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A GENETIC ANALYSIS OF YIELD IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.)

by

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A Dissertation Submitted to the
Graduate Faculty in Partial Fulfillment of
The Requirements for the Degree of
DOCTOR OF PHILOSOPHY

Major Subject: Genetics

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INTRODUCTION

The plant breeder, as applied geneticist, faces one of his most important as well as most difficult tasks in efficiently selecting for the complex trait, yield. In most crop plants the development of varieties with superior yielding abilities is generally the principal objective, though characteristics other than yield, such as quality and adaptiveness, also are important. The difficulty of the problem lies in the generality of the trait and its consequent complexity; such a generalized trait reacts with its environment in a complex way rendering the correspondence between phenotype and genotype rather tenuous. This is another way of saying that in most situations, heritability for yield is relatively low.

Consequently, it is desirable to develop a means of more accurately assessing the genotype for the complex trait, yield, than is possible by simply measuring the phenotypic expression of the trait. Manning (6) has shown that in Upland cotton, Gossypium hirsutum (the subject of this investigation), selection for yielding ability of individual F_2 plants was of little value in his material, as judged by the relationship in yielding ability between

F_2 plants and subsequently derived lines. This points up the problem and the utility of a solution, since an effective means of selecting for individual plants would be of greater value than yield testing of derived lines at some later stage of development.

Richmond (9) points out that the breeder should seek to maintain the ratio of genetic variability to environmental variability as large as possible in order that selection can be effective. This can be done either by purposely increasing the genetic variability through outcrossing or by reducing the environmental variability through a refinement in techniques, that is by the

> ...development of more precision in the breeding program through refinements in method and design to provide more discriminatory statistical tests and the establishment of indices which will measure the genetically potential performance rather than the actual end-result behavior;....

(9, p. 219) Since the level of performance for yield of most Upland cotton varieties is very high (9), outcrossing to induce genetic variability alone is not the entire answer.

One approach to this problem is to select a group of other, simpler traits which can be considered as related to the general trait, yield. These traits can be utilized to develop a selection index. The index is developed in such

a way that the heritability of the index will be higher than that for yield and will be correlated with yield, thus providing a more efficient selection criterion. The theoretical basis of the selection index has been considered by Hazel (2) and will be described only briefly here in terms of the present problem.

The assumption is made that the material studied fits an additive genetic model for yield and that therefore the genotype for yield is a linear function of the genotypes of the subordinate traits considered. Since these genotypes cannot be measured directly, a correlated variable (the index) based on the phenotypes for these several traits is used. This index is evaluated as a linear function of the phenotypic measurements, though other alternatives are discussed. The coefficients of these measurements used to obtain the index are multiple regression coefficients chosen so as to maximize the correlation between the index and the genotype for yield. In this way the index provides a closer assessment of the genotype than does the yield phenotype, which, as Manning (6) has shown, is ineffective. The exact methodological procedure will be described later.

The approach used in this study was to subdivide yield into component sub-traits (see page 8) and to

develop a series of selection indexes from these sub-traits at several levels of subdivision. If the assumption of an additive genetic model is valid, one expects that progressive subdivision will result in progressively simpler genetic control of the sub-traits and that heritabilities will increase with progressive subdivision. Thus the assumption is subject to test. With such progressively simpler control one might further expect that the derived indexes will be most efficient when they include sub-traits derived from the most extensive subdivision.

MATERIALS AND METHODS

This study comprises an analysis of data obtained from four hundred spaced cotton plants which were planted in the following way. Each replication (there being five replications) consisted of eighty plants planted in two rows of forty each. (The rows were spaced forty inches apart and the plants within the row were forty-one inches apart.) Each replication was divided into eight blocks of ten plants each (two rows by five plants) and a plot consisted of a single plant. The eight blocks were allocated as follows: one block each of two parental varieties (designated P_1 and P_2) and six blocks of F_2 plants. The parental blocks were located at random. There were thus fifty plants of each parental variety and three hundred F_2 plants.

The analyses of variance and covariance thus had the following structure (for the purposes intended in this study.)

Source of variation	d.f.	E(M.S.)
Replications	4	
Blocks within replications	35	
Within blocks	360	
Within P_1 blocks	45	σ_E^2
Within P_2 blocks	45	σ_E^2
Within F_2 blocks	270	$\sigma_E^2 + \sigma_G^2$
Total	399	

The specified components (σ_G^2 = genetic variance and σ_E^2 = environmental or non-genetic variance) would be estimated from the within block mean squares and are the items of principal interest.

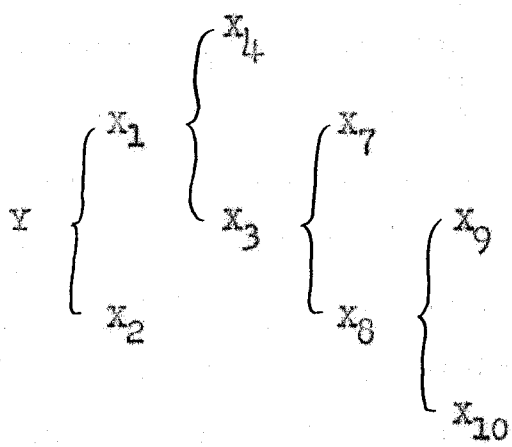
The parental varieties used were chosen on somewhat unrelated grounds, but were well adapted to this study. The P_1 parent was a strain having the designation 19-14-6-3 (see Figure 1, page 43 for pedigree). It was a strain of the Acala type, though a gene B_7 for resistance to the bacterial blight disease had been incorporated into its genotype from the variety Stoneville 20 through a back-crossing scheme. The P_2 parent was a selection from the variety Hartsville having the designation W-1-CF-9-1. These parents can be considered as representative of what are now considered to be the two distinct groups of the American Upland biotype of Gossypium hirsutum (5) and as such can be considered as relatively representative of the germ plasm generally available to and used by cotton breeders in this country. These two types are generally recognized as the Acala cottons which are grown in the irrigated areas of the southwestern United States and the "southeastern" cottons which are grown in the remainder of the cotton belt. These two groups differ not only in adaption to their own areas but in other traits as well,

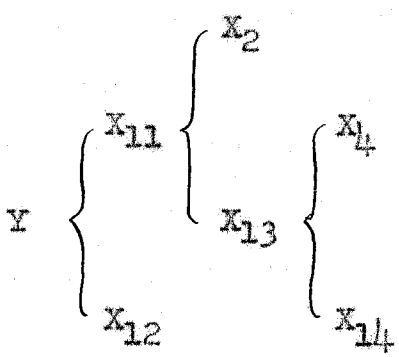
including fiber properties.

The plants were started in the greenhouse and transplanted to the field individually on May 26 and 27, 1953. The seedlings were then in about the first leaf stage. The field to which they were transplanted was a portion of the New Mexico Agricultural Experiment Station agronomy farm and was a field of good fertility which was essentially disease free (which principally means that Verticillium albo-atrum was not prevalent in the soil.) Through the remainder of the growing season they received the usual practices of irrigation and cultivation. The plants were harvested individually and completely after frost and data were taken at this time on the number of bolls harvested and also on the mean locule number per boll, as measured on a sample of the first ten bolls harvested. Selfed seed was obtained on most plants and harvested separately.

The samples of seed cotton were then allowed to come to equilibrium in a humidity controlled laboratory and subsequently weighed. A representative portion of each sample was ginned on a small laboratory gin to separate the seed and lint and to permit a determination of the percent lint (by weight). Seed weight was measured at this time. All weights were measured in grams.

From this information it was possible to evaluate the thirteen variables considered in this study (see below). The relationships existing among these variables are shown in the following two diagrams





where the brackets indicate one variable to be the product of two others and the variables are defined as follows:

Y - weight of lint per plant (grams),

X_1 - weight of lint per boll (grams),

X_2 - number of bolls per plant,

X_3 - weight of lint per locule (grams),

X_4 - number of locules per boll,

X_7 - lint index (1/100)[1]

X_8 - number of seed per locule,

X_9 - weight of seed per locule (grams),

X_{10} - reciprocal of weight per seed (grams),

X_{11} - weight of seed cotton per plant (grams),

X_{12} - percent lint,

X_{13} - weight of seed cotton per boll (grams),

X_{14} - weight of seed cotton per locule (grams).

As is evident from the diagram, two alternative systems of subdivision were considered. It was of interest to determine if the method of subdivision had any influence on its effectiveness in providing information on yield, the trait subdivided. Cotton lends itself well to alternative systems of breakdown.

Analyses of variance and covariance were computed for each variable and analyses of covariance for each pair of variables which were to be associated in a given selection index.

Groups of variables were then utilized to construct selection indexes by taking a group at each level of subdivision. Using both systems of subdivision this gave

[1] Lint index is defined as the weight of lint (in grams) per hundred seed, and is a frequently used measure of lint quantity. It is often preferred over lint percent measurements in that it is physically independent of seed size.

seven selection indexes. An additional seven were obtained by including the variable Y in each of the first seven indexes giving a total of fourteen indexes, as follows:

$$I_1 = b_2X_2 + b_4X_4 + b_7X_7 + b_9X_9 + b_{10}X_{10}$$

$$I_2 = b_2X_2 + b_4X_4 + b_7X_7 + b_8X_8$$

$$I_3 = b_2X_2 + b_3X_3 + b_4X_4$$

$$I_4 = b_1X_1 + b_2X_2$$

$$I_5 = b_2X_2 + b_4X_4 + b_{12}X_{12} + b_{14}X_{14}$$

$$I_6 = b_2X_2 + b_{12}X_{12} + b_{13}X_{13}$$

$$I_7 = b_{11}X_{11} + b_{12}X_{12}$$

$$I_8 = b_2X_2 + b_4X_4 + b_7X_7 + b_9X_9 + b_{10}X_{10} + b_YY$$

$$I_9 = b_2X_2 + b_4X_4 + b_7X_7 + b_8X_8 + b_YY$$

$$I_{10} = b_2X_2 + b_3X_3 + b_4X_4 + b_YY$$

$$I_{11} = b_1X_1 + b_2X_2 + b_YY$$

$$I_{12} = b_2X_2 + b_4X_4 + b_{12}X_{12} + b_{14}X_{14} + b_YY$$

$$I_{13} = b_2X_2 + b_{12}X_{12} + b_{13}X_{13} + b_YY$$

$$I_{14} = b_{12}X_{12} + b_{11}X_{11} + b_YY$$

The indexes were constructed in the following way. For each index a set of simultaneous equations was set up. These equations are

$$b_1p_{11} + b_2p_{12} + \cdots + b_np_{1n} = g_{1Y}$$
$$b_1p_{21} + b_2p_{22} + \cdots + b_np_{2n} = g_{2Y}$$
$$\cdot$$
$$\cdot$$
$$\cdot$$
$$b_1p_{n1} + b_2p_{n2} + \cdots + b_np_{nn} = g_{nY}$$

where the p values are the phenotypic variances and covariances of the variables denoted by the subscripts and the g values are the genetic covariances of yield with the several sub-traits. These values were available from the analyses of variance and covariance which were computed. These equations were then solved for the b values which are the coefficients desired to form the selection index.

In order to compare the effectiveness of the several indexes, the amount of improvement expected from the use of each of the selection indexes was computed from the relationship

$$\begin{matrix}\text{expected genetic advance} \\ \text{(per generation)}\end{matrix} = \begin{matrix}\text{selection} \\ \text{differential}\end{matrix} \times \begin{matrix}\text{heritability} \\ \text{of the index}\end{matrix}$$

where the selection differential is most conveniently expressed in standard deviation units and the heritability of the index is obtained as $\sqrt{\Sigma b_i G_{iY}}$ using the symbols as before.

---

[1] The selection differential is a function of the percent selected and can be evaluated in standard units from tables of areas and ordinates of the normal curve. The ratio of the ordinate at the point of truncation to the percent selected provides the desired value, which is in fact the difference between the means of the selected group and of the original population expressed in standard deviation units.

RESULTS

The analyses of variance and covariance presented in Table 1 contain only the within block variance estimates. The entries in the "degrees of freedom" columns are somewhat variable because of missing data. (A simple missing plot formula[1] was developed from a least squares approach to meet this problem.)

In examining these data it was found that the two parental lines did not agree in the magnitude of the variances and covariances they exhibited. The P_1 parent generally was found to have larger variances than the P_2 parent and to have variances and covariances which were generally in the direction of the magnitude of those of the F_2 population. This suggested that P_1 was not genotically homogeneous relative to P_2, a supposition that was borne out by an examination of the pedigree of P_1 (see Figure 1, page 43). It appears that sufficient inbreeding had not occurred in P_1 to effectively reduce and stabilize the genetic variability which had been induced through outcrossing. The P_2 parent on the other hand was a long established, stabilized line with no outcrossing in

---

[1] The missing plot was estimated as the mean of the remainder of the observations in the same block.

Table 1. Analyses of Variance and Covariance
(variables identified in text)

	X_1		X_2		X_3	
	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
Within P_1 blocks	41	.0659	41	152.0	41	.0039
Within P_2 blocks	44	.0389	44	214.8	44	.0024
Within F_2 blocks	260	.0723	262	181.4	259	.0038

	X_4		X_7		X_8	
	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
Within P_1 blocks	42	.045	42	.000068	41	2.75
Within P_2 blocks	44	.029	45	.000073	44	.61
Within F_2 blocks	265	.057	264	.000060	259	1.08

	X_9		X_{10}		X_{11}	
	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
Within P_1 blocks	41	.0314	42	.000095	42	10101
Within P_2 blocks	44	.0044	45	.000040	45	7922
Within F_2 blocks	259	.0201	266	.000085	266	10064

	X_{12}		X_{13}		X_{14}	
	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
Within P_1 blocks	42	3.2821	41	.4864	41	.0332
Within P_2 blocks	45	5.6860	44	.1419	44	.0088
Within F_2 blocks	264	6.9063	261	.6509	260	.0339

	Y		$X_1 - X_2$		$X_1 - X_3$	
	d.f.	M.S.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	42	1033.48	41	.53	41	.0172
Within P_2 blocks	45	1039.58	44	.02	44	.0090
Within F_2 blocks	264	1224.02	260	.25	259	.0146

Table 1. (Continued)

	$X_1 - X_4$		$X_1 - Y$		$X_2 - X_3$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	-.027	41	6.154	41	.160
Within P_2 blocks	44	-.004	44	2.507	44	-.078
Within F_2 blocks	259	.009	260	4.007	259	.108

	$X_2 - X_4$		$X_2 - X_7$		$X_2 - X_8$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	.20	41	-.00005	41	.23
Within P_2 blocks	44	.11	44	-.01502	44	.30
Within F_2 blocks	261	-.44	260	.00024	259	.95

	$X_2 - X_9$		$X_2 - X_{10}$		$X_2 - X_{11}$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	-.269	41	.0190	41	1197
Within P_2 blocks	44	-.136	44	.0187	44	1259
Within F_2 blocks	259	-.234	262	.0257	262	1234

	$X_2 - X_{12}$		$X_2 - X_{13}$		$X_2 - X_{14}$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	4.45	41	.72	41	.30
Within P_2 blocks	44	.48	44	.05	44	-.20
Within F_2 blocks	260	10.65	261	-.18	260	-.37

	$X_2 - Y$		$X_3 - X_4$		$X_3 - X_7$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	378.3	41	-.0045	41	.00018
Within P_2 blocks	44	432.5	44	-.0038	44	.00025
Within F_2 blocks	260	431.1	259	-.0025	259	.00022

Table 1. (Continued)

	$X_3 - X_8$		$X_3 - Y$		$X_4 - X_7$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	.032	41	.918	42	.00024
Within P_2 blocks	44	.010	44	.390	44	-.00020
Within F_2 blocks	259	.033	259	.959	262	-.00005

	$X_4 - X_8$		$X_4 - X_9$		$X_4 - X_{10}$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	-.102	41	-.0305	42	.00005
Within P_2 blocks	44	-.043	44	-.0043	44	.00001
Within F_2 blocks	260	-.089	259	-.0078	265	-.00024

	$X_4 - X_{12}$		$X_4 - X_{13}$		$X_4 - X_{14}$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	42	.072	41	-.015	41	-.019
Within P_2 blocks	44	-.066	44	.001	44	-.008
Within F_2 blocks	262	.008	260	.035	260	-.012

	$X_4 - Y$		$X_7 - X_8$		$X_7 - X_9$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	42	-1.05	41	-.0163	41	-.000236
Within P_2 blocks	44	1.48	44	-.0040	44	-.000185
Within F_2 blocks	262	-2.23	259	-.0038	259	-.000012

	$X_7 - X_{10}$		$X_7 - Y$		$X_8 - X_9$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	42	-.000061	42	.0330	41	.1974
Within P_2 blocks	45	-.000028	45	.0338	44	.0381
Within F_2 blocks	264	-.000034	264	.0771	259	.0876

Table 1. (Continued)

	$X_8 - X_{10}$		$X_8 - Y$		$X_9 - X_{10}$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	.0092	41	4.03	41	-.00026
Within P_2 blocks	44	.0037	44	-11.72	44	.00004
Within F_2 blocks	259	.0035	259	6.82	259	-.00080

	$X_9 - Y$		$X_{10} - Y$		$X_{11} - X_{12}$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	-.1531	42	.0379	42	33.46
Within P_2 blocks	44	.2274	45	.0363	45	1.09
Within F_2 blocks	259	.3402	264	.0352	264	10.42

	$X_{11} - X_{13}$		$X_{11} - Y$		$X_{12} - X_{13}$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	23.80	42	3159.7	41	.0866
Within P_2 blocks	44	10.10	45	2724.2	44	.1672
Within F_2 blocks	261	21.96	264	3336.5	260	-.8508

	$X_{12} - X_{14}$		$X_{12} - Y$		$X_{13} - X_{14}$	
	d.f.	Cov.	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	-.0047	42	20.46	41	.1153
Within P_2 blocks	44	.0222	45	20.97	44	.0303
Within F_2 blocks	259	-.2305	264	34.85	260	.1350

	$X_{13} - Y$		$X_{14} - Y$	
	d.f.	Cov.	d.f.	Cov.
Within P_1 blocks	41	7.03	41	1.89
Within P_2 blocks	44	3.42	44	7.76
Within F_2 blocks	260	4.71	259	1.30

its known history. Consequently, it was concluded that a more accurate estimate of the environmental and genetic components could be had by considering only the F_2 data in estimating the environmental (non-genetic) variance. This practice was followed throughout the remainder of the study.

From these analyses it is possible to estimate the genotypic components of variance and covariance as the difference between the F_2 and P_2 variance and covariance estimates. These values are presented in Table 2, together with the phenotypic estimates which are the F_2 estimates directly.

Table 2 provides the information from which one can construct the proposed indexes. The details of the construction of one of the indexes (I_6) will be presented by way of example. This index was constructed from the variables X_2, X_{12}, and X_{13}. Taking the appropriate values from Table 2, the set of normal equations becomes

$$181.4b_2 + 10.65b_{12} - 0.18b_{13} = -0.40$$
$$10.65b_2 + 6.91b_{12} - .8508b_{13} = 13.88$$
$$-0.18b_2 - .8508b_{12} + .6509b_{13} = 1.29$$

where 181.4 is the phenotypic variance of X_2, 10.65 is the phenotypic covariance of X_2 and X_{12}, -0.40 is the genetic

Table 2. Phenotypic and Genetic Variance and Covariance Estimates

	Phenotypic	Genetic
X_1 (variance)	.0723	.0334
X_1 and X_2	.25	.23
X_1 and X_3	.0146	.0056
X_1 and X_4	.009	.013
X_1 and Y	4.007	1.500
X_2 (variance)	181.4	-33.4
X_2 and X_3	.108	.186
X_2 and X_4	-.44	-.55
X_2 and X_7	.00024	.01526
X_2 and X_8	.95	.65
X_2 and X_9	-.234	-.098
X_2 and X_{10}	.0257	.0070
X_2 and X_{11}	1234	-25
X_2 and X_{13}	-.18	-.23
X_2 and X_{14}	-.37	-.17
X_2 and Y	431.1	-.40
X_3 (variance)	.0038	.0014
X_3 and X_4	-.0025	.0013
X_3 and X_7	.00022	-.00003
X_3 and X_8	.033	.023
X_3 and Y	.959	.569
X_4 (variance)	.057	.028
X_4 and X_7	-.00005	.00015
X_4 and X_8	-.089	-.046
X_4 and X_9	-.0078	-.0035
X_4 and X_{10}	-.00024	-.00025
X_4 and X_{12}	.008	.074
X_4 and X_{13}	.035	.034
X_4 and Y	-2.23	-3.71
X_7 (variance)	.000060	-.000013
X_7 and X_8	-.0038	.0002
X_7 and X_9	-.000012	.000173
X_7 and X_{10}	-.000034	-.000006
X_7 and Y	.0771	.0433

Table 2. (Continued)

	Phenotypic	Genetic
X_8 (variance)	1.08	.47
X_8 and X_9	.0876	.0495
X_8 and X_{10}	.0035	-.0002
X_8 and Y	6.82	18.54
X_9 (variance)	.0201	.0157
X_9 and X_{10}	-.00080	-.00084
X_9 and Y	.3402	.1128
X_{10} (variance)	.000085	.000045
X_{10} and Y	.0352	-.0011
X_{11} (variance)	10064	2142
X_{11} and X_{12}	10.42	9.33
X_{11} and X_{13}	21.96	11.86
X_{11} and Y	3336.5	612.3
X_{12} (variance)	6.91	1.22
X_{12} and X_{13}	-.8508	-1.0182
X_{12} and X_{14}	-.2305	-.2527
X_{12} and Y	34.85	13.88
X_{13} (variance)	.6509	.5090
X_{13} and X_{14}	.1350	.1047
X_{13} and Y	4.71	1.29
X_{14} (variance)	.0339	.0251
X_{14} and Y	1.30	-6.46
Y (variance)	1224.02	184.44

covariance of X_2 and Y, and so forth. The solutions of this set of equations give the multiple regression coefficients desired, which are

$$b_2 = -.17 ,$$

$$b_{12} = 2.99 , \text{ and}$$

$$b_{13} = 5.85 .$$

These solutions were obtained by carrying six decimal places through the computations to avoid the accumulation of rounding errors, but the solutions were rounded to two decimal places in that this provided sufficient accuracy for the indexes. The index thus becomes

$$I_6 = -.17 X_2 + 2.99 X_{12} + 5.85 X_{13}$$

The remainder of the indexes were constructed in a similar way and are listed below.

$$I_1 = -.18X_2 - 72.56X_4 + 469.60X_7 - 37.37X_9 - 326.49X_{10}$$

$$I_2 = -.19X_2 - 29.92X_4 + 2106.65X_7 + 22.28X_8$$

$$I_3 = -.22X_2 + 115.39X_3 - 61.73X_4$$

$$I_4 = 20.85X_1 - .03X_2$$

$$I_5 = -.51X_2 - 128.69X_4 - 6.66X_{12} - 287.84X_{14}$$

$$I_6 = -.17X_2 + 2.99X_{12} + 5.85X_{13}$$

$$I_7 = .06X_{11} + 1.92X_{12}$$

$$I_8 = 6.72X_2 - 61.93X_4 + 7351.49X_7 + 309.64X_9 + 4882.39X_{10} - 3.02Y$$

$$I_9 = -47.02X_2 + 16.46X_4 - 38098.76X_7 - 202.16X_8 + 20.27Y$$

$I_{10} = -1.45X_2 + 16.56X_3 - 54.03X_4 + .55Y$

$I_{11} = -123.25X_1 - 7.05X_2 + 3.04Y$

$I_{12} = 34.00X_2 - 166.90X_4 + 63.01X_{12} + 1114.01X_{14} - 15.08Y$

$I_{13} = -2.75X_2 - .64X_{12} - 8.06X_{13} + 1.17Y$

$I_{14} = -.97X_{11} - 12.42X_{12} + 3.15Y$

In order to compare these indexes, the expected genetic advance based on the use of each index was computed for each, according to the formula on page 11. These values are given in Table 3 together with the genetic advance to be expected from selection for the phenotypic expression of yield itself.

Of interest both in themselves and in connection with the present problem are the correlation coefficients which can be computed from the data given in Table 2. These are calculated from the formula

$$r_{XY} = \frac{Cov_{XY}}{\hat{\sigma}_X \cdot \hat{\sigma}_Y}$$

where genetic or phenotypic correlations can be obtained by using the appropriate components of variance and covariance. These correlation coefficients are found in Table 4.

It was stated earlier that the assumption of an additive genetic model was in part subject to verification

Table 3. Genetic Advance Expected from Use of Indexes

	Expected genetic advance (grams lint per plant)	Percent of Y
Y	10.86	100.0
I_1	34.81	320.5
I_2	51.11	470.6
I_3	35.37	325.7
I_4	11.52	106.1
I_5	97.79	900.5
I_6	14.44	133.0
I_7	16.32	150.3
I_8	8.73	80.4
I_9	86.051	-----
I_{10}	36.38	335.0
I_{11}	43.82	403.5
I_{12}	190.261	-----
I_{13}	28.96	266.7
I_{14}	28.041	-----

by the evaluation of the heritabilities of sub-traits at successive levels of subdivision of the trait, yield. These heritabilities are calculated as the percent of the total (F_2) variability which can be ascribed to the genetic component, and are presented in Tables 5 and 6.

Table 4. Phenotypic (r_P) and Genetic (r_G) Correlation Coefficients

			r_P	r_G
X_1	and	X_2	.07	*
X_1	and	X_3	.88	.82
X_1	and	X_4	.14	.42
X_1	and	Y	.43	.60
X_2	and	X_3	.13	*
X_2	and	X_4	-.14	*
X_2	and	X_7	.00	*
X_2	and	X_8	.07	*
X_2	and	X_9	-.12	*
X_2	and	X_{10}	.21	*
X_2	and	X_{11}	.91	*
X_2	and	X_{12}	.30	*
X_2	and	X_{13}	.02	*
X_2	and	X_{14}	-.15	*
X_2	and	Y	.91	*
X_3	and	X_4	-.17	.21
X_3	and	X_7	.46	*
X_3	and	X_8	.52	.88
X_3	and	Y	.44	1.12
X_4	and	X_7	-.03	*
X_4	and	X_8	-.36	-.40
X_4	and	X_9	-.23	-.17
X_4	and	X_{10}	-.11	-.22

* A lack of genetic variability for one variable vitiated the measurement of a genetic correlation.

Table 4. (Continued)

		r_P	r_G
X_4	and X_{12}	.01	.40
X_4	and X_{13}	.18	.29
X_4	and X_{14}	-.27	-.15
X_4	and Y	-.27	-1.63
X_7	and X_8	-.47	*
X_7	and X_9	-.01	*
X_7	and X_{10}	-.48	*
X_7	and Y	.28	*
X_8	and X_9	.59	.58
X_8	and X_{10}	.37	-.04
X_8	and Y	.19	1.99
X_9	and X_{10}	-.61	-1.00
X_9	and Y	.07	.07
X_{10}	and Y	.11	-.01
X_{11}	and X_{12}	.04	.18
X_{11}	and X_{13}	.27	.36
X_{11}	and Y	.95	.97
X_{12}	and X_{13}	-.40	-1.29
X_{12}	and X_{14}	-.48	-1.44
X_{12}	and Y	.38	.92
X_{13}	and X_{14}	.91	.93
X_{13}	and Y	.17	.13
X_{14}	and Y	.20	-3.00

* A lack of genetic variability for one variable vitiated the measurement of a genetic correlation.

Table 5. Percent Heritability of Variables Obtained from Subdivision (1) by Level of Subdivision

Level of subdivision	Y	X_1	X_2	X_3	X_4	X_7	X_8	X_9	X_{10}	Mean
0	15.1									15.1
1		46.2	0							23.1
2				36.8	49.1					43.0
3						0	43.5			21.8
4								78.1	52.9	65.5

Table 6. Percent Heritability of Variables Obtained from Subdivision (2) by Level of Subdivision

Level of subdivision	Y	X_2	X_4	X_{11}	X_{12}	X_{13}	X_{14}	Mean
0	15.1							15.1
1				21.3	17.7			19.5
2		0				78.2		39.1
3			49.1				74.0	61.6

Table 7. Means of Thirteen Variables for P_1, P_2, and F_2 Populations and Calculated Mid-parent Values*

	P_1	P_2	F_2	MP
X_1**	2.34	2.13	2.34	2.24
X_2	43.6	70.3	51.1	57.0
X_3	.53	.46	.52	.50
X_4	4.46	4.60	4.52	4.53
X_7	.059	.064	.062	.062
X_8	9.3	7.3	8.4	8.3
X_9	1.24	.85	1.10	1.05
X_{10}	.075	.086	.077	.081
X_{11}	336.0	424.1	374.7	380.1
X_{12}	30.2	35.3	32.2	32.8
X_{13}	7.74	6.03	7.29	6.89
X_{14}	1.74	1.31	1.61	1.53
Y	101.1	150.5	120.4	125.8

* X_2, X_4, and X_8 are expressed as absolute value; X_{12} is expressed as percent; the remainder are expressed in grams.

** The symbols denoting the variables are defined on pages 8 and 9.

In this same connection it is of interest to examine the mean values for the several variables studied. Table 7 presents these data together with the mid-parental values for each variable. The magnitudes exhibited by the variables and their degrees of intermediacy are shown here. The level of yield and its components is seen to be high, as a result of the good fertility of the field used, and the absence of disease.

DISCUSSION

Richmond (8) showed that by substituting the genotype FnFn (smooth seed) for fnfn (normal fuzzy seed) he was able to evaluate in a more sensitive manner the remainder of the genotype for certain modifier gene complexes which affect lint quantity in Gossypium hirsutum. Silow (11) with Asiatic cotton (G. arboreum and G. herbaceum) found a similar situation in using the locus $h_a h_a$, described as "glabrous lintless", which has effects phenotypically similar to the FnFn locus. Richmond (8) proposed a breeding system based on this approach, which is designed to accumulate modifier complexes for lint quantity so as to increase yield. However, this concerns only a portion of the complex trait, yield, viz. lint per seed or lint index. Consequently, unless information is available on the relationship of this trait to yield and to its other sub-traits, an exact specification of the expected response of yield to this breeding system cannot be made, though the method does have usefulness for screening otherwise unknown material (e.g., introductions) for potential value.

Mather (7) points out that somatic analysis (subdivision of a trait such as yield) is generally of little

value when one is concerned with the resolution of the genetical architecture of a complex trait into simpler, comprehensible parts. However, such an approach can have value where the investigator is interested in predicting average breeding behavior, in that the masking effects of non-genetic variation frequently can be reduced by a consideration of the sub-traits (as was found to be the case with this material in Tables 5 and 6.

The fact that the majority of cotton breeders give consideration to yield components (such as boll size, lint index, etc.), and that this has been so since the early days of organized cotton breeding, has been pointed out by Hutchinson (4). However, it is the writer's observation that this consideration is frequently given in an unsystematic way. The development of the discriminant function and its application to plant selection (Smith, 13) provides the means for a more rational approach to the use of information on the components of yield. Simlote (12) has made such an application in the case of durum wheat in order to more objectively consider the components of yield in that crop.

Cotton lends itself well to a study of this sort, in that cotton yield can be subdivided into numerous

components and can be subdivided in more than one way. Thus, from the same experimental material one can compare the effectiveness of alternative procedures. Table 3 provides the information for such a comparison.

It is evident that the results to be expected from the use of the several indexes are quite variable. Indeed, the expected genetic advance for three of the indexes (I_9, I_{12}, and I_{14}) is an imaginary number. This is impossible to interpret, of course, in biological terms. The explanation seems to lie in errors of estimation. A consideration of Table 2, in which negative components of variance occur, and of Table 4, in which several correlation coefficients (based on variance and covariance components) are found lying outside the expected range of from negative one to positive one, indicates that errors of sampling were quite appreciable in estimating these components. Since we are dealing with components of variance, where negative estimates are possible though not meaningful, and since the quantity $\Sigma b_i g_{iY}$ is of the nature of a sum of squares due to regression, it is concluded that while a negative value for $\Sigma b_i g_{iY}$ is computationally possible, it can only be interpreted as an error deviation from zero. Consequently, the genetic advance calculated for a given

index must also be interpreted as zero when the quantity $\Sigma b_i G_{iY}$ takes on a negative value.

A consideration of the several indexes from the point of view of the level of subdivision responsible for their composition does not reveal any consistent pattern. Similarly, the two alternative methods of breakdown which have been considered show no clear difference in the efficiency of the indexes derived from them. Indeed, the variability of the predictions based on these indexes is quite large, ranging from the zero estimates just discussed to an estimated genetic advance (for I_5) which is nine times as great as that expected for Y.

The values tend to be greater than that for Y alone (as one would expect from the development of a selection index) having a mean percentage efficiency value of approximately 250 percent. However, any variability due to true differences in efficiency between these indexes is masked by variability due to errors of estimation, which, as has been pointed out, are of an appreciable but unknown magnitude. Until it is possible to evaluate a standard error associated with an estimated response to selection, it will be difficult to draw objective con-

clusions from a comparison of several indexes. This seems particularly true in that no trend is apparent.

It is possible, of course, that one might detect a pattern if indexes were constructed from all possible combinations of the variables considered here. Such a pattern might enable one to discriminate in some manner between the indexes obtained. This is in part what was done by Robinson et al.(10), though they were not dealing with yield components. However, in the present case the construction of more than eight thousand indexes would be involved and this is not feasible.

Consequently, the only conclusion that seems justified from these data is that while the indexes as a group provide a more efficient selection criterion than does yield alone, the selection of any one index over the remainder cannot be done objectively. Rather, an arbitrary decision (based, say, on ease of application in a given situation) must be arrived at in order to make a choice.

It was stated earlier that the assumption of an additive genetic model for yield was subject to test. This test is not of a definitive sort, but is nevertheless of interest. The test stems from the following argument. If

the additive model holds, progressive subdivision of the trait should achieve progressively simpler genetic control. With a progressively simpler genetic mechanism, the gap between phenotype and genotype should be progressively reduced, from a reduced opportunity for environmental agencies to influence expression. Therefore, heritabilities should progressively increase. A comparison of mean heritabilities with level of subdivision in Tables 5 and 6 indicates that this, in general, is the case. Consequently, it is concluded that no marked deviation from additivity has been detected.

However, the test is not conclusive in that deviations from additivity can occur in a variety of ways and not all such deviations will necessarily have an effect on heritability measurements. Therefore, it can only be concluded that no deviations from additivity have been detected by a relatively insensitive test.

A consideration of the phenotypic correlations found in Table 4 indicates that where comparisons are possible with values previously reported in the literature (3, 1,14, 15, 16, and 6) agreement is generally found. Some disagreement is found for the following, where the first figure is taken from Table 4 and the second from the source cited.

correlation between X_4 and X_8	-.36	-.05	(1)
correlation between X_4 and X_{13}	.18	.53	(1)
correlation between X_7 and X_8	-.47	-.08	(1)
correlation between X_7 and Y	.28	.00	(6)

These differences are not wide and probably are based on the fact that different material was studied.

The genetic correlation between X_{10} and Y of -.01 differs from that found by Manning (6) between seed weight and lint yield of -.58 (the mean of two estimates). This difference, again, is probably based on the study of different material.

It is instructive to consider the limitations of this study. Firstly, a certain limitation is encountered in the amount of data available from which σ_E^2 can be estimated. Since it was considered necessary to ignore the data collected from P_1, there remain only five blocks of ten plants each from which this estimation is made. A number of blocks as small as five could easily be inadequately randomized, resulting in a non-random position effect on the within block variance estimates. This difficulty might have been remedied by increasing the size of the experiment or by using an experimental design which could effectively reduce such an effect. A more fortunate choice

of experimental material, of course, would have aided in this instance by allowing the retention of the P_1 data.

Simlote (12) developed a selection index from yield components in durum wheat by the use of a logarithmic transformation. It can be argued that this transformation makes more effective use of relationships existing among the sub-traits than does the use of arithmetic data. If so, the indexes so developed will have an even higher efficiency (relative to the use of Y alone) than those developed from arithmetic data. The magnitude of this difference will depend upon how well the arithmetic model approximates the geometric model for the variables considered.

The desirability of pursuing a study of this sort through many advanced generations is apparent. In this way one could obtain new estimates of the genetic and environmental components by means of a between and within family variance comparison and a regression analysis of F_n on F_{n-1}. The agreement of these values with those described in this study could be checked. One would be able, in fact, to compare predicted behavior with actual behavior.

SUMMARY AND CONCLUSIONS

1. A series of fourteen selection indexes was developed for yield in Upland cotton. The thirteen variables from which these indexes were developed are yield components.

2. This study is based on data obtained from an F_2 population derived from a cross between strains of the two varieties, Hartsville and Acala.

3. Subdivision of the trait yield in general resulted in a successive increase of the heritabilities of the sub-traits obtained at succeeding levels of subdivision. It is indicated that this is in agreement with the assumption of an additive genetic model for yield.

4. The genetic advance per generation expected from the use of each index is used as the criterion of comparison. These values are compared to the expected advance based on selection for yield alone.

5. No pattern is detectable in comparing indexes developed from successive levels of subdivision of yield, nor in comparing those developed from two alternative methods of subdivision.

6. Selection based on the indexes tends to be more efficient than selection for yield alone, the fourteen indexes having a mean value (as percent of that for yield) of 250 percent.

7. It was not considered possible to objectively choose between the indexes, in that variability was high for the expected genetic advance values. No measure of the standard error of these values was available.

8. The genetic and phenotypic correlations between variables were found to agree in general with values previously reported, where comparisons were possible. Several of the genetic correlations were found outside of the range of from minus one to plus one. Errors of estimation were appreciable, therefore, and contributed to the variability mentioned in 7 (above).

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ACKNOWLEDGEMENT

The data reported herein were collected by the author at the New Mexico Agricultural Experiment Station as a portion of the work of that organization. The permission to use these data as the basis upon which this thesis is developed, which was generously granted by the administrators of that organization, is hereby gratefully acknowledged.

Thanks are also due Mr. John H. Porter and Mr. F. A. Kazi who assisted materially in the collection of the data.

APPENDIXES

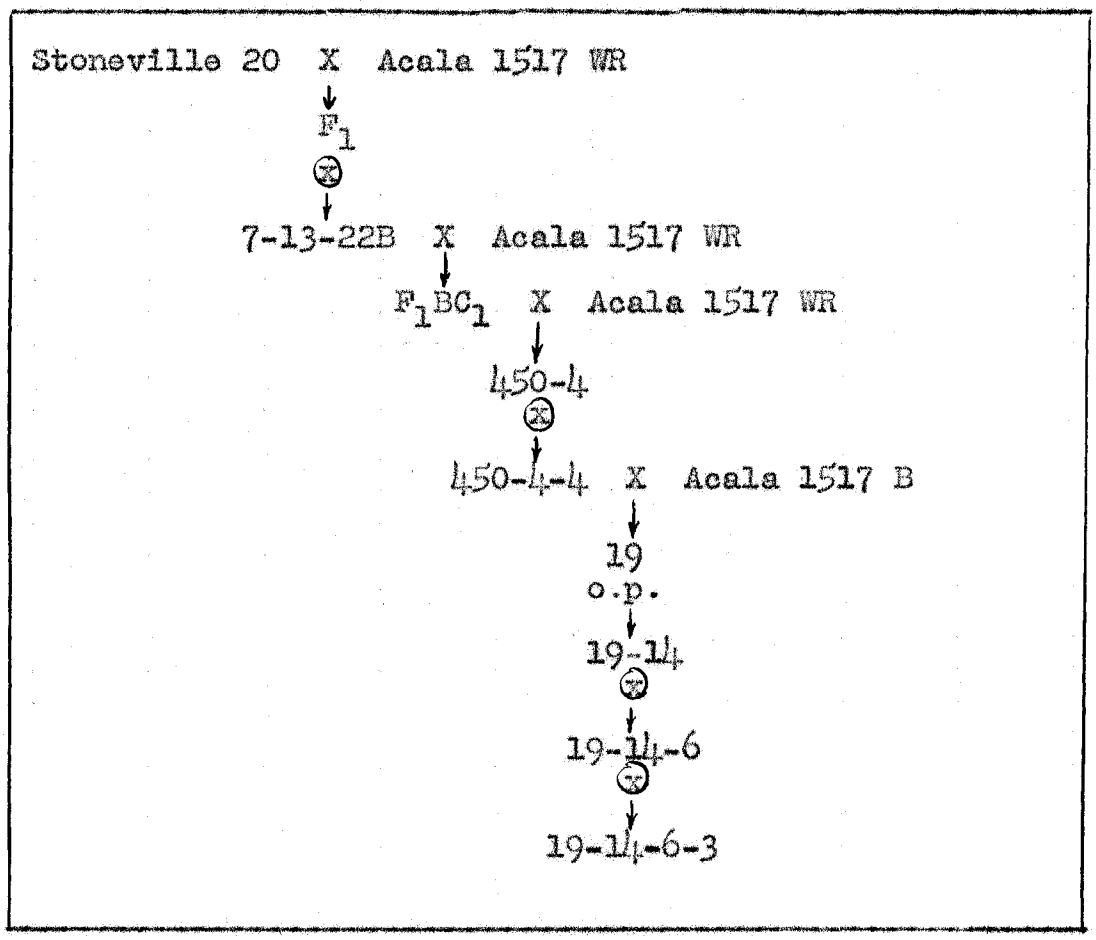

Figure 1. Pedigree of 19-14-6-3 or P_1.*

* Selection was practiced at all stages of this pedigree for the gene B_7 derived from the Stoneville 20 parent and for the "agronomic type" of the Acala parents. This included not only adaptability to New Mexico conditions but certain fiber properties as well.

F_2	P_1	F_2	F_2	F_2
F_2	F_2	F_2	F_2	F_2
F_2	F_2	F_2	P_1	F_2
P_1	F_2	F_2	F_2	P_2
F_2	F_2	P_2	F_2	F_2
P_2	F_2	F_2	F_2	F_2
F_2	F_2	P_1	F_2	P_1
F_2	P_2	F_2	P_2	F_2

The following notes are in explanation of Tables 8 - 20.

[a] The arrangement of the data corresponds to the field planting which is figured above.

[b] The variables are defined and their interrelationships described on pages 8 and 9.

[c] These data were supplied with the use of the missing plot formula and are, in fact, the mean of the remaining observations in their respective blocks.

Figure 2. Field arrangement of blocks (each block consisting of ten plants), being an explanation of the arrangement of the data presented in Tables 8 through 20.

Table 8[a]. Yield of Lint (grams) per Plant (Y)[b]

57.6	47.5	80.4	77.2[c]	126.0	177.0	206.2	101.0	66.6[c]	115.5
132.3	74.8	90.1	59.6	113.3	74.4	110.2	56.2	99.6	52.1
96.0	103.7	95.8	62.3	114.9	59.2	109.4	49.8	67.7	37.5
133.0	84.6	82.5	58.3	76.0	66.6	97.2	69.3	77.8	38.4
147.2	99.4	76.8	89.2	60.4	78.4	89.4	87.6	71.4	39.0
95.5	101.2	111.8	84.4	64.1	70.0	94.1	50.4	78.8	50.0
148.3	92.6	102.7	83.7	79.7	52.5	72.2	59.0	74.7	42.0
132.2	100.8	93.7[c]	82.5	73.5	55.1	53.6	67.8	53.9	47.9
152.2	100.8	98.0	113.1	75.1	88.6	86.3	86.4	92.4	44.1
124.7	102.0	84.3	82.7	91.9	94.0	77.4	53.6	35.3	42.9
101.6	69.4	115.9	108.2	93.6	91.8	57.3	81.2	73.1	44.4
140.7	143.6	100.1	98.9	73.9	70.4	80.8	72.2	64.0	51.7
146.3	113.0	194.9	148.3	170.8	132.1	97.7	63.9	96.0	75.3
146.6	119.1	115.2	70.9	149.6	147.9	134.3	122.7	76.2[c]	75.4
169.3	125.5	155.6	120.0	85.8	159.7	89.7	67.0	103.6	102.2
108.9	71.7	115.7	186.8	148.4	200.9	130.6	116.6	114.8	66.2
196.2	114.9	240.2	131.4	167.4	147.2	125.0	134.2[c]	159.3	119.2
153.4	83.4	135.8	146.0	157.4	25.3	142.0	146.4	150.3	148.3
107.3	67.6	170.4	77.3	150.7	125.4	187.4	142.8	97.0	131.2
52.5	97.3	185.8	127.9	235.8	147.2	111.7	105.6	138.0	158.1
234.9	136.5	122.4	110.5	154.2	177.0	179.4	106.5	163.2	74.5
119.0	131.1	128.5	142.6	53.4	188.1	97.6	149.6	161.7	119.5
173.1	144.2	101.0	97.7	180.2	190.1	163.5	123.1	76.8	101.1
160.5	102.4	133.7	159.7	146.8	163.0	183.1	106.9	186.0	114.8
82.7	130.2	136.8	170.8	165.3	64.9	160.4	129.7	137.7	180.2
166.9	141.6	155.9	178.5	101.8	240.7	147.4	149.0	156.1	86.0
153.6	106.9	163.8	179.3	164.3[c]	174.9	78.3	114.5	155.9	105.9
197.8	141.3	152.3	161.4	164.9	245.0	79.8	123.4	108.6	108.5
199.8	109.1	154.2	139.8	157.2	164.5	100.8	161.8	88.2	90.2
164.3	134.6	99.2	153.7	134.1	96.0	125.8	162.2	92.7	170.0
117.8	107.7	104.5	114.4	140.2	122.2	84.5	87.0	145.2	78.5
154.4	160.3	182.9	150.1	116.1	161.4	164.1	137.0	124.7	116.0
148.0	139.4	129.8[c]	27.6	136.6[c]	143.8	134.8	177.6	80.1	47.5
128.1	109.2	110.7	169.5	136.6[c]	155.1	79.9	123.0	101.7	117.3
161.7	143.9	152.0	156.8	57.6	196.1	214.1	146.4	74.1	116.5
207.6	106.8	121.8	175.1	73.7	193.4	150.7	144.7	155.3	156.2
189.5	147.6	158.5	180.9	236.9	230.2	138.9	155.1	181.5	51.4
148.8	152.1	182.3	152.6	134.8	181.0	165.6	149.9	140.4	120.5
140.5	110.6	177.3	144.1	144.6	134.8	157.4	172.1	128.5	111.0
128.8	150.6	164.6	188.0	167.6	262.0	214.5	149.8	172.0	169.8

[a,b,c] These symbols are explained on page 44.

Table 9[a]. Weight of Lint (grams) per Boll (X_1)[b]

2.31	2.64	2.44	2.40[c]	2.17	2.77	2.90	2.52	2.27[c]	2.61
2.54	2.02	2.82	2.84	2.41	2.33	2.45	1.94	2.12	2.48
2.67	2.30	2.23	2.08	2.46	2.11	2.96	2.37	2.42	2.09
2.22	2.12	2.23	2.65	2.23	2.38	2.16	2.10	2.29	2.26
2.68	2.69	2.40	1.94	2.32	2.80	2.18	2.65	2.23	1.95
2.98	2.35	2.03	2.34	2.07	1.94	2.41	1.80	2.63	2.09
2.56	2.37	2.39	2.46	2.42	1.94	2.49	1.97	2.41	2.00
2.28	2.40	2.30[c]	1.83	2.30	2.40	1.91	2.26	2.45	2.00
2.62	2.10	2.39	2.46	2.03	2.46	2.62	2.22	2.43	2.59
2.23	2.22	2.16	2.67	2.39	2.22[c]	2.50	2.33	2.21	2.04
2.16	2.10	2.58	2.21	2.13	2.62	2.20	2.26	2.36	2.12
2.27	2.18	2.71	3.00	2.38	2.13	2.31	2.26	1.88	1.92
2.57	2.51	2.47	2.39	2.41	2.40	2.57	2.06	2.29	2.04
2.62	2.05	2.30	2.29	2.45	2.11	2.53	2.36	2.20[c]	2.79
2.73	2.20	2.59	2.55	2.00	2.58	2.19	2.03	2.16	2.27
2.59	2.24	2.36	2.46	2.65	2.45	2.56	1.91	2.21	1.95
2.80	2.25	3.25	2.53	2.43	2.50	2.31	2.21[c]	2.18	2.34
2.61	2.38	2.34	2.25	2.35	1.80	2.49	2.40	1.83	2.70
2.98	2.60	2.84	2.41	2.47	1.74	2.43	2.20	1.64	1.96
1.88	2.56	2.65	2.37	2.43	2.26	1.93	1.70	1.89	2.17
2.50	2.10	1.91	2.35	1.88	2.19	2.53	2.01	2.15	1.86
2.24	2.47	2.85	2.38	2.05	2.27	1.41	2.17	2.57	2.34
2.84	2.62	2.24	1.81	2.17	2.16	2.44	2.24	2.33	2.15
2.63	2.21	2.26	2.71	2.45	1.99	2.26	1.91	2.35	2.25
2.07	2.60	2.38[c]	2.90	1.97	1.91	2.06	2.00	2.19	2.25
2.29	2.32	2.56	2.48	2.37	2.35[c]	2.34	2.44	2.11	2.46
1.94	1.78	2.16	2.04	2.35[c]	2.57	2.01	2.24	2.36	2.72
2.47	2.11	2.58	2.41	2.58	2.53	2.22	2.28	2.26	2.29[c]
2.13	2.06	2.41	2.74	2.07	2.32	2.52	2.22	2.15	2.00
2.00	2.10	2.11	2.79	2.16	2.18	2.29	2.19	2.11	2.46
2.87	2.56	2.13	2.16	2.34	2.22	2.11	2.07	2.20	2.07
2.29	2.63	2.20	2.27	2.25[c]	2.37	2.56	2.08	2.40	2.32
2.21	2.97	2.14[c]	1.45	2.25[c]	2.36	2.54	2.02	2.29	1.90
2.51	2.18	2.05	2.46	2.25[c]	2.22	2.50	2.12	2.37	2.39
2.53	2.72	2.34	2.21	2.06	2.18	2.35	2.36	1.85	2.77
2.44	2.74	2.10	2.04	1.99	2.61	2.18	2.14[c]	2.04	2.26
2.34	2.20	2.30	2.38	2.69	2.62	2.24	2.13	2.33	2.06
2.86	2.62	2.40	2.01	2.70	2.01	2.20	2.14	2.23	2.27
2.56	2.46	2.33	2.09	2.37	2.45	2.06	2.21	2.22	2.06
1.81	2.90	2.25	2.24	2.30	2.46	2.19	1.92	2.39	3.14

a,b,c These symbols are explained on page 44.

Table 10[a]. Number of Bolls per Plant (X_2)[b]

25	18	33	33[c]	58	64	71	40	29[c]	43
52	37	32	21	47	32	45	29	47	21
36	45	43	30	33	25	37	21	28	18
60	40	37	22	35	28	45	33	34	17
55	37	32	46	26	28	41	33	32	20
32	43	55	36	31	36	39	28	30	24
58	39	43	34	33	27	29	30	31	21
58	42	41[c]	45	32	23	28	30	22	24
58	48	41	46	37	36	33	39	38	17
56	46	39	31	37	32[c]	31	23	16	21
47	33	45	49	44	35	26	36	31	21
62	66	37	33	31	33	35	32	34	27
57	45	79	62	71	55	38	31	42	37
56	58	50	31	61	70	53	52	35[c]	27
62	57	60	47	43	62	41	33	48	45
42	32	49	76	56	82	51	61	52	34
70	51	74	52	69	59	54	51	73	51
58	35	58	65	67	14	57	61	82	55
36	26	60	32	61	72	77	61	59	67
28	38	70	54	97	65	58	62	73	73
94	65	64	47	82	81	71	53	76	40
53	53	45	60	26	83	69	69	63	51
61	55	45	54	83	88	67	55	33	47
61	45	58	59	60	82	81	56	79	51
40	50	55[c]	59	84	34	78	65	63	80
73	61	61	72	43	66[c]	63	61	74	35
79	60	76	88	66[c]	68	39	51	66	39
80	67	59	67	64	97	36	54	48	51[c]
94	53	64	51	76	71	40	73	41	45
82	64	47	55	62	44	55	74	44	69
41	42	49	53	60	55	40	42	66	38
66	61	83	66	62[c]	68	64	66	52	50
67	47	70	19	62[c]	61	53	88	35	25
51	50	54	69	62[c]	70	32	58	43	49
64	53	65	71	28	90	91	62	40	42
85	39	58	86	37	74	69	74[c]	76	69
81	67	69	76	88	88	62	73	78	25
52	58	76	76	50	90	77	70	63	53
55	45	76	69	61	55	59	78	58	54
71	52	73	84	73	108	98	78	72	54

[a,b,c] These symbols are explained on page 44.

Table 11[a]. Weight of Lint (grams) per Locule (X_3)[b]

.55	.56	.50	.54[c]	.50	.62	.66	.56	.52[c]	.57
.59	.48	.63	.66	.48	.52	.53	.42	.49	.58
.57	.50	.51	.47	.56	.47	.64	.52	.56	.50
.50	.48	.56	.53	.51	.54	.54	.48	.52[c]	.49
.61	.60	.52	.46	.49	.65	.46	.63	.54	.43
.65	.50	.46	.48	.41	.46	.59	.41	.60	.42
.54	.54	.52	.56	.55	.54	.55	.45	.54	.44
.51	.52	.50[c]	.37	.50	.52	.42	.50	.54	.40
.57	.45	.53	.55	.44	.55	.55	.47	.53	.52
.47	.53	.50	.56	.54	.50[c]	.51	.50	.47	.45
.49	.46	.53	.49	.48	.55	.49	.49	.49	.45
.49	.51	.62	.67	.53	.47	.51	.49	.43	.40
.57	.61	.53	.56	.52	.49	.57	.47	.50	.49
.52	.51	.56	.48	.54	.49	.56	.54	.48[c]	.57
.65	.49	.58	.57	.43	.54	.50	.42	.45	.53
.58	.52	.55	.55	.56	.56	.58	.44	.51	.41
.65	.51	.69	.54	.52	.53	.53	.50[c]	.48	.52
.57	.54	.50	.51	.50	.37	.54	.53	.39	.63
.68	.62	.59	.50	.59	.38	.57	.54	.36	.43
.41	.53	.58	.55	.50	.49	.40	.36	.40	.46
.58	.50	.43	.48	.39	.49	.54	.43	.49	.41
.48	.54	.59	.51	.46	.50	.34	.53	.57	.54
.59	.57	.49	.40	.49	.44	.51	.53	.53	.49
.57	.51	.54	.62	.53	.43	.51	.42	.53	.49
.43	.57	.52[c]	.62	.39	.43	.49	.48	.51	.55
.50	.52	.53	.50	.52	.51[c]	.53	.49	.50	.53
.42	.39	.49	.44	.51[c]	.52	.45	.49	.50	.63
.53	.47	.57	.56	.52	.60	.48	.50	.48	.51[c]
.44	.44	.54	.67	.42	.54	.51	.49	.45	.48
.43	.46	.44	.63	.50	.47	.46	.49	.47	.53
.65	.53	.43	.53	.54	.52	.47	.45	.47	.45
.56	.55	.46	.54	.52[c]	.53	.60	.46	.57	.49
.49	.69	.48[c]	.31	.52[c]	.54	.54	.49	.52	.43
.61	.45	.53	.50	.52[c]	.54	.53	.44	.55	.54
.59	.62	.52	.49	.46	.51	.51	.49	.41	.64
.57	.60	.47	.46	.43	.56	.46	.47[c]	.46	.53
.54	.46	.47	.49	.58	.58	.49	.47	.55	.47
.65	.61	.49	.42	.57	.40	.49	.50	.48	.54
.60	.56	.49	.48	.48	.56	.44	.48	.49	.47
.40	.62	.50	.51	.49	.55	.46	.43	.53	.64

[a,b,c]. These symbols are explained on page 44.

Table 12[a]. Number of Locules per Boll (X_4)[b]

4.2	4.7	4.9	4.5[c]	4.3	4.5	4.4	4.5	4.4[c]	4.6
4.3	4.2	4.5	4.3	5.0	4.5	4.6	4.6	4.3	4.3
4.7	4.6	4.4	4.4	4.4	4.5	4.6	4.6	4.3	4.2
4.4	4.4	4.0	5.0	4.4	4.4	4.0	4.4	4.4[c]	4.6
4.4	4.5	4.6	4.2	4.7	4.3	4.7	4.2	4.1	4.5
4.6	4.7	4.4	4.9	5.0	4.2	4.1	4.4	4.4	5.0
4.7	4.4	4.6	4.4	4.4	3.6	4.5	4.4	4.5	4.5
4.5	4.6	4.6[c]	4.9	4.6	4.6	4.5	4.5	4.2	5.0
4.6	4.7	4.5	4.5	4.6	4.5	4.8	4.7	4.6	5.0
4.7	4.2	4.3	4.8	4.4	4.7	4.9	4.7	4.7	4.5
4.4	4.6	4.9	4.5	4.4	4.8	4.5	4.6	4.8	4.7
4.6	4.3	4.4	4.5	4.5	4.5	4.5	4.6	4.4	4.8
4.5	4.1	4.7	4.3	4.6	4.9	4.5	4.4	4.6	4.2
5.0	4.0	4.1	4.8	4.5	4.3	4.5	4.4	4.6	4.9
4.2	4.5	4.5	4.5	4.6	4.8	4.4	4.8	4.8	4.3
4.5	4.3	4.3	4.5	4.7	4.4	4.4	4.3	4.3	4.7
4.3	4.4	4.7	4.7	4.7	4.7	4.4	4.7	4.5	4.5
4.6	4.4	4.7	4.4	4.7	4.9	4.6	4.5	4.7	4.3
4.4	4.2	4.8	4.8	4.2	4.6	4.3	4.1	4.5	4.6
4.6	4.8	4.6	4.3	4.9	4.6	4.8	4.7	4.7	4.7
4.3	4.2	4.4	4.9	4.8	4.5	4.7	4.7	4.4	4.5
4.7	4.6	4.8	4.7	4.5	4.5	4.2	4.1	4.5	4.3
4.8	4.6	4.6	4.5	4.4	4.9	4.8	4.2	4.4	4.4
4.6	4.3	4.2	4.4	4.6	4.6	4.4	4.6	4.4	4.6
4.3	4.6	4.6	4.7	5.0	4.4	4.2	4.2	4.3	4.1
4.6	4.5	4.8	5.0	4.6	4.5	4.4	5.0	4.2	4.6
4.6	4.6	4.4	4.6	4.6[c]	4.9	4.5	4.6	4.7	4.3
4.7	4.5	4.5	4.3	5.0	4.2	4.6	4.6	4.7	4.5[c]
4.8	4.7	4.5	4.1	4.9	4.3	4.9	4.3	4.6	4.2
4.6	4.6	4.8	4.4	4.3	4.6	5.0	4.5	4.5	4.6
4.4	4.8	4.9	4.1	4.3	4.3	4.5	4.6	4.7	4.6
4.1	4.8	4.8	4.2	4.9	4.5	4.3	4.5	4.2	4.7
4.5	4.3	5.2	4.7	4.4[c]	4.4	4.7	4.1	4.4	4.4
4.1	4.8	3.9	4.9	4.4[c]	4.1	4.7	4.8	4.3	4.4
4.3	4.4	4.5	4.5	4.5	4.3	4.6	4.8	4.5	4.3
4.3	4.6	4.5	4.4	4.6	4.7	4.7	4.6[c]	4.4	4.3
4.3	4.8	4.9	4.7	4.6	4.5	4.6	4.5	4.2	4.4
4.4	4.3	4.9	4.8	4.7	5.0	4.5	4.3	4.6	4.2
4.3	4.5	4.8	4.4	4.9	4.4	4.7	4.6	4.5	4.4
4.5	4.7	4.5	4.4	4.7	4.5	4.8	4.5	4.5	4.9

a,b,c. These symbols are explained on page 44.

Table 13[a]. Lint Index x 1/100 (X_7)[b]

.060	.064	.074	.063[c]	.066	.091	.070	.074	.063[c]	.067
.062	.057	.067	.072	.066	.063	.058	.058	.060	.074
.071	.057	.061	.055	.071	.070	.087	.061	.067	.059
.060	.070	.064	.056	.068	.064	.052	.059	.054	.064
.065	.074	.063	.052	.070	.067	.059	.070	.064	.056
.058	.064	.061	.065	.060	.054	.074	.050	.070	.062
.064	.060	.072	.060	.062	.056	.076	.055	.060	.065
.065	.062	.064[c]	.054	.060	.056	.055	.064	.076	.046
.067	.063	.064	.063	.061	.066	.068	.073	.071	.061
.061	.064	.071	.063	.064	.069	.067	.060	.065	.058
.058	.062	.072	.052	.068	.055	.062	.083	.057	.055
.068	.059	.067	.062	.076	.055	.058	.048	.065	.062
.064	.073	.068	.067	.065	.063	.063	.050	.051	.058
.062	.054	.066	.055	.043	.060	.063	.056	.061[c]	.079
.070	.068	.066	.068	.049	.057	.057	.057	.061	.058
.060	.049	.067	.064	.075	.060	.069	.052	.065	.060
.070	.037	.073	.063	.064	.054	.057	.061[c]	.068	.072
.048	.060	.065	.054	.073	.044	.067	.064	.059	.104
.062	.060	.077	.067	.054	.051	.076	.060	.059	.064
.046	.070	.056	.060	.067	.052	.056	.047	.049	.063
.059	.055	.051	.059	.057	.057	.058	.065	.056	.051
.054	.051	.063	.058	.071	.067	.065	.064	.068	.053
.071	.066	.057	.053	.069	.063	.063	.064	.061	.063
.064	.056	.066	.071	.060	.067	.067	.058	.065	.054
.070	.061	.063	.072	.060	.058	.056	.047	.057	.060
.062	.062	.065	.070	.065	.103	.061	.064	.051	.066
.066	.043	.061	.057	.064[c]	.063	.060	.068	.066	.068
.062	.063	.066	.059	.065	.056	.057	.059	.065	.050
.056	.062	.048	.063	.056	.058	.085	.057	.056	.061
.066	.072	.053	.080	.055	.056	.060	.059	.055	.064
.055	.069	.057	.056	.066	.056	.061	.058	.049	.058
.069	.071	.061	.067	.068	.068	.068	.054	.055	.052
.057	.069	.061[c]	.061	.063[c]	.069	.053	.058	.051	.052
.060	.058	.055	.063	.063[c]	.061	.070	.050	.054	.062
.060	.070	.064	.064	.060	.056	.066	.059	.047	.041
.049	.066	.065	.052	.042	.068	.065	.064	.060	.054
.064	.066	.077	.061	.065	.061	.064	.063	.065	.054
.059	.076	.065	.057	.068	.061	.065	.054	.068	.064
.065	.067	.069	.062	.059	.070	.066	.072	.059	.045
.057	.073	.061	.067	.054	.059	.066	.061	.053	.069

a,b,c These symbols are explained on page 44.

Table 14[a]. Number of Seed per Locule (X_8)[b]

9.2	8.7	6.8	8.5[c]	7.6	6.8	9.5	7.6	8.2[c]	8.7
9.6	8.5	9.4	9.2	7.4	8.3	9.2	7.3	8.2	7.9
8.1	8.8	7.7	8.5	7.9	6.7	7.4	8.4	8.4	8.3
8.2	6.9	8.7	9.6	7.4	8.4	10.2	8.1	8.2[c]	7.6
9.4	8.0	8.2	8.8	7.2	9.8	7.8	9.0	8.5	7.7
11.2	7.8	7.6	7.3	6.9	8.6	7.9	8.3	8.5	6.7
8.4	9.0	7.1	9.3	9.1	9.7	7.1	8.2	8.9	6.8
7.8	8.4	7.9[c]	6.9	8.3	9.2	7.7	7.9	7.8	8.7
8.5	7.1	8.3	8.7	7.2	8.3	8.0	6.5	7.4	8.4
7.8	8.3	7.0	8.8	8.8	8.5[c]	8.2	8.3	7.2	7.8
8.5	7.3	7.2	9.5	7.1	9.9	7.9	5.9	8.6	8.1
7.2	8.6	9.3	10.7	6.9	8.7	8.8	10.1	6.5	6.4
8.8	8.4	7.7	8.3	8.0	7.8	10.6	9.4	9.8	8.3
8.5	9.5	8.5	8.6	12.5	8.2	9.0	9.5	7.9[c]	7.2
9.2	7.1	8.6	8.3	8.9	9.4	8.8	7.4	7.3	9.1
9.6	10.7	8.1	8.5	7.5	9.2	8.4	8.5	7.9	6.9
9.2	13.9	9.5	8.6	8.1	9.8	9.2	8.2[c]	7.1	7.2
12.1	9.1	7.6	9.5	6.9	8.3	8.1	8.3	6.6	6.0
10.9	10.2	7.7	7.5	10.9	7.3	7.4	9.4	6.2	6.6
8.8	7.7	10.3	9.2	7.3	9.5	7.1	7.8	8.2	7.3
9.8	9.1	8.4	8.1	6.8	8.4	9.3	6.6	8.7	8.1
8.8	10.4	9.4	8.7	6.4	7.5	5.2	8.3	8.4	10.3
8.3	8.6	8.5	7.5	7.2	7.0	8.0	8.3	8.6	7.8
8.9	9.4	8.1	8.6	8.9	6.4	7.6	7.1	8.2	9.0
6.1	9.2	8.4[c]	8.5	6.5	7.4	8.7	10.0	8.9	9.2
8.0	8.3	8.1	7.1	7.9	8.7[c]	8.8	7.6	9.7	8.2
6.5	8.8	8.0	7.8	8.7[c]	8.3	7.4	7.1	7.6	9.2
8.3	7.5	8.6	9.5	7.9	10.8	8.4	8.4	7.4	8.3[c]
7.9	7.1	11.3	10.5	7.6	9.3	6.0	8.6	7.9	7.5
6.6	6.4	8.3	8.0	9.2	8.5	7.6	8.2	8.5	8.4
11.8	7.7	7.6	9.5	8.3	9.3	7.6	7.8	9.6	7.8
8.3	7.7	7.6	8.0	8.4[c]	7.8	8.8	8.5	10.4	9.5
8.5	10.1	7.9[c]	5.1	8.4[c]	7.8	10.2	8.4	10.2	14.5
10.2	7.8	9.5	8.0	8.4[c]	8.8	7.6	8.8	10.1	8.7
9.8	8.8	8.2	7.7	7.6	9.1	7.7	8.3	8.7	15.6
11.5	9.0	7.2	8.8	10.3	8.2	7.1	7.3[c]	7.8	9.8
8.5	6.9	6.1	7.9	9.9	9.5	7.6	7.5	8.4	8.7
11.0	8.6	7.5	7.3	8.5	8.6	7.4	9.2	7.1	8.4
9.2	8.1	7.1	7.6	8.2	7.9	6.6	6.7	8.3	10.3
7.1	8.4	8.2	7.5	10.0	9.3	6.9	6.9	10.0	9.4

a,b,c. These symbols are explained on page 44.

Table 15[a]. Weight of Seed (grams) per Locule (X_9)[b]

1.19	1.31	1.09	1.18[c]	1.22	1.08	1.04	1.14	1.16[c]	1.31
1.25	0.99	1.31	1.19	0.81	0.91	1.10	0.87	1.15	1.10
1.21	1.05	1.15	1.11	1.11	0.87	1.11	1.09	1.34	1.16
1.15	0.83	1.30	1.15	0.81	1.26	1.12	0.89	1.16[c]	1.07
1.22	0.88	1.15	1.15	0.93	0.98	0.94	1.26	1.11	1.00
1.45	0.93	0.84	0.88	0.96	0.86	0.87	0.99	1.02	0.94
1.01	1.08	1.07	1.02	1.09	1.26	0.78	0.98	1.25	0.88
1.01	1.09	0.99[c]	0.76	0.91	1.29	1.08	1.10	1.24	0.96
1.11	0.78	1.16	1.13	1.08	1.08	1.04	0.71	0.89	1.18
1.17	1.24	0.91	1.14	1.06	1.07	1.06	1.24	0.94	0.94
1.19	1.10	1.01	1.04	1.14	1.29	1.03	1.06	1.03	1.14
1.01	1.03	1.21	1.28	0.97	1.04	1.06	1.11	1.11	0.90
1.15	1.09	0.92	1.16	0.88	0.93	1.27	1.32	1.17	1.08
1.10	1.14	1.19	1.12	1.25	0.98	0.99	1.23	1.07[c]	1.08
1.29	1.07	1.21	1.25	1.07	0.94	1.14	0.96	1.10	1.00
1.34	1.28	1.30	1.11	1.05	1.01	1.34	1.10	0.95	0.76
1.29	1.25	1.23	1.20	1.13	1.27	1.29	1.14[c]	0.85	0.86
1.33	1.27	1.07	1.24	1.10	0.91	1.22	1.24	0.79	0.72
1.63	1.43	1.08	1.12	1.31	1.17	1.04	1.22	0.81	0.79
1.06	1.15	0.93	1.10	0.88	1.04	1.07	0.78	0.90	0.80
1.28	1.18	1.09	1.05	0.75	0.84	1.12	0.92	1.04	0.81
1.15	1.25	1.41	1.04	0.77	0.90	0.67	0.99	1.18	1.23
1.16	1.12	1.19	0.75	0.86	0.84	0.96	1.08	1.20	1.09
1.33	1.22	1.14	1.21	0.98	0.77	1.07	1.00	0.90	1.17
0.92	1.29	1.13[c]	1.28	0.72	0.89	0.96	1.10	1.16	1.10
0.96	0.99	1.21	1.07	1.18	1.17[c]	1.23	1.21	0.97	1.06
0.84	0.97	0.96	1.01	1.17[c]	1.25	1.04	1.00	0.99	1.47
1.00	0.82	0.95	1.14	1.10	1.40	1.01	1.17	0.96	1.10[c]
0.79	0.85	1.13	1.47	0.91	1.12	0.84	1.20	1.03	1.13
0.79	0.89	0.99	1.20	1.19	1.19	1.06	0.98	1.10	1.18
1.53	1.16	1.06	1.14	1.32	1.39	1.06	0.93	1.06	1.09
1.16	1.23	0.99	1.04	1.27[c]	1.17	1.14	1.02	1.35	1.14
1.11	1.51	1.08[c]	0.87	1.27[c]	1.24	1.22	1.01	1.33	2.03
1.43	1.17	1.42	1.04	1.27[c]	1.41	1.07	1.06	1.21	1.30
1.37	1.14	1.06	1.08	1.07	1.27	1.08	1.00	1.04	1.56
1.27	1.35	0.86	0.88	1.03	1.23	0.85	0.86[c]	0.93	1.17
0.94	1.04	0.79	0.79	1.08	1.23	0.91	0.90	1.18	1.13
1.32	1.28	0.83	0.80	1.44	0.79	0.89	0.92	0.92	1.09
1.19	1.22	0.85	0.84	1.06	1.03	0.79	0.80	1.24	1.24
0.99	1.26	0.90	0.83	1.20	0.93	0.83	0.83	1.20	1.31

a,b,c These symbols are explained on page 44.

Table 16[a]. Reciprocal of Weight per Seed (grams) (X_{10})[b]

.077	.067	.063	.073[c]	.063	.063	.091	.067	.072[c]	.067
.077	.091	.071	.077	.091	.091	.083	.083	.071	.071
.067	.083	.067	.077	.071	.077	.067	.077	.063	.071
.071	.083	.067	.083	.091	.067	.091	.091	.083	.071
.077	.091	.071	.077	.077	.100	.083	.071	.077	.077
.077	.083	.091	.083	.071	.100	.091	.083	.083	.071
.083	.083	.067	.091	.083	.077	.091	.083	.071	.077
.077	.077	.081[c]	.091	.091	.071	.071	.071	.063	.091
.077	.091	.071	.077	.067	.077	.077	.091	.083	.071
.067	.067	.077	.077	.083	.091	.071	.067	.077	.083
.071	.067	.071	.091	.063	.077	.077	.056	.083	.071
.071	.083	.077	.083	.071	.083	.083	.091	.059	.071
.077	.077	.083	.071	.091	.083	.071	.071	.083	.077
.077	.083	.071	.077	.100	.083	.091	.077	.074[c]	.067
.071	.067	.071	.067	.083	.100	.077	.077	.067	.091
.071	.083	.063	.077	.071	.091	.063	.077	.083	.091
.071	.111	.077	.071	.071	.077	.071	.083	.083	.083
.091	.071	.071	.077	.063	.091	.067	.067	.083	.083
.067	.071	.071	.067	.083	.063	.071	.077	.077	.083
.083	.067	.111	.083	.083	.091	.067	.100	.091	.091
.077	.077	.077	.077	.091	.100	.083	.071	.083	.100
.077	.083	.067	.083	.083	.083	.077	.083	.071	.083
.071	.077	.071	.100	.083	.083	.083	.077	.071	.071
.067	.077	.071	.071	.091	.083	.071	.071	.091	.077
.067	.071	.067	.067	.091	.083	.091	.091	.077	.083
.083	.083	.067	.067	.067[c]	.063	.071	.063	.100	.077
.077	.091	.083	.077	.073[c]	.067	.071	.071	.077	.063
.083	.091	.091	.083	.071	.077	.083	.071	.077	.077
.100	.083	.100	.071	.083	.083	.071	.071	.077	.067
.083	.071	.083	.067	.077	.071	.071	.083	.077	.071
.077	.067	.071	.083	.063	.067	.071	.083	.091	.071
.071	.063	.077	.077	.063	.067	.077	.083	.077	.083
.077	.067	.083	.059	.066[c]	.063	.083	.083	.077	.071
.071	.067	.067	.077	.066[c]	.063	.071	.083	.083	.067
.071	.077	.077	.071	.071	.071	.071	.083	.083	.100
.091	.067	.083	.100	.100	.067	.083	.083	.083	.083
.091	.067	.077	.100	.083	.077	.083	.083	.071	.077
.083	.063	.091	.091	.059	.083	.083	.100	.077	.077
.077	.067	.083	.091	.077	.077	.083	.083	.067	.083
.071	.067	.091	.091	.083	.100	.083	.083	.083	.071

a,b,c. These symbols are explained on page 44.

Table 17[a]. Weight of Seed Cotton (grams) per Plant (X_{11})[b]

183	159	257	249[c]	430	489	530	306	216[c]	375
412	220	279	167	303	205	337	172	332	151
300	322	313	209	242	169	298	156	228	126
442	230	275	185	203	222	299	198	250	132
442	246	246	312	174	196	271	263	217	129
309	290	314	239	213	200	234	172	213	163
425	278	314	237	238	175	174	188	249	126
397	311	278[c]	250	207	192	190	216	168	163
449	277	313	347	258	263	251	216	249	145
433	341	238	253	264	243	238	188	106	132
348	237	340	338	314	308	178	257	227	157
429	435	298	290	210	225	248	236	231	169
442	314	537	459	458	383	315	243	321	243
454	383	359	238	492	444	370	405	247[c]	218
504	401	483	386	297	440	295	219	356	297
363	248	391	566	424	566	431	405	327	187
584	395	669	424	533	499	431	359	440	317
508	279	427	500	503	88	461	488	454	319
365	224	480	250	486	514	531	449	312	376
189	307	485	384	655	457	409	332	448	432
753	458	431	352	451	485	552	335	510	221
406	437	434	436	144	524	293	431	496	388
502	428	347	279	493	551	474	373	251	326
535	339	410	474	416	454	565	366	500	389
260	427	462	524	467	198	476	431	453	541
491	414	511	563	335	614	488	519	459	256
457	375	486	588	518[c]	591	261	350	464	353
575	387	405	489	517	814	247	414	326	402
558	320	479	448	496	506	266	556	292	310
464	396	322	443	453	337	618	490	310	543
394	342	359	361	480	451	276	267	473	269
468	522	575	439	387	519	477	439	420	383
482	444	507	105	469[c]	476	439	543	285	176
427	390	410	520	469[c]	560	240	417	326	399
539	410	462	501	192	688	665	445	261	399
674	349	347	509	248	620	427	417	465	504
515	484	425	476	673	717	398	451	569	176
451	471	490	445	473	537	473	427	407	364
422	359	487	398	462	385	342	459	451	405
442	459	461	496	580	718	606	442	562	516

a,b,c These symbols are explained on page 44.

Table 18[a]. Percent Lint (X_{12})[b]

31.5	29.9	31.3	31.2[c]	29.3	36.2	38.9	33.0	31.2[c]	30.8
32.1	34.0	32.3	35.7	37.4	36.3	32.7	32.7	30.0	34.5
32.0	32.2	30.6	29.8	33.6	35.0	36.7	31.9	29.7	29.8
30.1	36.8	30.0	31.5	38.4	30.0	32.5	35.0	31.1	31.5
33.3	40.4	31.2	28.6	34.7	40.0	33.0	33.3	32.9	30.2
30.9	34.9	35.6	35.3	30.1	35.0	40.2	29.3	37.0	30.7
34.9	33.3	32.7	35.3	33.5	30.0	41.5	31.4	30.0	33.3
33.3	32.4	33.8[c]	33.0	35.5	28.7	28.2	31.4	32.1	29.4
33.9	36.4	31.3	32.6	29.1	33.7	34.4	40.0	37.1	30.4
28.8	29.9	35.4	32.7	34.8	38.7	32.5	28.5	33.3	32.5
29.2	29.3	34.1	32.0	29.8	29.8	32.2	31.6	32.2	28.3
32.8	33.0	33.6	34.1	35.2	31.3	32.6	30.6	27.7	30.6
33.1	36.0	36.3	32.3	37.3	34.5	31.0	26.3	29.9	31.0
32.3	31.1	32.1	29.8	30.4	33.3	36.3	30.3	30.9[c]	34.6
33.6	31.3	32.2	31.1	28.9	36.3	30.4	30.6	29.1	34.4
30.0	28.9	29.6	33.0	35.0	35.5	30.3	28.8	35.1	35.4
33.6	29.1	35.9	31.0	31.4	29.5	29.0	30.6[c]	36.2	37.6
30.2	29.9	31.8	29.2	31.3	28.7	30.8	30.0	33.1	46.5
29.4	30.2	35.5	30.9	31.0	24.4	35.3	31.8	31.1	34.9
27.8	31.7	38.3	33.3	36.0	32.2	27.3	31.8	30.8	36.6
31.2	29.8	28.4	31.4	34.2	36.5	32.5	31.8	32.0	33.7
29.3	30.0	29.6	32.7	37.1	35.9	33.3	34.7	32.6	30.8
33.8	33.7	29.1	35.0	36.4	34.5	34.5	33.0	30.6	31.0
30.0	30.2	32.0	33.7	35.3	35.9	32.4	29.2	37.2	29.5
31.8	30.5	29.6	32.6	35.4	32.8	33.7	30.1	30.4	33.3
34.0	34.2	30.5	31.7	30.4	39.2	30.2	28.7	34.0	33.6
33.6	28.5	33.7	30.5	31.5[c]	29.6	30.0	32.7	33.6	30.0
34.4	36.5	37.6	33.0	31.9	30.1	32.3	29.8	33.3	27.0
35.8	34.1	32.2	31.2	31.7	32.5	37.9	29.1	30.2	29.1
35.4	34.0	30.8	34.7	29.6	28.5	30.1	33.1	29.9	31.3
29.9	31.5	29.1	31.7	29.2	27.1	30.6	32.6	30.7	29.2
33.0	30.7	31.8	34.2	30.0	31.1	34.4	31.2	29.7	30.3
30.7	31.4	30.8[c]	26.3	29.2[c]	30.2	30.7	32.7	28.1	27.0
30.0	28.0	27.0	32.6	29.2[c]	27.7	33.3	29.5	31.2	29.4
30.0	35.1	32.9	31.3	30.0	28.5	32.2	32.9	28.4	29.2
30.8	30.6	35.1	34.4	29.7	31.2	35.3	34.7	33.4	31.0
36.8	30.5	37.3	38.0	35.2	32.1	34.9	34.4	31.9	29.2
33.0	32.3	37.2	34.3	28.5	33.7	35.0	35.1	34.5	33.1
33.3	30.8	36.4	36.2	31.3	35.0	35.6	37.5	28.5	27.4
29.0	32.8	35.7	37.9	28.9	37.0	35.4	33.9	30.6	32.9

a,b,c These symbols are explained on page 44.

Table 19[a]. Weight of Seed Cotton (grams) per Boll (X_{13})[b]

7.32	8.83	7.79	7.67[c]	7.41	7.64	7.46	7.65	7.32[c]	8.72
7.92	5.95	8.72	7.96	6.45	6.41	7.49	5.93	7.06	7.19
8.33	7.16	7.28	6.98	7.33	6.76	8.05	7.43	8.14	7.00
7.37	5.75	7.43	8.41	5.80	7.93	6.64	6.00	7.35	7.18
8.04	6.65	7.69	6.78	6.69	7.00	6.61	7.97	6.78	6.45
9.66	6.74	5.71	6.63	6.87	5.56	6.00	6.14	7.10	6.79
7.33	7.13	7.30	6.97	7.21	6.48	6.00	6.27	8.03	6.00
6.84	7.40	6.85[c]	5.55	6.47	8.35	6.78	7.20	7.64	6.79
7.74	5.77	7.63	7.55	6.97	7.31	7.61	5.54	6.55	8.53
7.73	7.41	6.10	8.17	7.14	6.93[c]	7.68	8.17	6.63	6.29
7.40	7.18	7.56	6.91	7.14	8.80	6.85	7.14	7.32	7.48
6.92	6.59	8.05	8.80	6.77	6.82	7.04	7.38	6.79	6.26
7.75	6.98	6.80	7.40	6.45	6.96	8.29	7.84	7.64	6.57
8.11	6.60	7.18	7.68	7.90	6.34	6.98	7.79	7.13[c]	8.07
8.13	7.04	8.05	8.20	6.91	7.10	7.20	6.64	7.42	6.60
8.64	7.75	7.98	7.45	7.57	6.90	8.45	6.64	6.29	5.50
8.34	7.75	9.04	8.16	7.72	8.46	7.98	7.04	6.03	6.22
8.76	7.97	7.36	7.71	7.51	6.29	8.09	8.00	5.54	5.80
10.14	8.62	8.00	7.80	7.97	7.14	6.90	7.36	5.29	5.61
6.75	8.08	6.93	7.12	6.75	7.03	7.05	5.35	6.14	5.92
8.01	7.05	6.73	7.48	5.50	5.99	7.77	6.32	6.71	5.53
7.66	8.25	9.63	7.28	5.54	6.31	4.25	6.25	7.87	7.61
8.39	7.78	7.70	5.17	5.96	6.26	7.07	6.78	7.61	6.94
8.77	7.53	7.06	8.04	6.93	5.54	6.98	6.54	6.33	7.63
6.50	8.54	7.55[c]	8.88	5.56	5.82	6.10	6.63	7.19	6.76
6.73	6.79	8.39	7.82	7.79	7.70[c]	7.75	8.51	6.20	7.31
5.78	6.25	6.41	6.68	7.70[c]	8.69	6.69	6.86	7.03	9.05
7.19	5.78	6.86	7.30	8.08	8.39	6.86	7.67	6.79	7.26[c]
5.94	6.04	7.48	8.78	6.53	7.13	6.65	7.62	7.12	6.89
5.66	6.19	6.85	8.69	7.31	7.66	7.60	6.62	7.05	7.87
9.61	8.14	7.32	6.81	8.00	8.20	6.90	6.36	7.17	7.08
7.09	8.56	6.92	6.65	7.73[c]	7.63	7.45	6.65	8.08	7.66
7.19	9.45	6.95[c]	5.53	7.73[c]	7.80	8.28	6.17	8.14	7.04
8.37	7.80	7.59	7.54	7.73[c]	8.00	7.50	7.19	7.58	8.14
8.42	7.74	7.11	7.06	6.86	7.64	7.31	7.18	6.53	9.50
7.93	8.95	5.98	5.92	6.70	8.38	6.19	6.06[c]	6.12	7.30
6.36	7.22	6.17	6.26	7.65	8.15	6.42	6.18	7.29	7.04
8.67	8.12	6.45	5.86	9.46	5.97	6.14	6.10	6.46	6.87
7.67	7.98	6.40	5.77	7.57	7.00	5.80	5.88	7.78	7.50
6.25	8.83	6.30	5.90	7.95	6.65	6.18	5.67	7.81	9.56

a,b,c These symbols are explained on page 44.

Table 20[a]. Weight of Seed Cotton (grams) per Locule (X_{14})[b]

1.74	1.88	1.59	1.72[c]	1.72	1.70	1.70	1.70	1.68[c]	1.90
1.84	1.42	1.94	1.85	1.29	1.42	1.63	1.29	1.64	1.67
1.77	1.56	1.65	1.59	1.67	1.50	1.75	1.62	1.89	1.67
1.68	1.31	1.86	1.68	1.32	1.80	1.66	1.36	1.68[c]	1.56
1.83	1.48	1.67	1.61	1.42	1.63	1.41	1.90	1.65	1.43
2.10	1.43	1.30	1.35	1.37	1.32	1.46	1.40	1.61	1.36
1.56	1.62	1.59	1.58	1.64	1.80	1.33	1.43	1.78	1.33
1.52	1.61	1.49[c]	1.13	1.41	1.82	1.51	1.60	1.82	1.36
1.68	1.23	1.70	1.68	1.52	1.62	1.59	1.18	1.42	1.71
1.64	1.76	1.42	1.70	1.62	1.57[c]	1.57	1.74	1.41	1.40
1.68	1.56	1.54	1.54	1.62	1.83	1.52	1.55	1.53	1.59
1.50	1.53	1.83	1.96	1.50	1.52	1.58	1.60	1.54	1.30
1.72	1.70	1.45	1.72	1.40	1.42	1.84	1.78	1.66	1.56
1.62	1.65	1.75	1.60	1.76	1.47	1.55	1.77	1.55[c]	1.65
1.94	1.56	1.79	1.82	1.50	1.48	1.64	1.38	1.55	1.53
1.92	1.80	1.86	1.66	1.61	1.57	1.92	1.54	1.46	1.17
1.94	1.76	1.92	1.74	1.64	1.80	1.81	1.50	1.34	1.38
1.90	1.81	1.57	1.75	1.60	1.28	1.76	1.78	1.18	1.35
2.30	2.05	1.67	1.63	1.90	1.55	1.60	1.80	1.18	1.22
1.47	1.68	1.51	1.66	1.38	1.53	1.47	1.14	1.31	1.26
1.86	1.68	1.53	1.53	1.15	1.33	1.65	1.34	1.53	1.23
1.63	1.79	2.01	1.55	1.23	1.40	1.01	1.52	1.75	1.77
1.75	1.69	1.67	1.15	1.35	1.28	1.47	1.61	1.73	1.58
1.91	1.75	1.68	1.83	1.51	1.20	1.59	1.42	1.44	1.66
1.35	1.86	1.65[c]	1.89	1.11	1.32	1.45	1.58	1.67	1.65
1.46	1.51	1.75	1.56	1.69	1.68[c]	1.76	1.70	1.48	1.59
1.26	1.36	1.46	1.45	1.68[c]	1.77	1.49	1.49	1.50	2.10
1.53	1.28	1.52	1.70	1.62	2.00	1.49	1.67	1.44	1.59[c]
1.24	1.29	1.66	2.14	1.33	1.66	1.36	1.69	1.48	1.64
1.23	1.35	1.43	1.98	1.70	1.67	1.52	1.47	1.57	1.49
2.18	1.70	1.49	1.66	1.86	1.91	1.53	1.38	1.53	1.54
1.73	1.78	1.44	1.58	1.78[c]	1.70	1.73	1.48	1.92	1.63
1.60	2.20	1.55[c]	1.18	1.78[c]	1.77	1.76	1.50	1.85	1.60
2.04	1.63	1.95	1.54	1.78[c]	1.95	1.60	1.50	1.76	1.85
1.96	1.76	1.58	1.57	1.52	1.78	1.59	1.50	1.45	2.21
1.84	1.95	1.33	1.35	1.46	1.78	1.32	1.33[c]	1.39	1.70
1.48	1.50	1.26	1.28	1.66	1.81	1.40	1.37	1.74	1.60
1.97	1.89	1.32	1.22	2.01	1.19	1.36	1.42	1.40	1.64
1.78	1.77	1.33	1.31	1.54	1.59	1.23	1.28	1.73	1.70
1.39	1.88	1.40	1.34	1.69	1.48	1.29	1.26	1.74	1.95

a,b,c These symbols are explained on page 44.