar{s}^2\right] - \textstyle\sum (n_i-1) \log s^2\right\}$$

$$= 2.3026 \left[-445.2448 - (-446.3572)\right]$$

$$= 2.3026 \quad (1.1124)$$

$$= 2.5614$$

Chi-square 0.05 df 2 : 5.99

0.01 df 2 : 9.21

Appendix 3. Test of homogeneity of the correlation coefficients for lint length and lint fineness

Population	ni	(n_i-3)	r_i	x_i	$(n_i-3)\,Z_i$	$Z_i-\bar{Z}_w$	$(Z_i-\bar{Z}_w)^2$	$(n_i-3)(Z_i-\bar{Z}_w)^2$
F_2	169	166	-0.3997	-0.4224	-70.1184	-0.0373	0.0014	0.2324
Parrott	156	153	-0.3055	-0.3150	-48.4950	+0.0701	0.0049	0.7497
Z-106	150	147	-0.3002	-0.3116	-45.8052	+0.0735	0.0054	0.7938
F_1	121	118	-0.4828	-0.4824	-61.7022	-0.0977	0.0095	1.1110
M-8948	148	145	-0.3591	-0.3769	-54.6505	+0.0260	0.0007	0.1015
Total	744	729			-280.7713			

X^2 : 2.9884

$$\bar{Z}_w = \frac{\sum (n_i-3)\,Z_i}{\sum (n_i-3)} = \frac{-280.7713}{729} = -0.3851$$

The pooled $r = -0.367$

X^2 .05 df 4 : 9.49

X^2 .01 df 4 : 13.3

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