THE INHERITANCE AND INTERRELATIONSHIP OF POD DEHISCENCE AND SOME OTHER AGRONOMIC CHARACTERS IN SOYBEANS

by

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I. INTRODUCTION

Pod dehiscence, or shattering, is an undesirable characteristic in cultivated soybeans (Glycine max (L) Merr.). There is variation in the degree of shatter resistance in cultivated soybeans. Before resistant varieties were developed, if weather conditions were favorable for shattering, soybean growers could lose over one-half of their crop (2). Just two pods shattering per square foot reduces yield by one bushel per acre.

Environmental factors such as relative humidity, temperature, soil type, and periods of wetting and drying affect shattering, with relative humidity and temperature affecting it the most (2). Progress in recent years has been made in developing soybean varieties that are shatter resistant allowing soybeans to be grown in many areas where a few years ago they were unprofitable to grow. Selection for shatter resistant types must be continued and conducted where weather conditions during harvest are favorable for shattering. More knowledge of how shattering is inherited and is related to other agronomic characters will assist soybean breeders in designing programs for producing shatter resistant varieties.

The main objective was to study the inheritance of shattering in soybeans and its relation to other agronomic characters. Inheritance of height, maturity, and seed weight were also studied.

II. LITERATURE REVIEW

Inheritance studies of pod dehiscence in soybeans are limited. Nagai (17) and Ting (22) found in hybrid progenies of cultivated soybeans crossed with wild soybeans that the shattering character was dominant to the non-shattering character. Piper and Morse (19) working with an intraspecific cross involving varieties of Glycine max, however, reported the nonshattering character to be dominant to the shattering character. Caviness (2,3) with intra- and interspecific crosses found partial dominance for the shattering character. Estimates of heritability for pod dehiscence are high (2,3,9). Caviness (2,3) reports shattering to be due to the action of several genes and some modifiers.

Inheritance of maturity varies as to the type of gene action controlling maturity. Several investigators have reported dominance in the direction of lateness (12,20,23,30) while others reported dominance in the direction of earliness (11,18). Others have reported additive gene action (9,10,14,29). The varying results of earlier reporters may be explained by two major genes (1) that control maturity, each acting in a different direction; a major gene for earliness and a major gene for lateness. As suggested by Bernard (1) some of the variability of earlier reports also could be due to the arbitrariness of the date chosen to distinguish early from late. Maturity is highly heritable (8,9,14,15,21,26,27,28,29). Most of these authors agree that selection for maturity can be carried out successfully in early generations.

In a cross between the wild species, Glycine ussuriensis, Regel and Maack and the cultivated species, Glycine max, Ting (22) reported that the genes for short plants are dominant to those for tall plants. In intraspecific

crosses with the cultivated species, Glycine max, however, dominance was in the direction of tallness (4,6,11,12,23,29,30). Woodworth (31) found indeterminant growth habit to be dominant to determinant. Height is highly heritable (4,8,9,14,15,21,27,28,29). Gopani and Kabaria (7), however, reported low heritability for height. This could be due to the small variation in height between the parents. Earlier studies indicate that a single major gene pair affects height but minor genes and/or modifying genes also affect plant height in soybeans (4,30).

The small seed size of the wild species, Glycine ussuriensis and Glycine formosana Hosokawa, is dominant to the larger seed size of the cultivated species, Glycine max, (12,17,21,22,26). In intraspecific crosses with Glycine max, (11) dominance was reported in the direction of large seed size while other workers reported additive gene action controlling seed weight (6,28). Most of the earlier studies have found seed weight to be a highly heritable character (7,9,21,28). Hanson and Weber (8) however, reported low heritability for seed weight. They further stated that environmental stresses at seed formation could affect seed weight. If this stress is confounded with the maturity range for a set of genotypes, considerable genotype by environmental interaction could be expected for seed weight, which could explain the low estimate of heritability. Caviness (3) also indicated that seed size was influenced by the environment. Weber (26) and Weber and Moorthy (28) report that there are a large number of genes that determine seed weight in soybeans.

Little information is available on the relationship of shattering with other agronomic characters. Johnson, Robinson and Comstock (10) indicated a positive correlation between height and shattering resistance. In a cross between the wild species, Glycine ussuriensis, and the cultivated species,

Caviness (3) reported a positive correlation between shattering and maturity while in crosses between varieties of Glycine max Johnson, et al. (10) reported a positive correlation between shattering resistance and maturity. Caviness (3), in intraspecific crosses, reported no correlation of shattering to maturity. Johnson, et al. (10) and Caviness (3) reported a positive correlation between shatter resistance and seed weight. However, in crosses between varieties of the cultivated species Caviness (3) reported a negative correlation. The positive correlation he found was in a cross between parents with medium and small seeds while the negative correlation occurred in a cross between medium and large seeded parents.

Positive correlations between maturity and height (10,12,15,21,28,29) have been reported. However, there was variation on the relation of maturity to seed weight from a positive correlation (10,12) in intraspecific crosses in the cultivated species to no correlation (26,28) to a negative correlation (21) in interspecific crosses between the wild and cultivated species. Likewise, reports on the relation of height to seed weight also varied from no correlation (7,10) to a negative correlation (21). Weber and Moorthy (28) reported height and seed weight to be negatively correlated in one cross and positively correlated in the other two crosses.

III. MATERIALS AND METHODS

Intraspecific crosses in soybeans were made in 1969 involving four varieties (Table 1 and 2). Methods of handling the various generations in all three crosses were the same unless otherwise noted. The F_1 seed was planted in 1970. One-half of the F_2 seed was planted in 1971 along with the parental varieties. Data on single F_2 plants and parents were collected on maturity, shattering (number of days from maturity to pod dehiscence), height at maturity, and seed weight. All unshattered F_2 plants remaining after 21 days in the 10S and 11S crosses and 28 days in the 9S cross were considered shatter resistant.

In 1972 F_3 progeny seed from F_2 plants grown in 1971 was planted along with the remaining F_2 seed, F_1 seed from crosses made in 1971, and seed from the parental varieties. The F_3 seed was planted in single rows 76 cm apart and 3.69 meters long and later trimmed to 2.46 meters. Parents were planted every tenth row and two check varieties, 'Amsoy' and 'Hark', were planted in every tenth row giving a check variety every fifth row. Plant density within a row was dependent upon the amount of seed available, ranging from 30 to 80 seeds per row. Parental check rows were planted at the same rates as the F_3 progeny rows while the other check varieties were planted at a constant rate of 60 seeds per row. Data on maturity, shattering, height, and seed weight were collected from progeny rows grown from one hundred randomly selected F_2 single plants from each cross. Maturity and shattering data were collected on individual F_3 plants while height and seed weight were measured as F_3 progeny row means. Data for the parents and checks were collected in the form of row means.

The F_2 and F_1 seed was planted at a rate of 50 seeds per 3.69 meter

Table 1. Description of the parental varieties comparing indicated characters.

Variety	Shattering	Maturity group	Height	Seed size
A 100	resistant	I	indeterminant	medium
Goldsoy	moderately resistant	O	indeterminant	medium
Burwell	susceptible	I	determinant	large
Giant Green	susceptible	I	determinant	large

Table 2. Cross numbers assigned and pedigree of the crosses.

Cross number	Cross
9S	A 100 x Goldsoy
10S	A 100 x Burwell
11S	A 100 x Giant Green

rows, however, due to poor germination in the F_2 caused by the age of the seed, plant spacing in the F_2 varied considerably. Data on single plants were collected on the F_2, F_1, and parents.

Methods of evaluating the different characters were:

Maturity date: when 95% of the pods on a single plant turned brown, or for parental row means when 75% of the plants within a row were mature.

Shattering date: when two to three pods on a single plant had shattered or, for parental row means when 75% of the plants within a row had shattered.

Height (cm): measured at maturity from ground level to the uppermost tip of the main stem.

Seed weight: the weight in grams per 100 seeds.

IV. METHODS OF ANALYSIS

Mather (16), used equations derived by Fisher, Immer and Tedin (5), to describe how to divide continuous variation in quantitative characters into additive, nonadditive, and environmental portions. The following equations were used to derive values for the additive or fixable portions of variance and nonadditive or unfixable portions:

$$\text{I.} \quad VF_2 = 1/2\ D + 1/4\ H + E_1$$

$$\text{II.} \quad \text{Cov}\ F_2/F_3 = 1/2\ D + 1/8\ H$$

where VF_2 is the variance of the F_2 population.

Cov F_2/F_3 is the covariance of F_2 single plants and their F_3 progeny row means

D is the additive portion of variance

H is the nonadditive portion of variance

E_1 is a measure of the environmental portion based on single plant measurements and calculated directly from the data by the formula:

$$E = \frac{VP_1 + VP_2 + VF_1}{3}$$

where VP_1 is the variance of the first parent

VP_2 is the variance of the second parent

VF_1 is the variance of the F_1 generation

Broad sense and narrow sense estimates of heritability were calculated. The broad sense estimate includes the additive and nonadditive portion of variance while the narrow sense estimate includes only the additive portion of variability (13). The formula used to calculate the broad sense estimates of heritability was:

$$H = \frac{VF_2 - E_1}{VF_2}$$

Three different methods all using regression of F_3 progeny row means on single F_2 plant values were used to estimate narrow sense heritability. The first of these methods was described by Mahmud and Kramer (14):

$$H = \frac{\bar{X}\, b_{yx}}{\bar{Y}} \times 100$$

where H is heritability

$\bar{X}$ is the mean of the F_2 generation

$\bar{Y}$ is the mean of the F_3 generation

b_{yx} is the regression of means of F_3 lines on individual F_2 plant values.

The second method was proposed by Waddle (24) and described by Caviness (3):

$$H = \frac{\frac{(\xi xy)^2}{\xi x^2}}{\xi y^2} \quad \text{or} \quad H = \frac{(\xi xy)^2}{\xi x^2 \cdot \xi y^2} \quad \text{or} \quad H = r^2$$

where H is heritability

$\frac{(\xi xy)^2}{\xi x^2}$ is the sum of squares due to regression of y on x

ξx^2 is the sum of squares for F_2 plant values

ξy^2 is the sum of squares for F_3 progeny means.

The third method made use of the D value calculated earlier with the use of Mather's formulas (16). This method was described by Warner (25):

$$H = \frac{1/2\ D}{VF_2}$$

The formulas used to calculate correlation coefficients are:

In the F_2 generation:

$$\text{phenotypic correlation} = \frac{Cov_{xy}}{\sqrt{Var_x}\ \sqrt{Var_y}}$$

$$\text{genotypic correlation} = \frac{Cov_{xy} - Cov\ E_{1xy}}{\sqrt{Var_x - E_{1x}}\ \sqrt{Var_y - E_{1y}}}$$

where Cov_{xy} is the covariance of two sets of data

Var_x is the variance of one set of data

Var_y is the variance of the other set of data

Cov E_{1xy} is the estimate of the environmental covariance calculated from the formula:

$$\frac{CovP_1 + CovP_2 + CovF_1}{3}$$

where $CovP_1$ is the covariance of parent one's data

$CovP_2$ is the covariance of parent two's data

$CovF_1$ is the covariance of the F_1 generation's data

E_{1x} and E_{1y} are, as defined earlier, the environmental effect for the various characters.

Phenotypic correlations in the F_3 generation are like those calculated in the F_2 generation. The genotypic correlation in the F_3 generation is essentially the same as for the F_2 except that the environmental portion is based on row means. The formula for calculating it is:

$$\frac{Cov_{xy} - Cov\ E_{2xy}}{\sqrt{Var_x - E_{2x}}\ \sqrt{Var_y - E_{2y}}}$$

where Cov_{xy}, Var_x, Var_y are as earlier defined

Cov E_{2xy} is an estimate of the environmental covariance based on row means.

E_{2x} and E_{2y} are the estimates of environmental variance based on row means for the different characters and calculated from the equation:

$$E_{2x \text{ or } y} = \frac{VP_1 \text{ row means} + VP_2 \text{ row means}}{2}$$

V. RESULTS AND DISCUSSION

Shattering

Frequency distributions (Figures 1-6) indicate additive gene action in the 9S cross and dominant gene action in the 10S and 11S crosses. The additivity is indicated by the normal distribution in the 9S F_2 and F_3 generations, while dominance is indicated by the skewed distributions in the 10S and 11S F_2 and F_3 generations. Also the fact that the means of the F_1, F_2, and F_3 generations fall closer to the mean of the susceptible parent in the two crosses indicate dominance in the direction of shattering. The means of the F_1, F_2, and F_3 generations in the 9S cross fall close to the center of the parents indicating additivity.

From looking at the frequency distributions (Figures 1-6), one would expect small D values for the 10S and 11S crosses and a large D value in the 9S cross. The D value (Table 3) for the 11S cross agreed with what was expected, being a negative value which was considered zero. In the 10S cross the D value, though not as small as that in the 11S, was still small when compared to its corresponding H value. The negative D value in the 9S cross was not expected. This negative value was the result of a very small covariance between F_2 plants and their F_3 progeny resulting from early termination of data collecting in the F_2 generation in 1971, which decreased the variance of the F_2 plants.

Except for the 1972 broad sense estimate in the 9S cross (Table 4), all of the broad sense estimates of heritability are high. The low value for the 9S cross in 1972 was the environmental affect on the shatter resistant genotypes causing large variation in the nonsegregating populations.

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Fig. 1. Frequency distributions of the parental populations and F_2 generation in 1971 for the 93 cross for shattering.

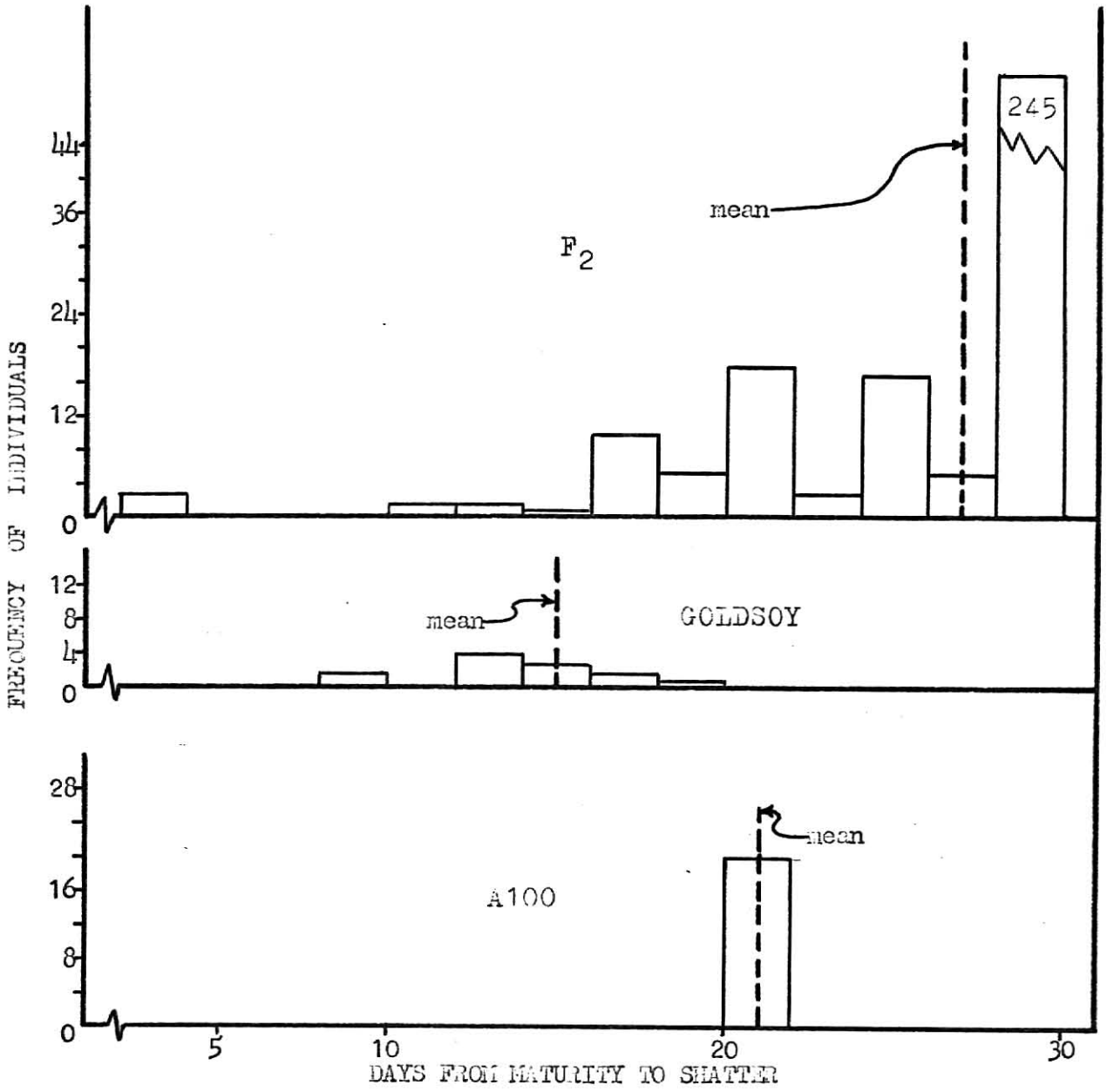


Fig. 2. Frequency distributions of all populations in 1972 for the 9S cross for shattering.

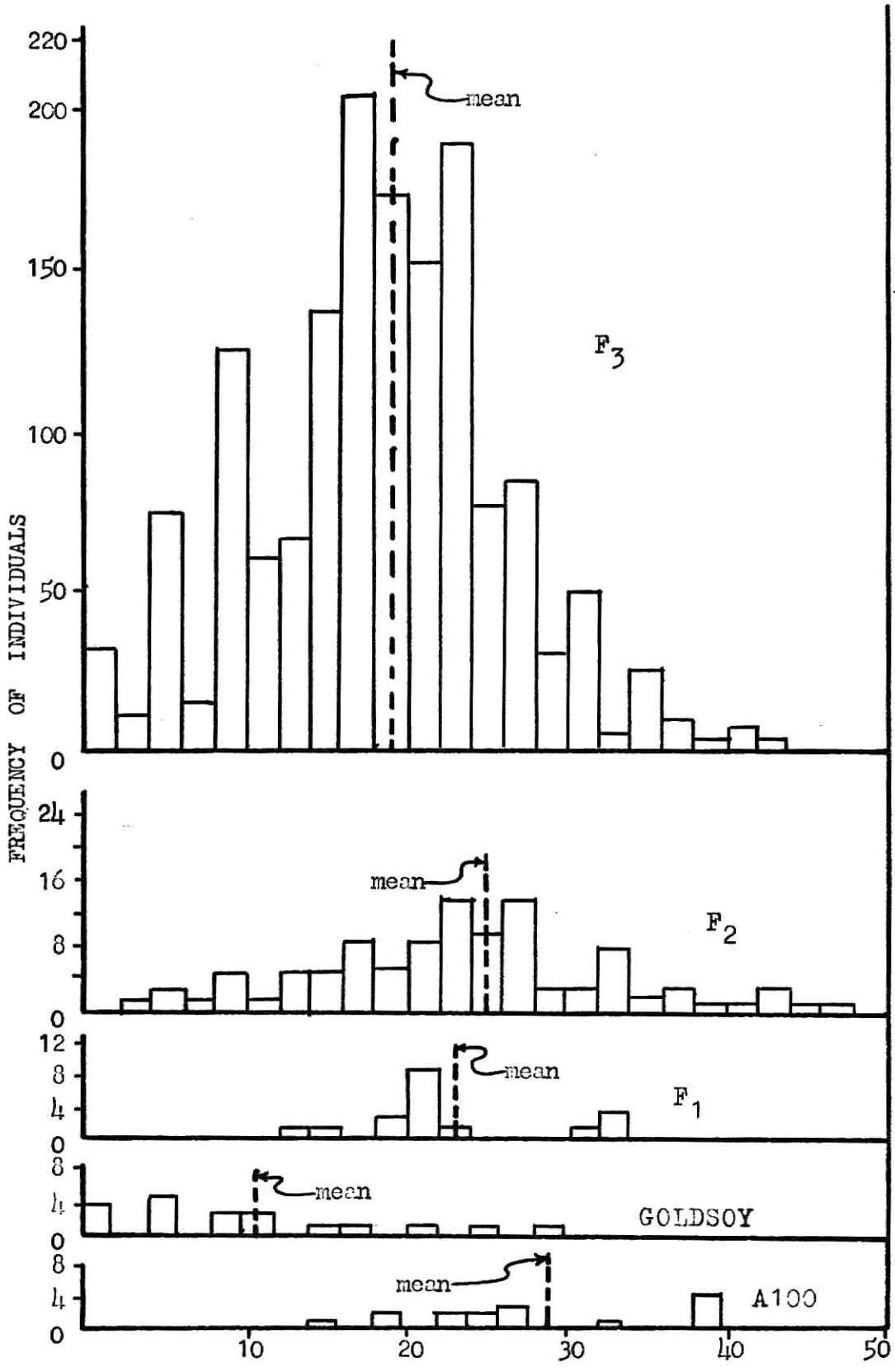


Fig. 3. Frequency distributions of the parental populations and F_2 generation in 1971 for the 10S cross for shattering.

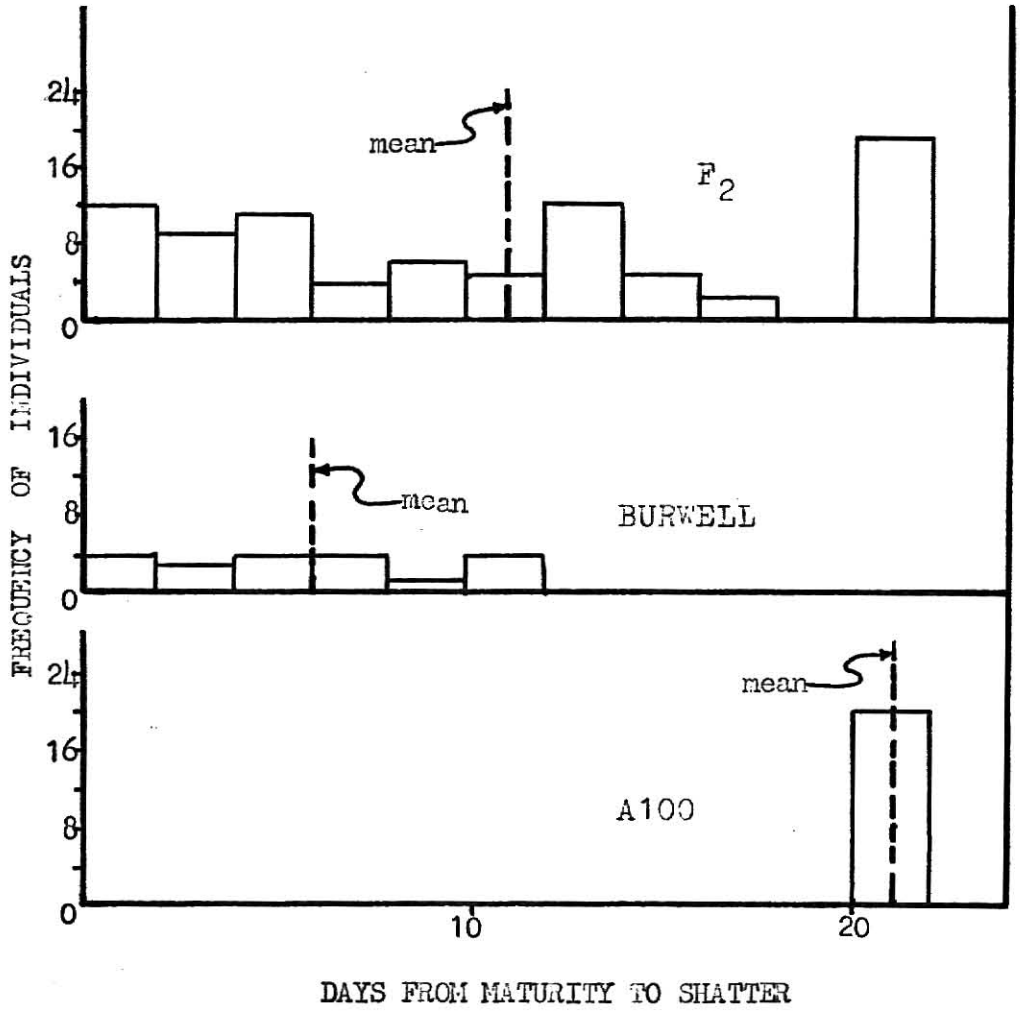


Fig. 4. Frequency distributions of all populations in 1972 for the 10S cross for shattering.

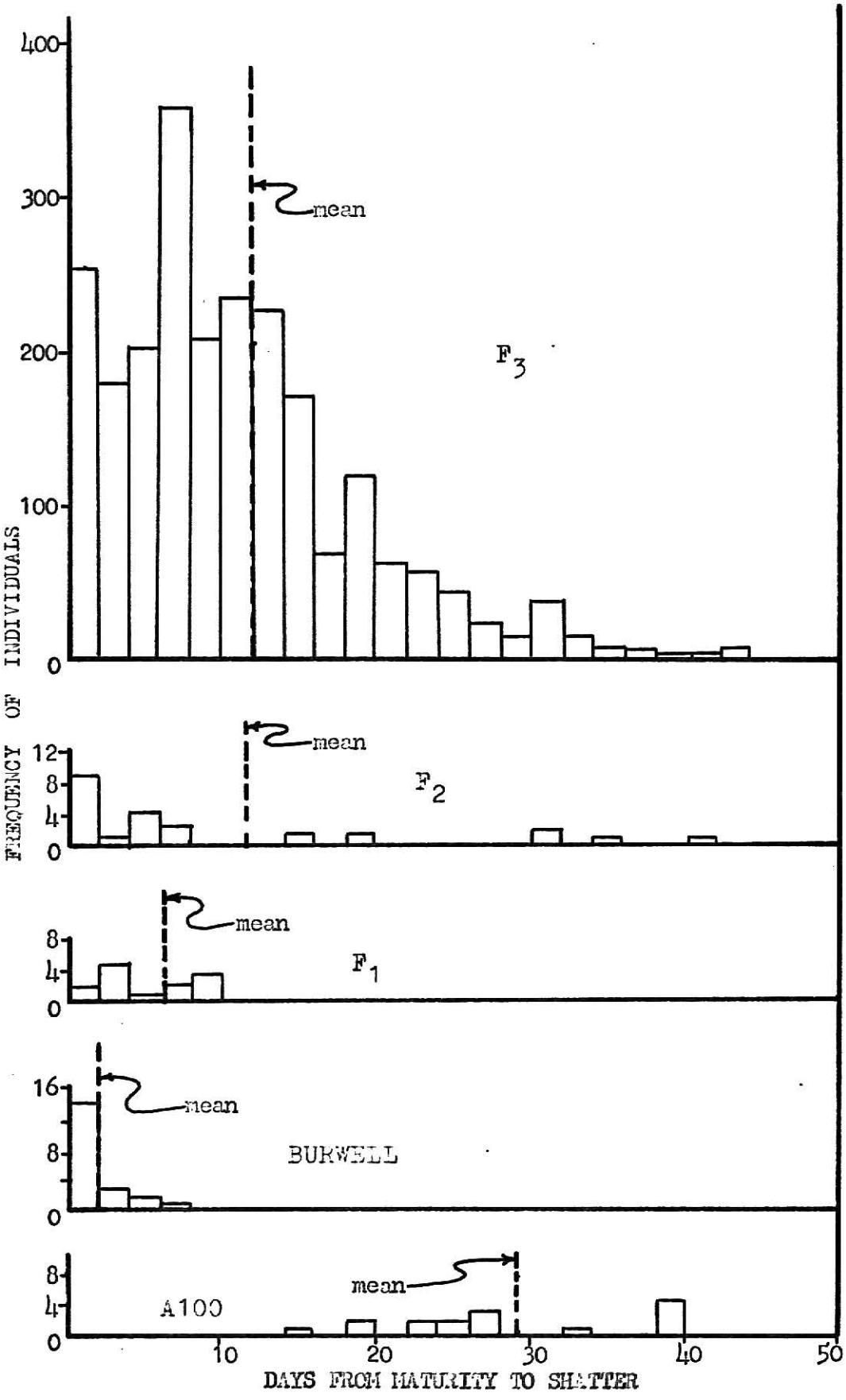


Fig. 5. Frequency distributions of the parental populations and F_2 generation in 1971 for the 118 cross for shattering.

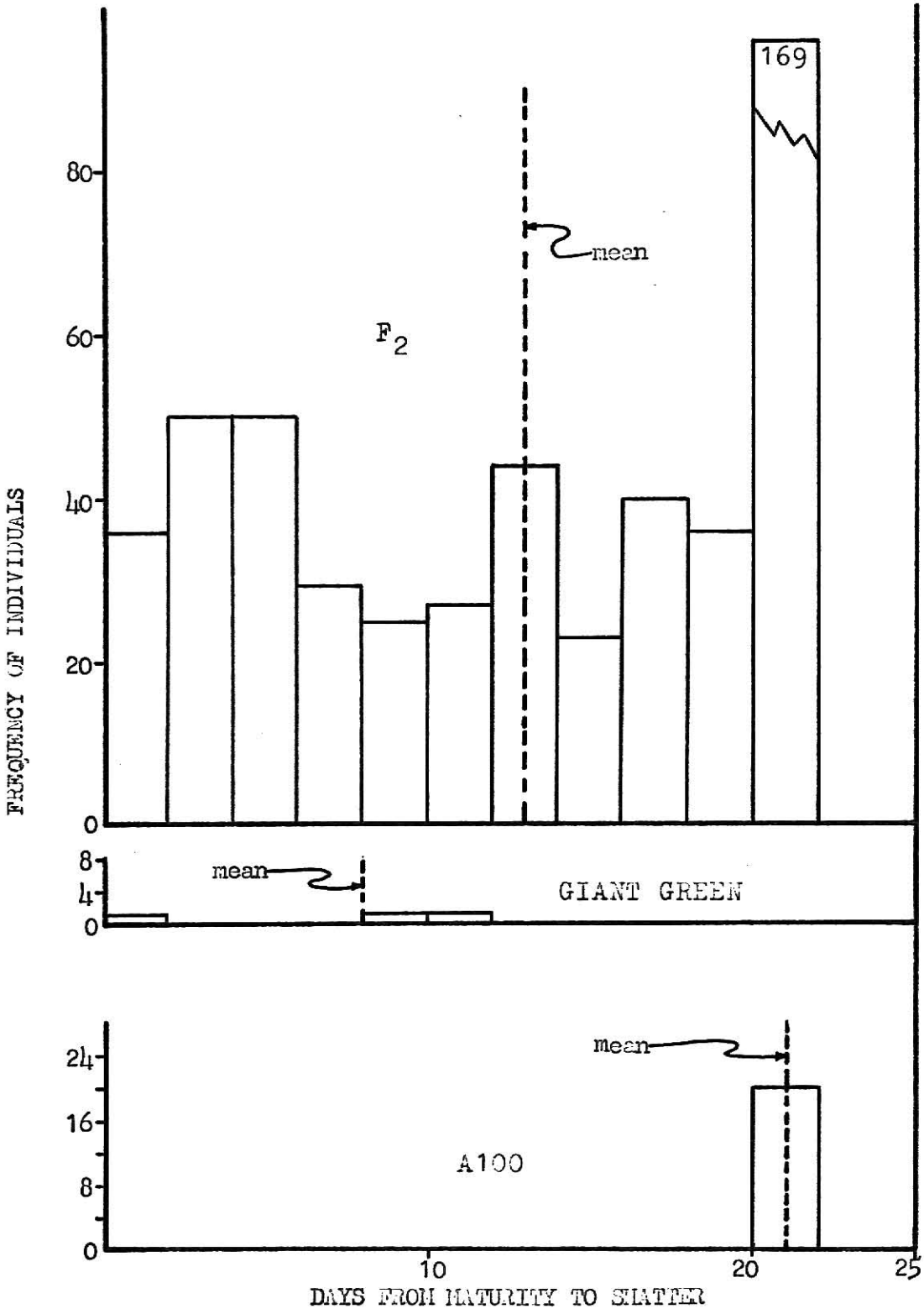
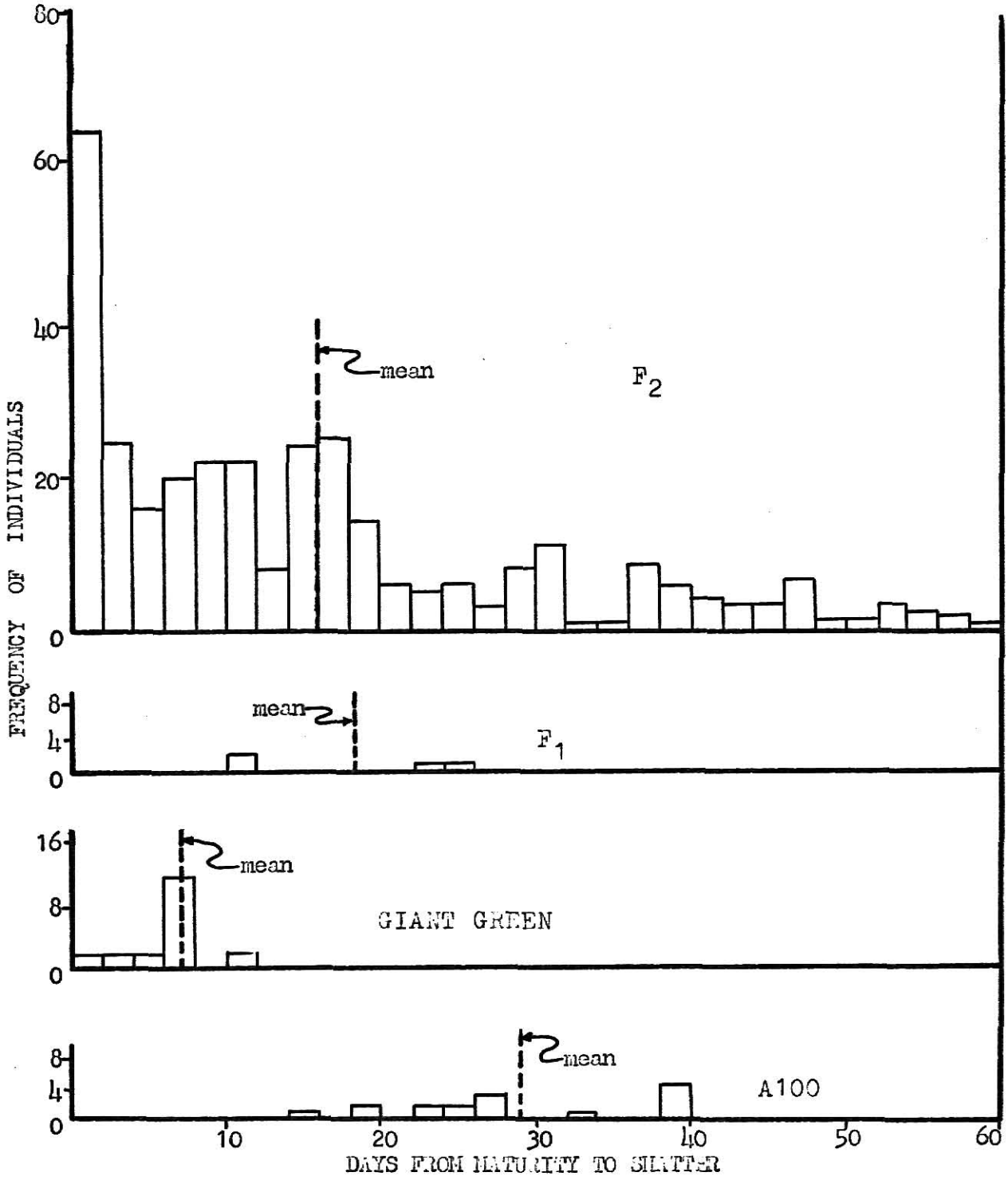


Fig. 6. Frequency distributions of all populations in 1972 for the 113 cross for shattering.



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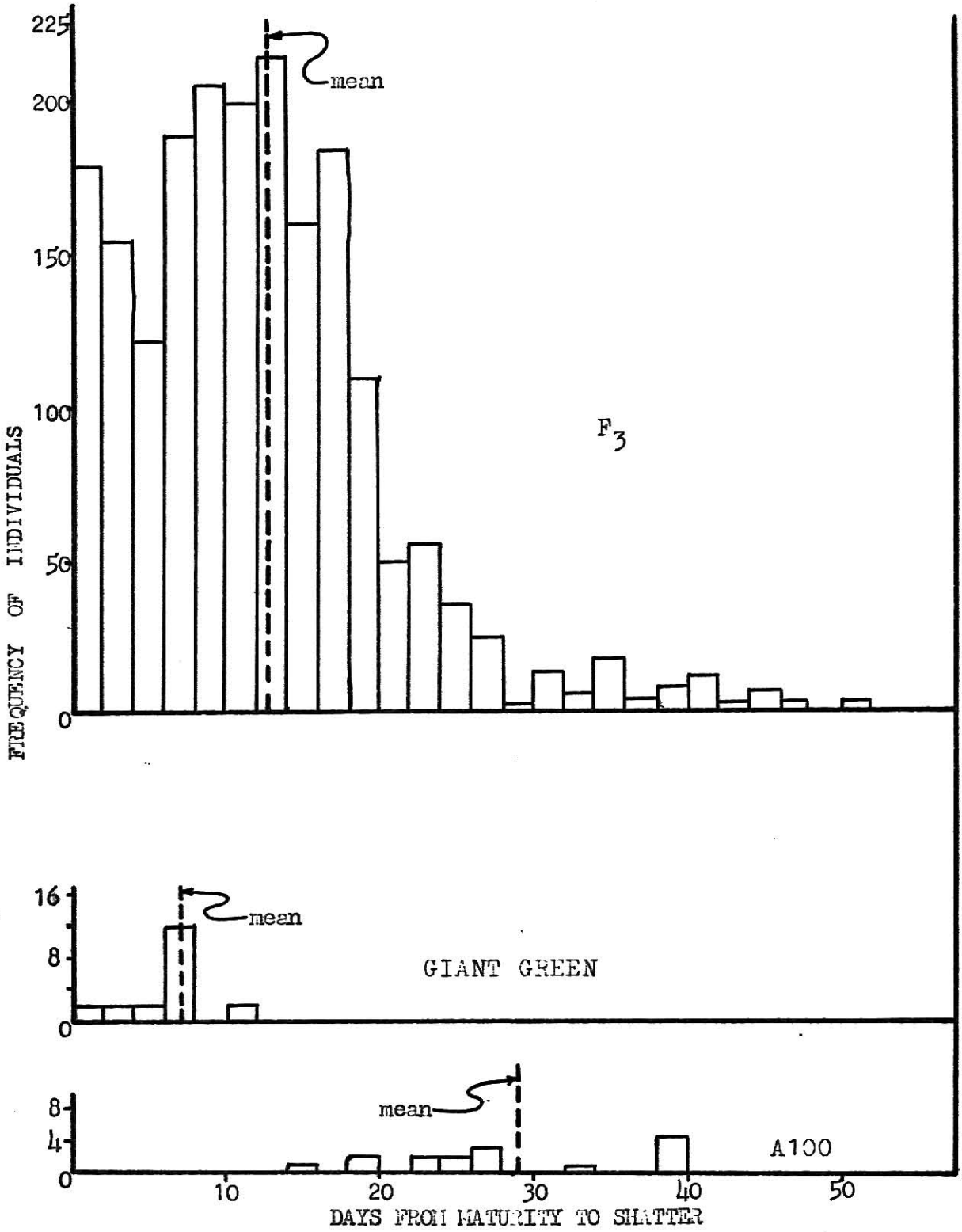


Table 3. Estimates of D and H for the indicated characters derived with Mather's equations for the three crosses.

Characters	Cross Numbers					
	9S		10S		11S	
	D	H	D	H	D	H
Shattering	-15.14	72.48	33.76	113.52	-19.56	210.96
Maturity	5.14	44.64	-9.24	193.52	92.38	108.08
Height	128.00	330.88	967.08	34.96	1621.64	-445.44
Seed weight	-7.20	33.52	-15.82	74.80	-43.06	170.48

Table 4. Broad sense estimates of heritability for two years for the indicated characters for the three crosses.

Characters	Cross Numbers					
	9S		10S		11S	
	1971	1972	1971	1972	1971	1972
Shattering	.75	.33	.89	.85	.77	.78
Maturity	.72	.53	.91	.56	.87	.74
Height	.59	.68	.87	.82	.93	.94
Seed weight	.93	.46	.97	.76	1.00	.31

Narrow sense estimates of heritability (Table 5) however, are low. Since these estimates were all based on the relationship of the F_2 to its F_3 progeny, the lowering of the variances of the F_2 generation by the early termination of data collecting in 1971 caused the low estimates of heritability. Another reason for these low narrow sense estimates could be the variation in weather conditions between the two years. Estimates in the 10S cross were higher than estimates in the other two crosses, for a larger percentage of the F_2 plants in this cross had shattered when the collection of data was terminated in 1971 than in the other two crosses.

Correlation coefficients between the F_2 and its F_3 progeny (Table 6) indicated a highly significant correlation in the 10S and 11S crosses but not in the 9S cross. The lack of correlation in the 9S cross is due to the environment's effect on the various genotypes in 1972.

Maturity

The distributions of the F_2 and F_3 generations in the frequency tables (Figures 7 and 8) indicate additive gene action for maturity in the 9S cross. In 1971 in the 9S and 10S crosses (Figures 7-10) there were larger differences between parents than in 1972. In the 10S cross in 1972 there were only two days difference in maturity while in 1971 there was an eight day difference between parental means. This difference was due to the difference in environmental conditions for the two years. In 1971 the means of the F_2 generations for all crosses (Figures 7-12) fell between the means of the two parents. In 1972, however, this was not the case, especially in the 10S and 11S crosses. In the 9S cross (Figures 7 and 8) the means of the F_1, F_2, and F_3 and parental populations in 1972 all fell within a six day span.

Table 5. Narrow sense estimates of heritability for the indicated methods and characters for the three crosses.

Method	Cross Numbers 9S	10S	11S
		Shattering	
Mather	0.00	0.33	0.00
Mahmud and Kramer	0.16	0.59	0.30
Waddle	0.06	0.41	0.07
		Maturity	
Mather	0.13	0.00	0.55
Mahmud and Kramer	0.40	0.38	0.69
Waddle	0.07	0.15	0.57
		Height	
Mather	0.26	0.84	1.06
Mahmud and Kramer	0.48	0.77	0.97
Waddle	0.20	0.58	0.76
		Seed Weight	
Mather	0.00	0.00	0.00
Mahmud and Kramer	0.09	0.11	0.00
Waddle	0.00	0.00	0.00

Table 6. Correlation coefficients for the same character between F_2 plants and their F_3 progeny for the three crosses.

Character	Cross number		
	9S	10S	11S
Shattering	.08	.64**	.27**
Maturity	.27**	.39**	.76**
Height	.45**	.76**	.87**
Seed weight	.00	.13	-.02

** significant at the 1% level

Fig. 7. Frequency distributions of the parental populations and F_2 generation in 1971 for the 9S cross for maturity.

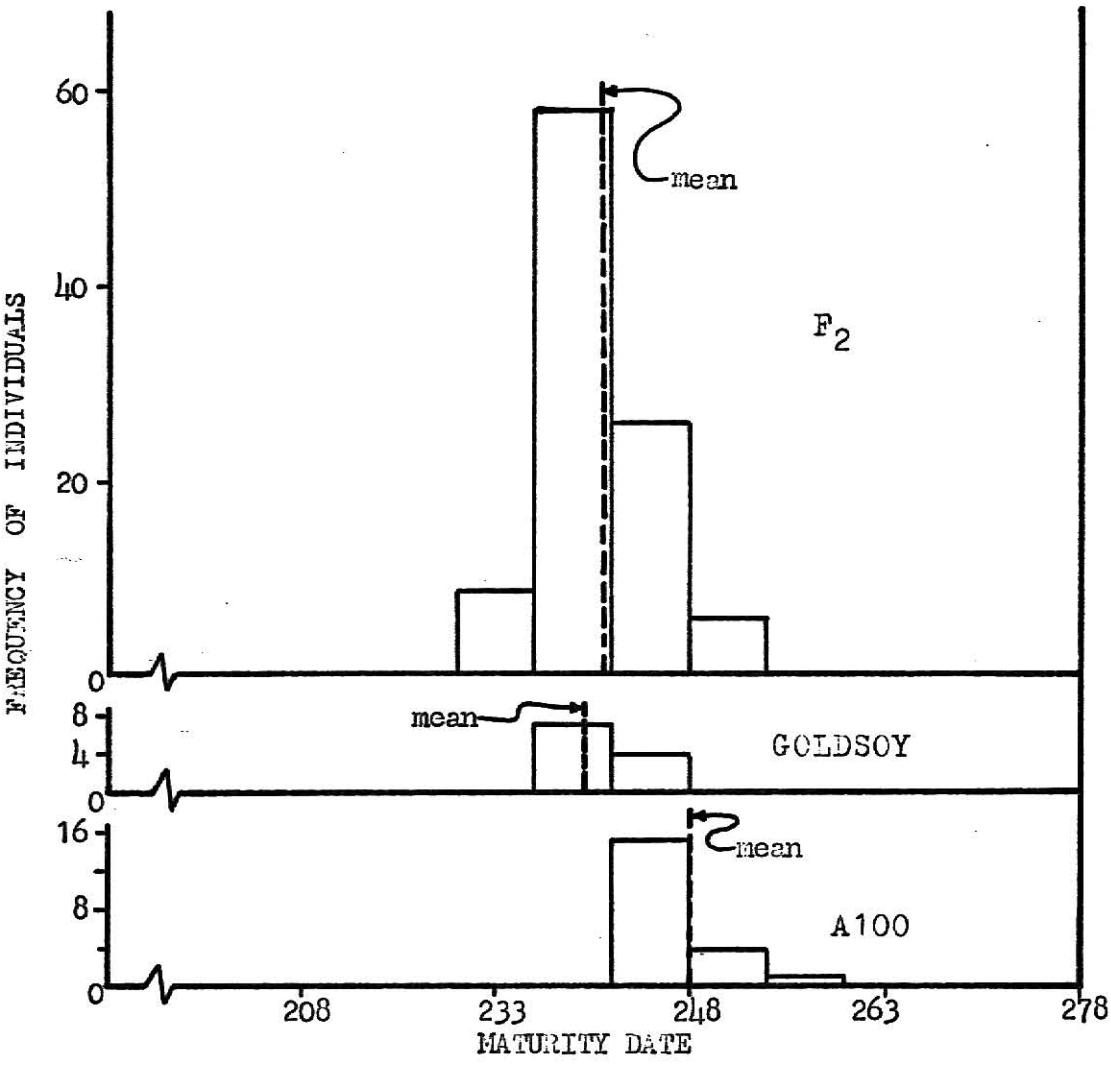


Fig. 8. Frequency distributions of all populations in 1972 for the 9S cross for maturity.

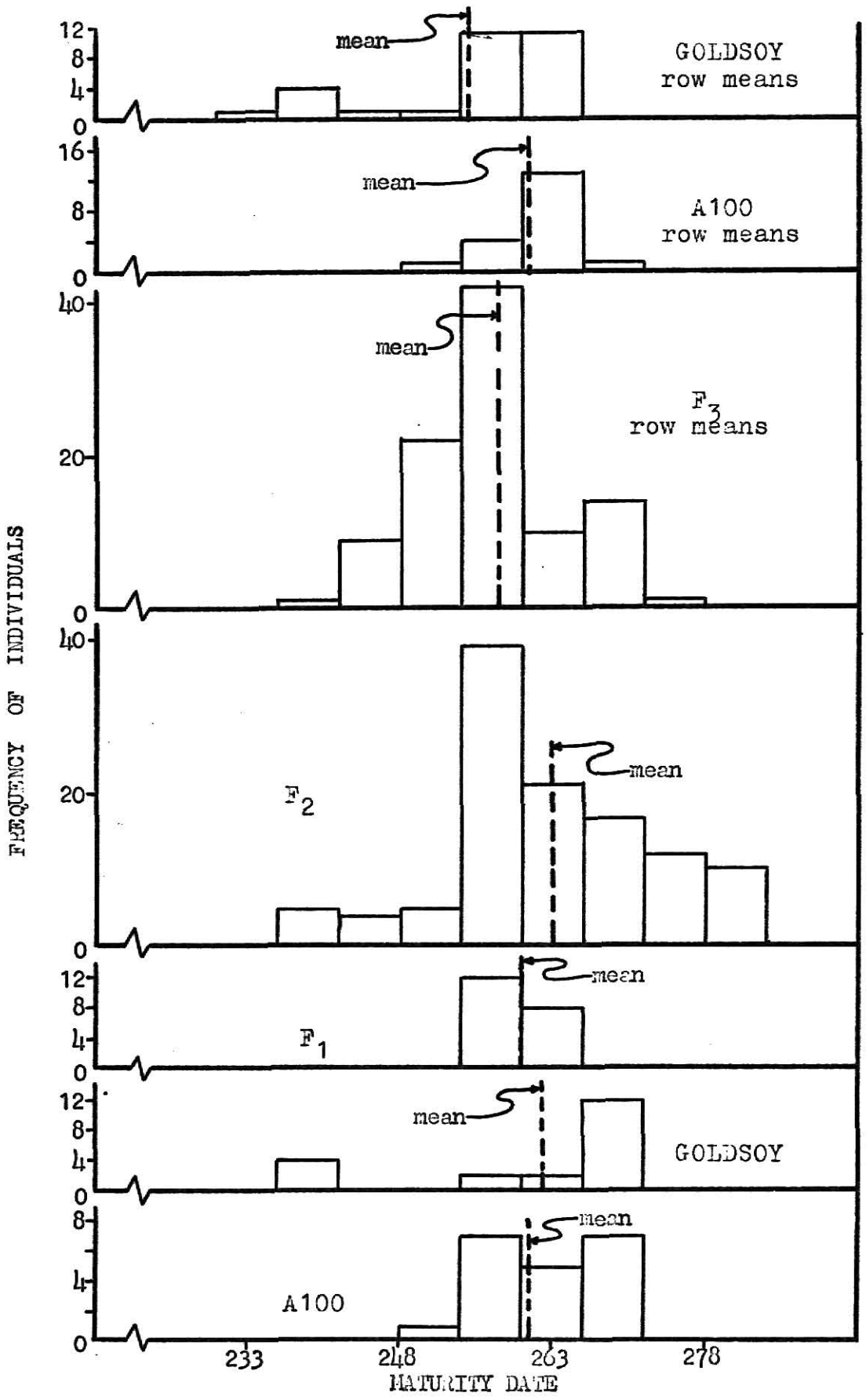


Fig. 8. (continued).

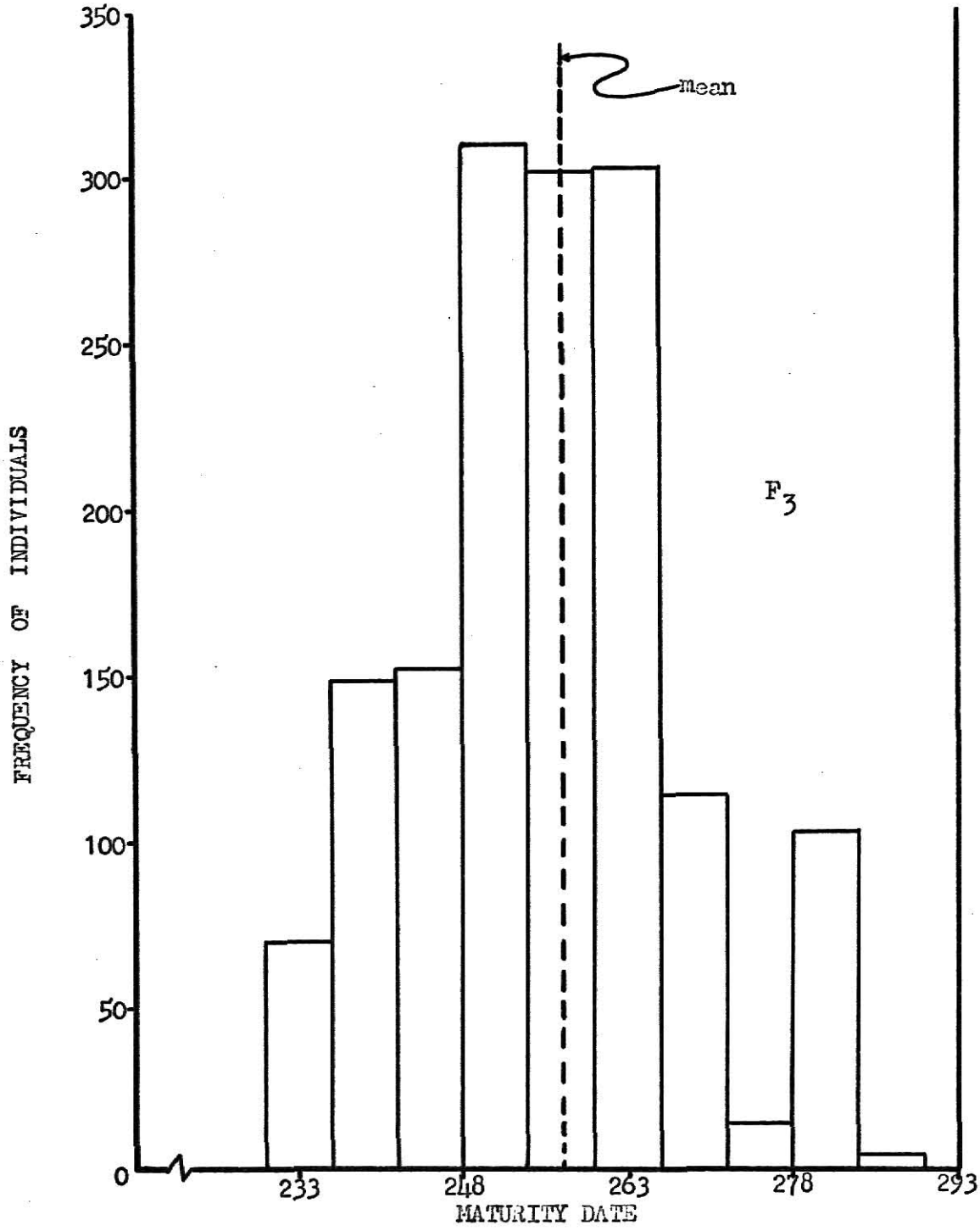


Fig. 9. Frequency distributions of the parental populations and F_2 generation in 1971 for the 10S cross for maturity.

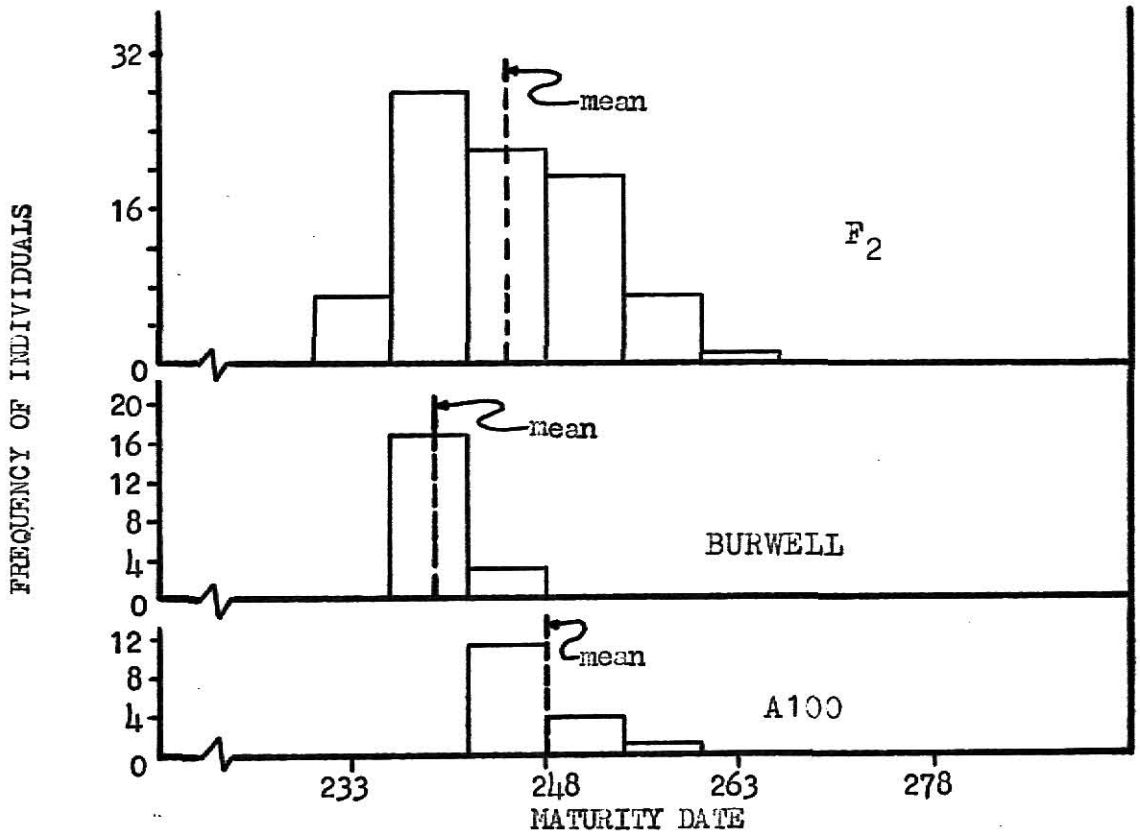


Fig. 10. Frequency distributions of all populations in 1972 for the 10S cross for maturity.

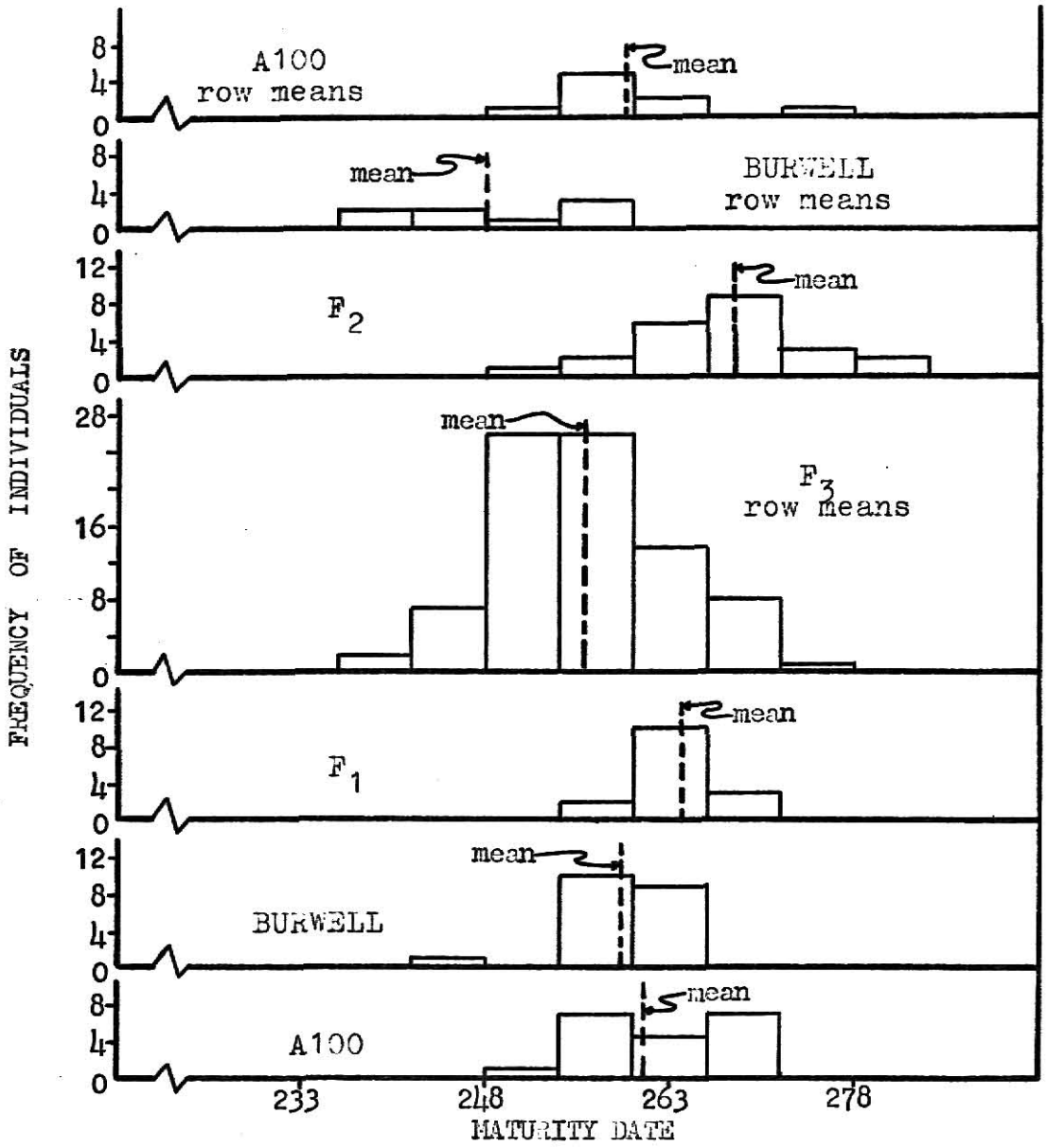


Fig. 10. (continued).

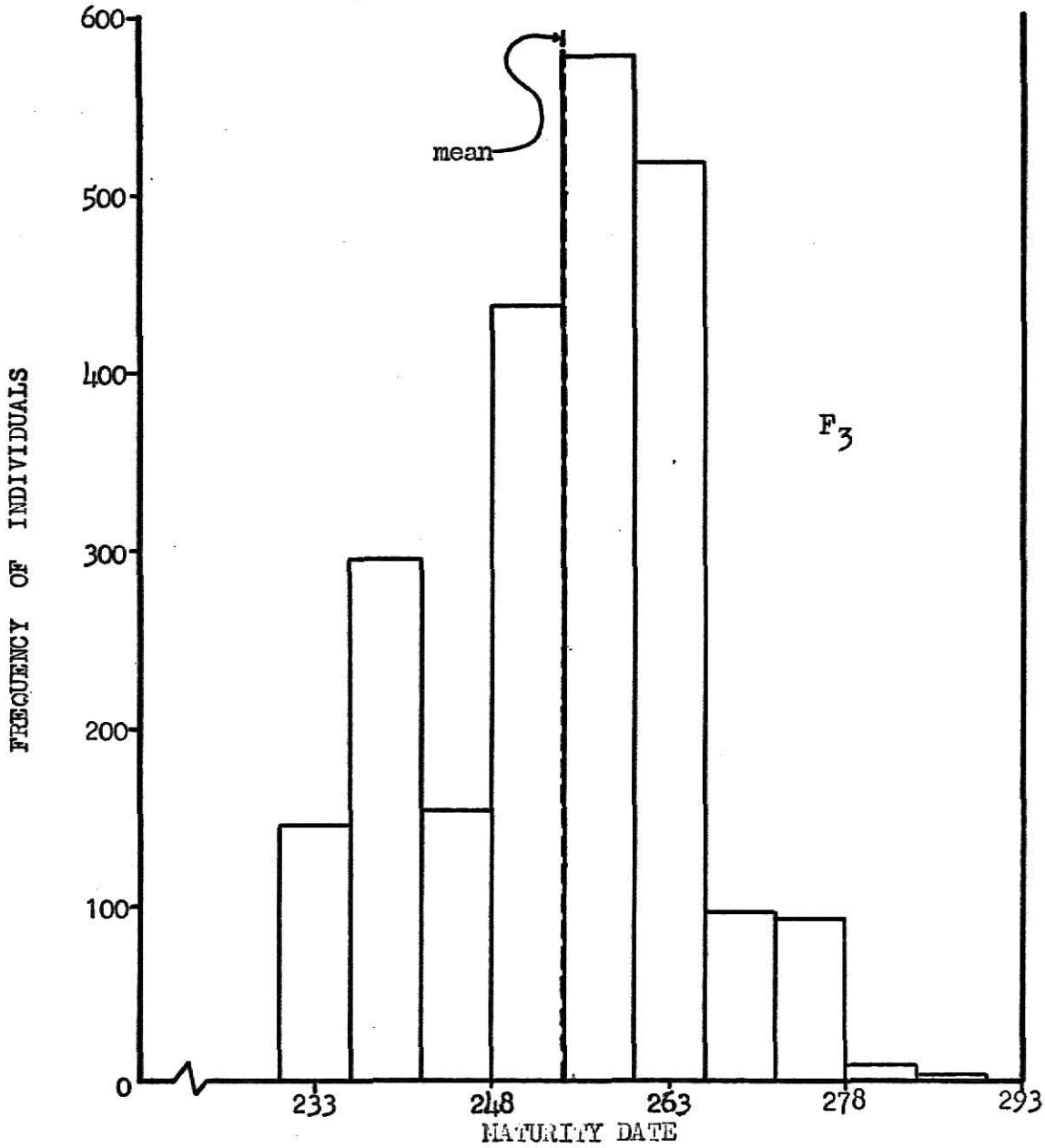


Fig. 11. Frequency distributions of the parental populations and F_2 generation in 1971 for the 11S cross for maturity.

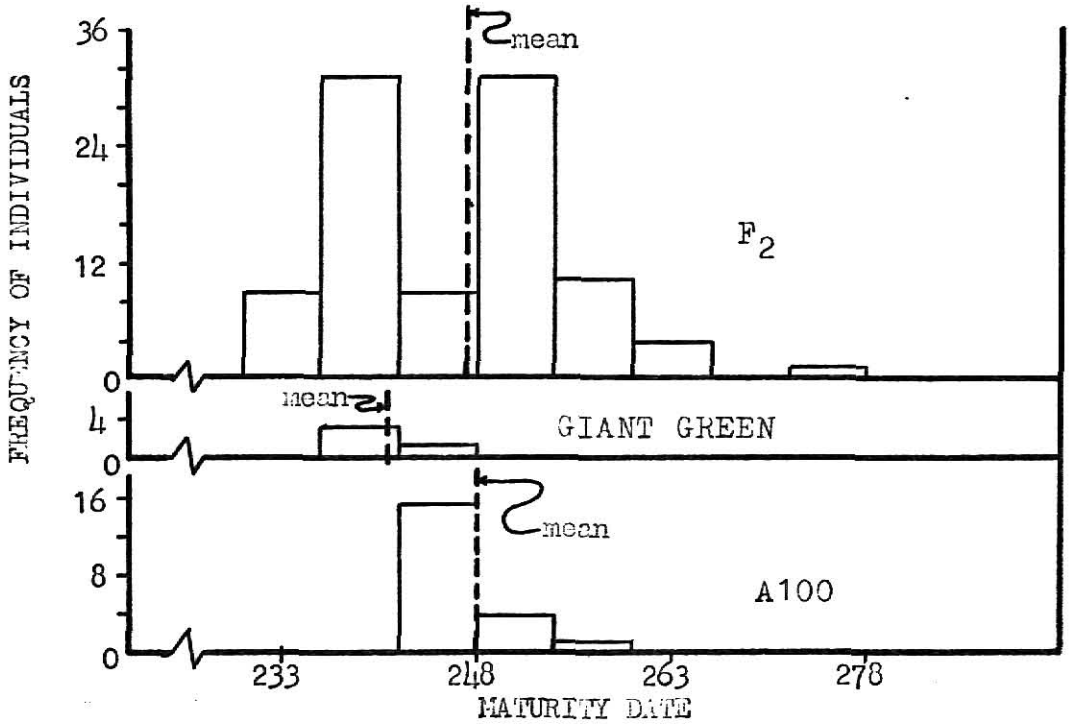


Fig. 12. Frequency distributions of all populations for 1972 for the 118 cross for maturity.

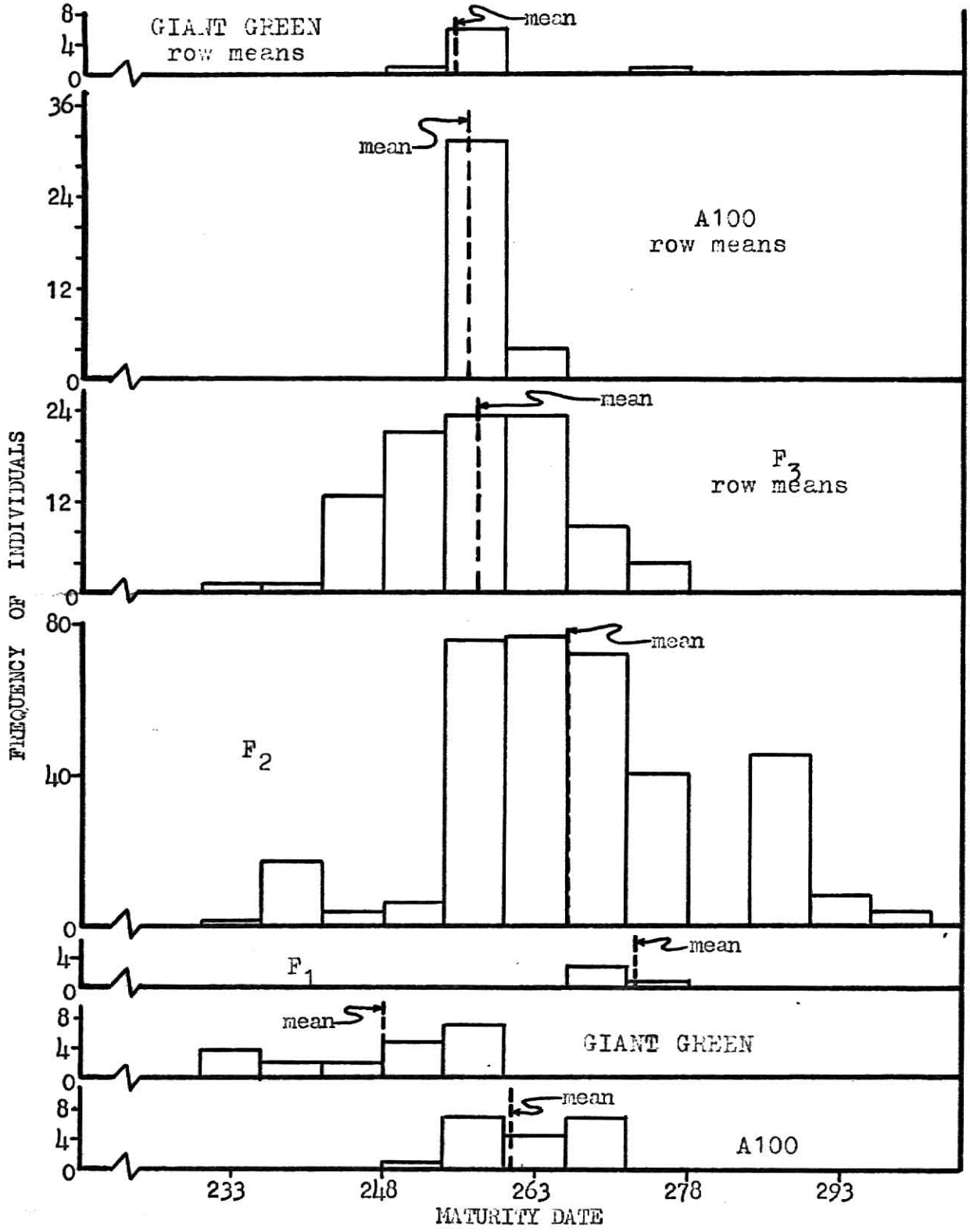
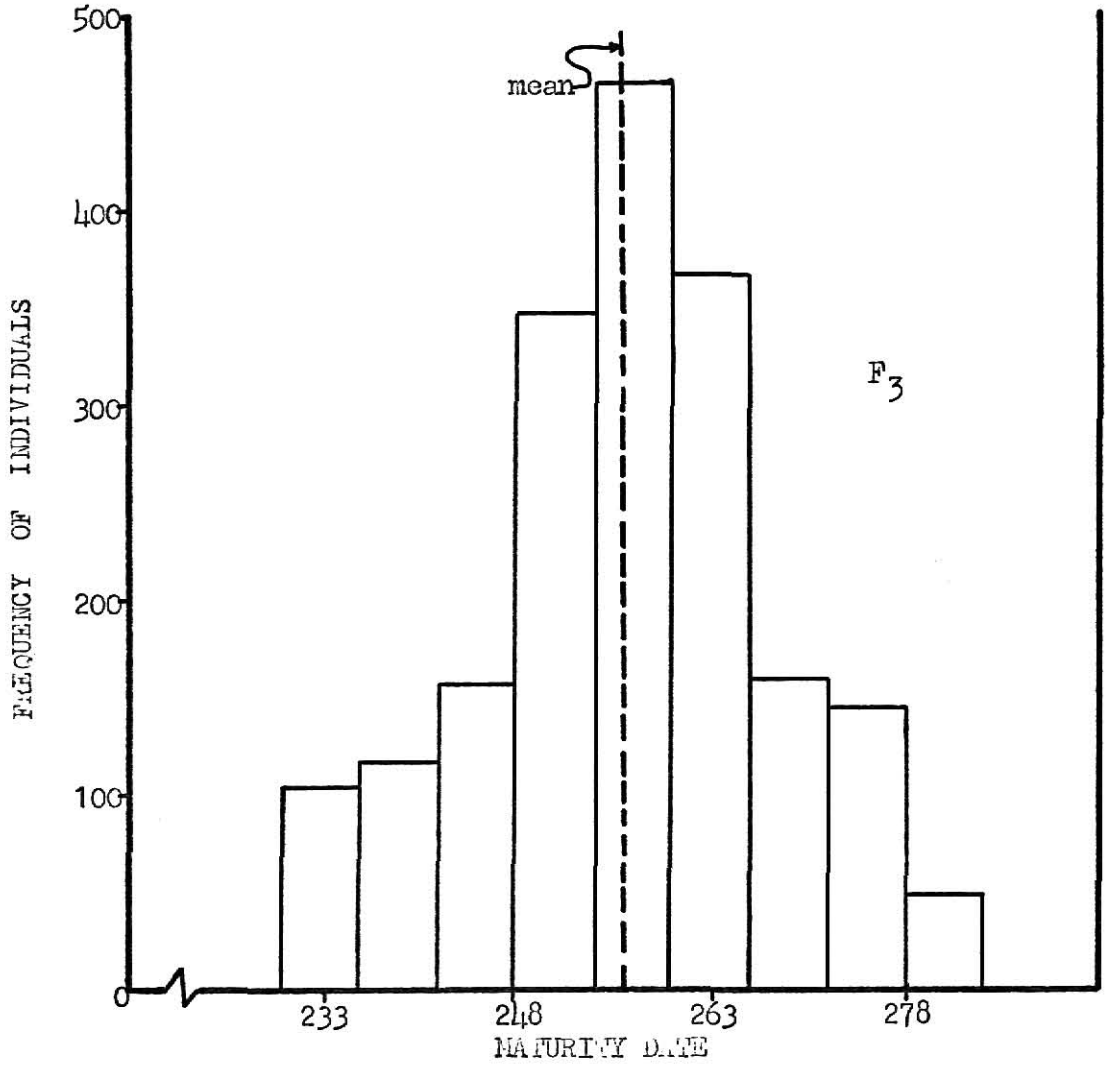


Fig. 12. (continued).



This and the transgressive segregation occurring in the F_2 and F_3 generations indicate that the parents are phenotypically similar but genotypically different.

In the 10S cross in 1972 (Figure 10) the mean of the F_2 generation was later than the late maturing parent. This could be due to poor germination of the F_2 seed resulting in a small plant number on which to collect data. The F_1 generation mean was later than the late maturing parent indicating perhaps a small amount of heterosis. Again in this cross transgressive segregation was shown in the F_2 and F_3 generations.

As in the other two crosses, in the 11S F_2 generation for both years and the F_3 generation for 1972 (Figures 11 and 12) there appears to be transgressive segregation. Heterosis is indicated by the mean of the F_1 generation being twelve days later than the latest parent. Bernard (1) described two genes that control maturity in soybeans that act in opposite directions; a major gene for earliness and a major gene for lateness. The interaction of these genes could give the normal distributions shown in the frequency tables (Figures 7-12), and may also help explain the differences in the additive portion of variance in the various crosses (Table 3). In the 9S and 10S crosses the additive portion is small while in the 11S cross it is fairly high. The small additive portion in the 9S and 10S crosses is due to small covariance values between F_2 plants and their F_3 progeny for these two crosses. In the 9S cross it is especially due to a low variance of the F_2 generation and a high variance in the F_3 generation.

Broad sense estimates (Table 4) are high in 1971 and slightly lower in 1972 due to the genotype's interaction with the environment. Compared to previous works (8,14,21,26,27), narrow sense estimates appear to be low with

the highest being in the 11S cross. The low heritabilities in the 9S and 10S crosses could be due to the genotypic similarity of the parental varieties. As could be expected from previous reports, correlations between F_2 plants and their F_3 progeny row means are all highly significant.

Height

In the 9S cross between two indeterminant types, frequency distributions (Figure 13) indicated additive gene action by the normal distributions in the F_2 generations. There was very little difference between parental varieties in 1971. The F_2 generation showed a large amount of transgressive segregation with its mean falling above that of the tallest parent. In 1972 a larger difference was shown in the means of the parents. The differences of the means of the two parents in the two years was due to the different environmental conditions in the two years. The means of the F_1 and F_2 generations in 1972 fell in between the parents indicating additive gene action. In the 10S cross between a determinant type and an indeterminant type, the distributions (Figure 14) indicate dominance in the direction of tallness. There were not enough F_2 plants available in 1972 to show any trends. The mean of the F_1 generation is closer to the mean of the tall parent also indicating dominant gene action in the direction of tallness. In 1971 and 1972 a small amount of transgressive segregation appeared in both directions indicating that the parents are phenotypically similar and genotypically different.

In the 11S cross also between a determinant and indeterminant type, there appeared to be partial dominance toward tallness (Figure 15). In both F_2 populations there was a large amount of transgressive segregation especially

Fig. 13. Frequency distributions of all populations for 1971 and 1972 in the 9S cross for height.

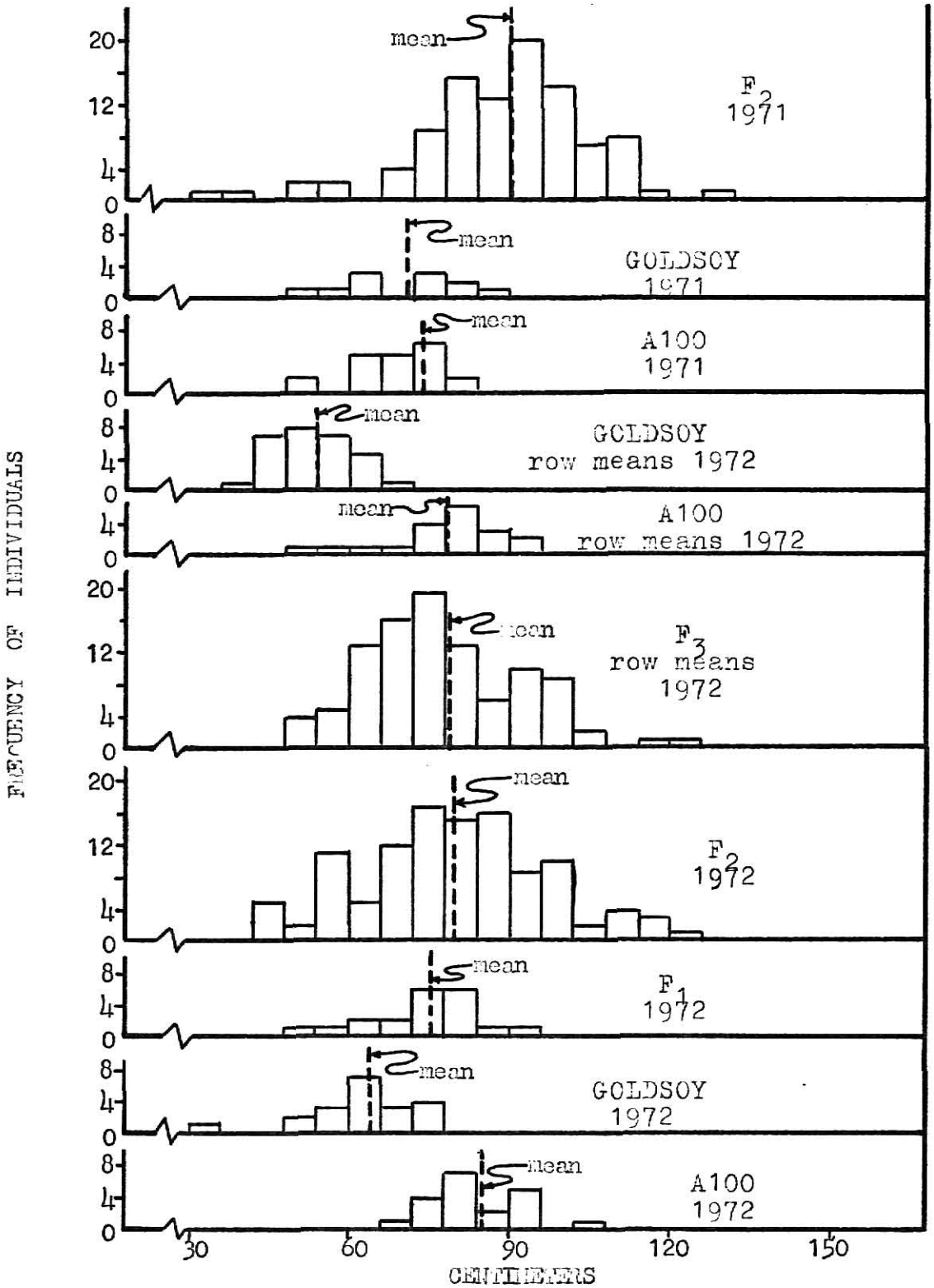


Fig. 14. Frequency distributions of all populations for 1971 and 1972 in the 10S cross for height.

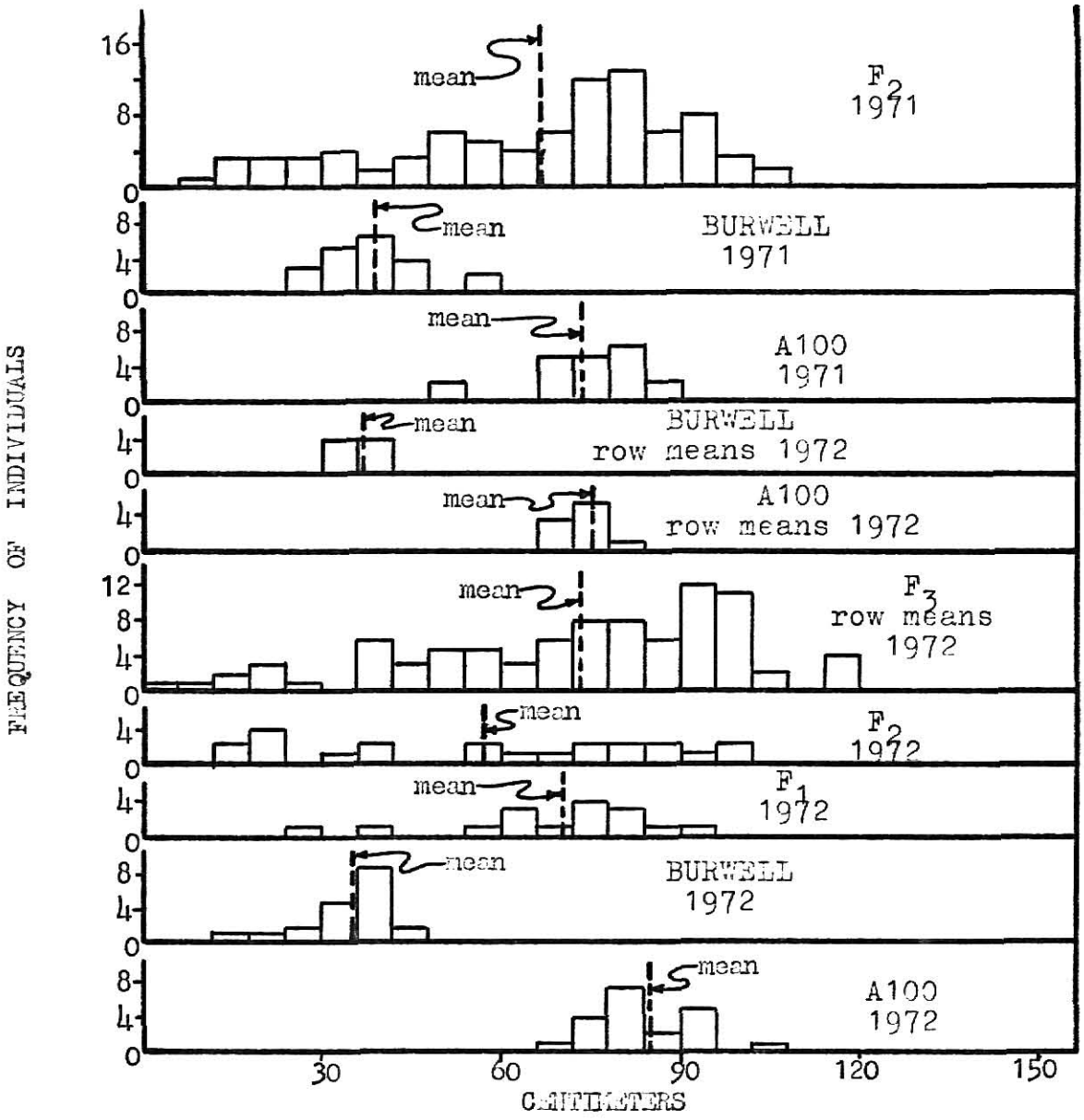
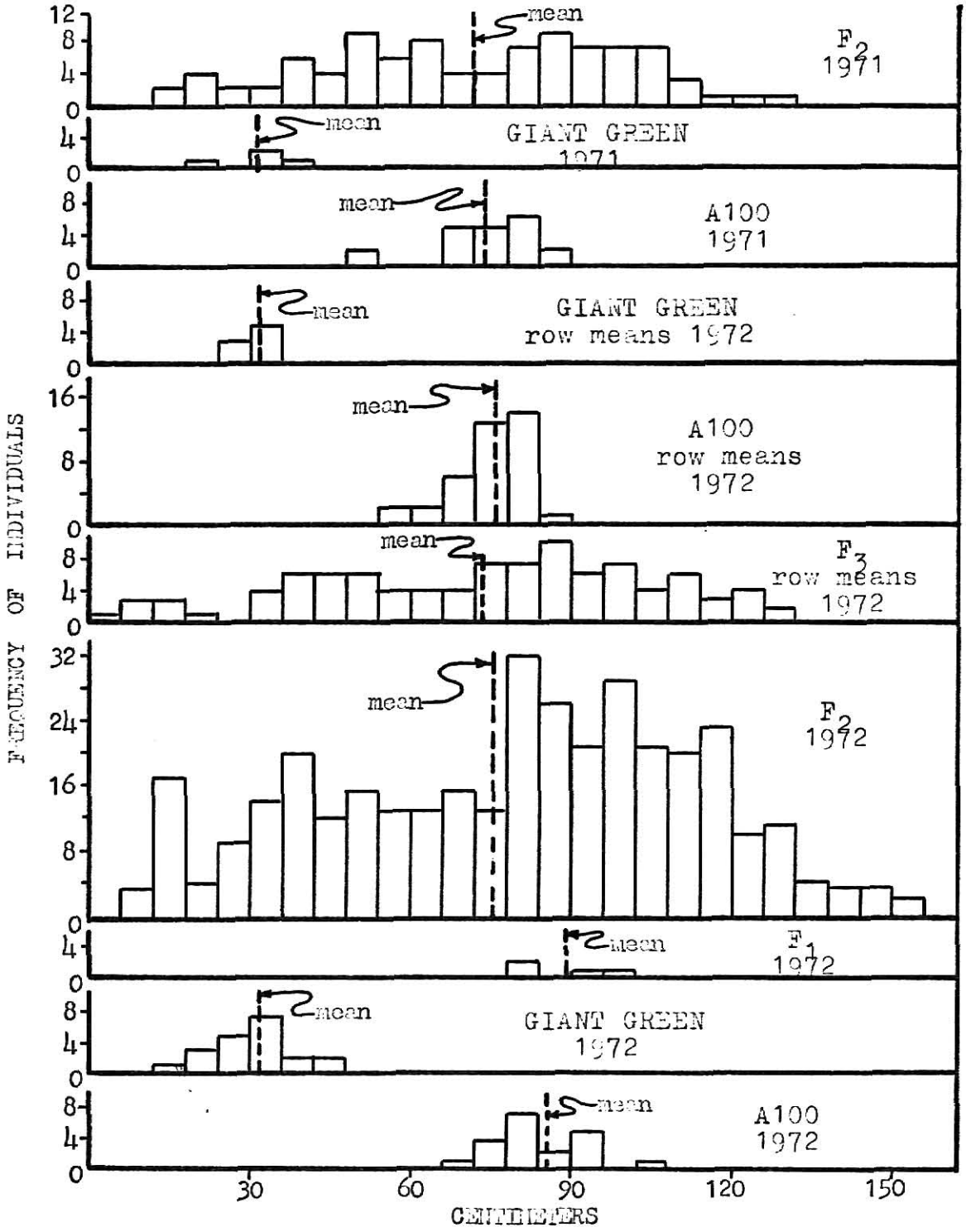


Fig. 15. Frequency distributions of all populations for 1971 and 1972 in the 11S cross for height.



in the direction of tallness which would indicate that the genotype of the parents contain different genes which interact with the environment to produce similar phenotypes. The F_1 generation shows slight heterosis by being slightly taller than the tallest parent. The means of the F_2 generation are between the parental means but much closer to the mean of the tallest parent, again indicating dominance for tallness.

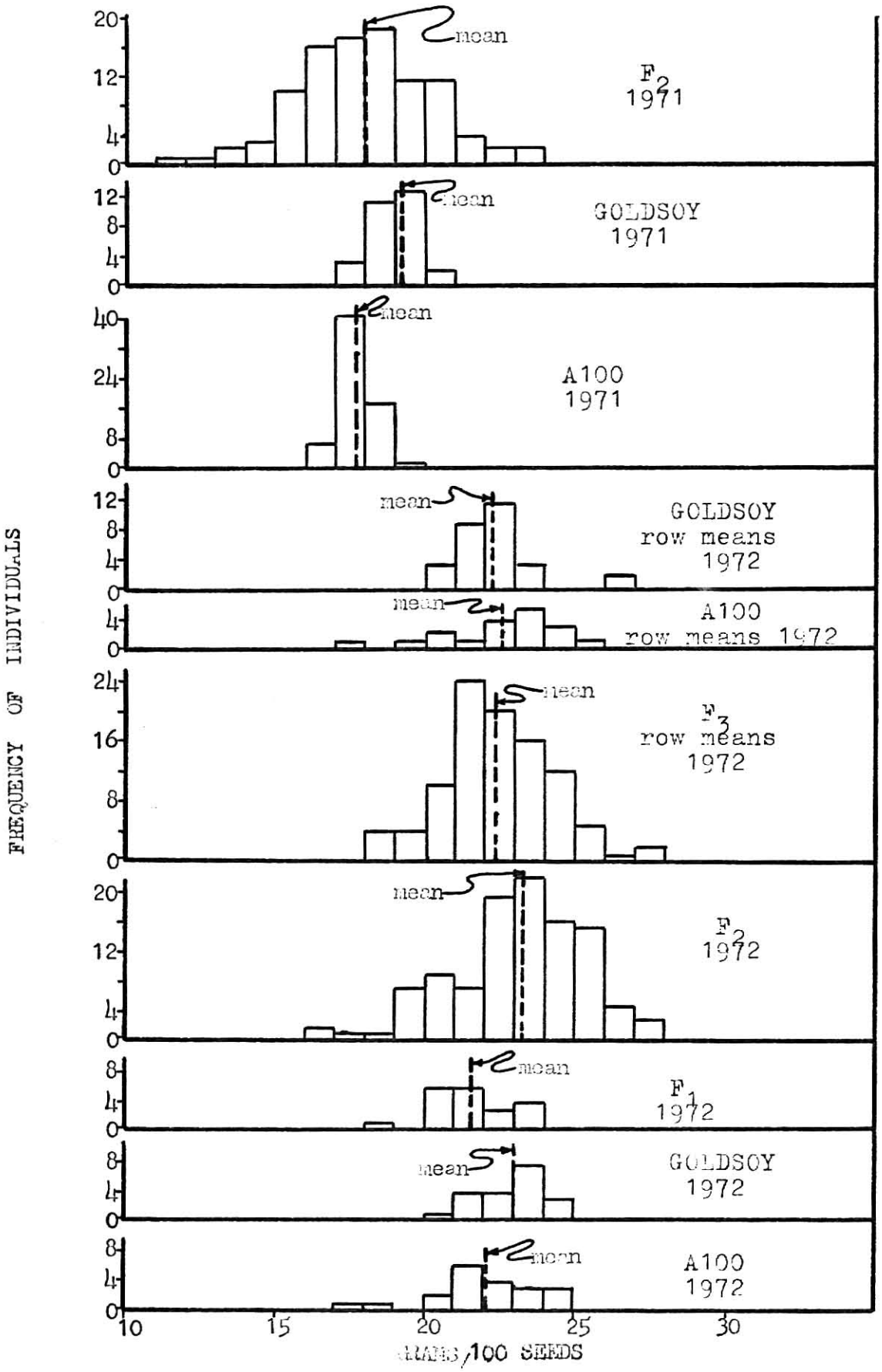
D and H values (Table 3) indicate additive gene action in all three crosses with large values of D. From the frequency distributions (Figure 13) this is what would have been expected for the 9S cross. However, for the other two crosses (Figures 14 and 15) just the opposite would have been expected. The large values in the 10S and 11S crosses could be due to the very large covariance values in these two crosses.

Broad sense estimates (Table 4) are high and estimates in the two years agree. In the 10S and 11S crosses narrow sense estimates (Table 5) are high which agrees with previous work (4,8,14,21,27). Estimates for the 9S cross however are low. These low values could be due to the parental lines being genetically similar thus lowering the heritability estimate. Correlations between the F_2 and its F_3 progeny (Table 6) are all statistically highly significant indicating that height is a highly heritable character.

Seed Weight

In the 9S frequency distributions (Figure 16) the F_2 generations for both years indicate additive gene action. Both of these F_2 distributions exhibit transgressive segregation. In 1972 the F_1 mean fell below the small seeded parent and the F_2 mean above the large seeded parent however, the difference between the means of the F_1 and F_2 generations was only 1.6 grams

Fig. 16. Frequency distributions of all populations for 1971 and 1972 in the 9S cross for seed weight.



per 100 seeds.

In the 10S cross (Figure 17) in 1972 there was variation in the large seeded type due to a genotype by environment interaction. In 1971 the F_2 distribution appeared to be normal while in 1972 it appeared to be slightly skewed. However, if the large amount of variation in the large seeded type is taken into consideration, it could cancel out the skewness in the 1972 F_2 frequency table. Also the F_3 row means, which should have a normal distribution as in the F_2 in 1971, turned out to have a slightly skewed distribution. The means of the F_1 and F_2 distributions, however, are closer to the small seeded parent indicating partial dominant gene action in the direction of small seed size.

In the 11S cross, F_2 frequency distributions (Figure 18) are unimodal approaching a normal type of distribution, and means of the F_2 generations are intermediate between the parents indicating additivity. In both distributions transgressive segregation occurs. As with the large seeded type in the 10S cross, the large seeded parent in this cross has a large amount of variation in 1972 due to genotype by environment interaction. The mean of the F_1 generation exceeds the large parent indicating heterosis.

Values for D and H (Table 3) however indicate nonadditive gene action. Previous work by Weber (26) indicates that several genes control the inheritance of seed size. The frequency distributions indicating additivity could be the result of many genes interacting among themselves and with the environment resulting in the normal distributions (Figures 16,17,18).

Broad sense estimates of heritability in 1971 (Table 4) are all high but in 1972 they are lower, due to the adverse weather conditions in 1972. Narrow sense estimates (Table 5) are all low. This low heritability as Hanson

Fig. 17. Frequency distributions of all populations for 1971 and 1972 in the 10S cross for seed weight.

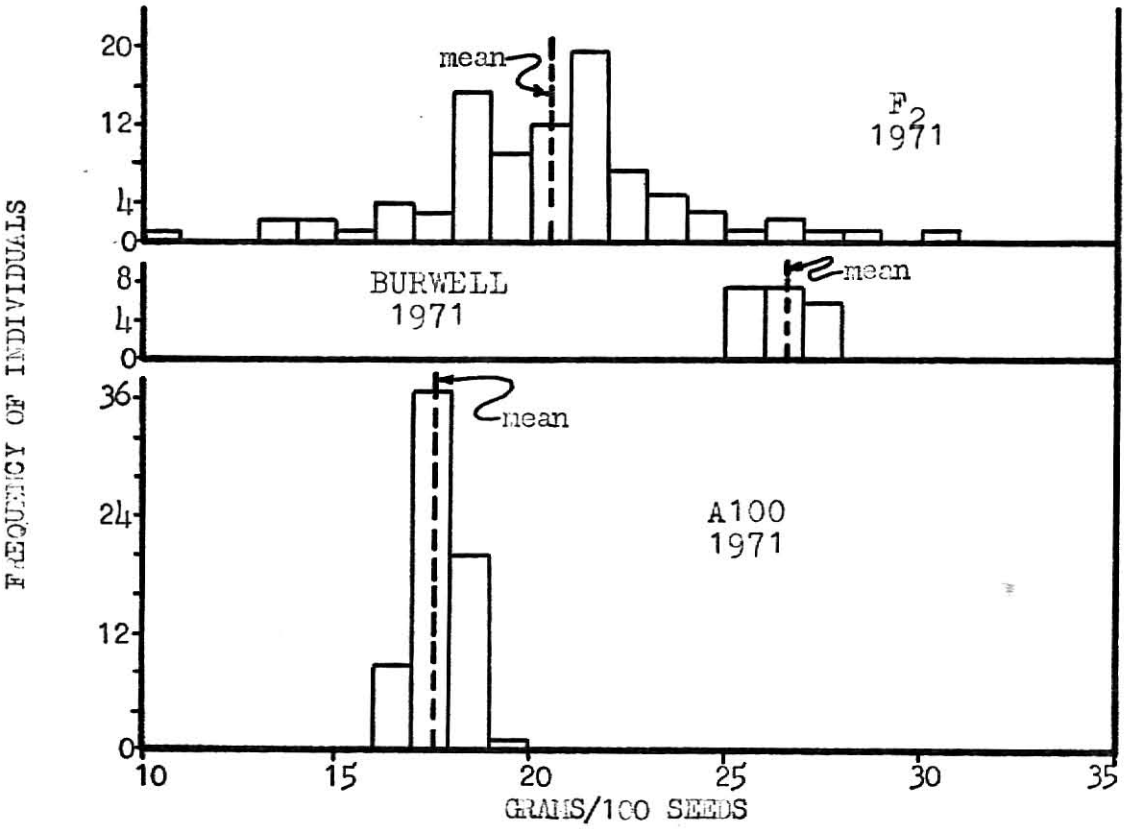


Fig. 17. (continued).

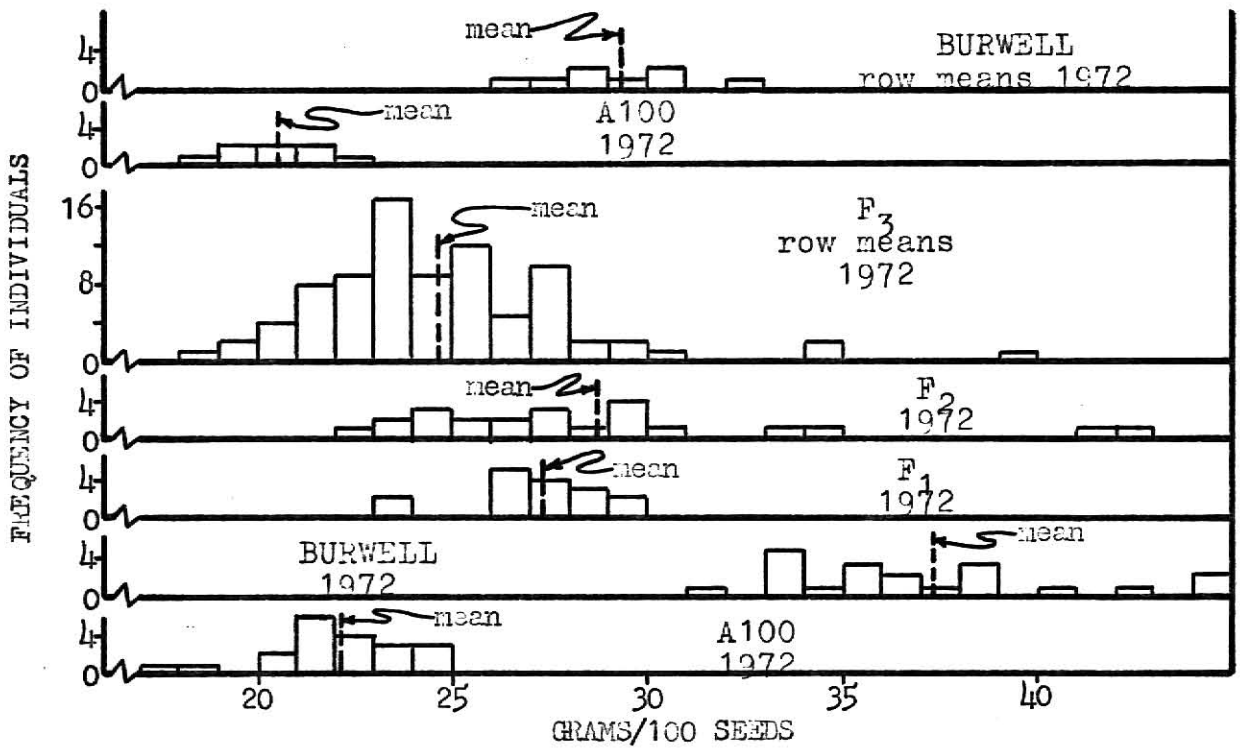
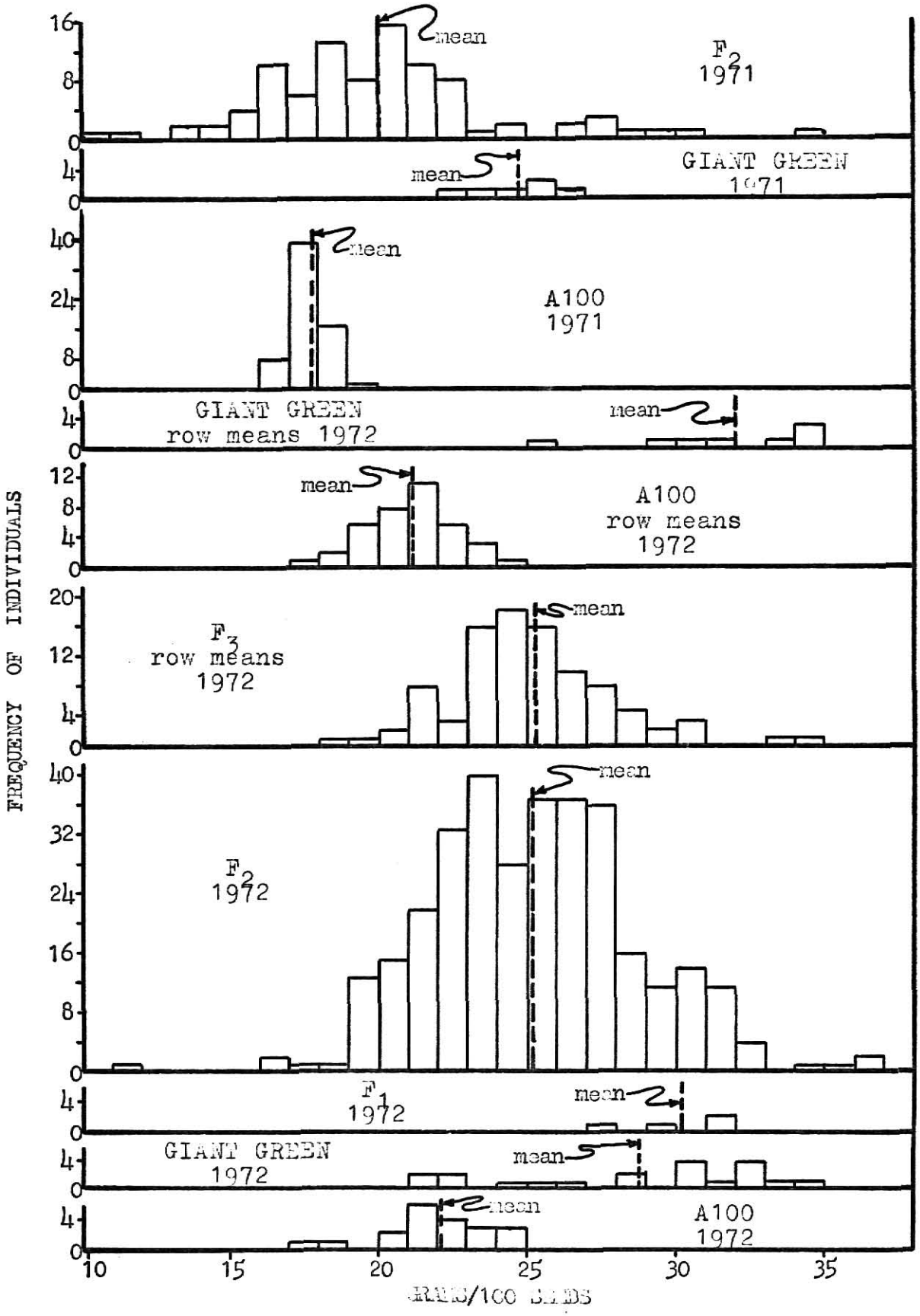


Fig. 18. Frequency distributions of all populations for 1971 and 1972 in the 11S cross for seed weight.



and Weber (8) indicated can be due to environmental stresses during seed development confounded with the maturity ranges of different genotypes causing considerable genotype by environment interactions. Also another factor in this study could be the large variation in weather conditions between the two years which resulted in no correlations between the F_2 generation and its F_3 progeny in any of the crosses.

Correlations

Selection against shattering will result in selection for late maturing tall lines or lines with large seed size, for there are positive correlations between these characters (Table 7). There is a negative correlation though between seed size and height. If a soybean breeder is interested in taller plants with large seed size he will have difficulty in reaching his goal due to the negative correlation. The genotypic correlations are higher than the phenotypic correlations indicating that the relationships between the characters is genetic.

Table 7. Genotypic and phenotypic correlation coefficients for the F_2 and F_3 generations between the indicated characters for the three crosses.

Cross number	F_2		F_3	
	Genotypic	Phenotypic	Genotypic	Phenotypic
		Shattering x Maturity		
9S	+.43**	-.15	+1.06**	-.16
10S	+.28	+.037	+ .49**	+.076
11S	-.21**	-.22**	+ .15	+.12
		Shattering x Height		
9S	+.29**	+.23*	+1.03**	+.40**
10S	+.18	+.16	- .04	+.02
11S	-.23**	-.22**	+ .31**	+.29**
		Shattering x Seed Weight		
9S	+.29**	-.01	+ .37**	+.01
10S	+.15	+.06	- .20	-.19
11S	+.41**	-.18**	- .12	-.20
		Height x Maturity		
9S	+.37**	+.33**	- .32**	+.21*
10S	+.24	+.13	- .05	+.06
11S	+.49**	+.47**	+ .62**	+.58**
		Seed Weight x Maturity		
9S	+.65**	+.65**	+2.56**	+.55**
10S	+.53**	+.49*	+ .35**	+.46**
11S	+.34**	+.46**	- .06	+.08
		Seed Weight x Height		
9S	+.38*	+.37**	- .01	+.26**
10S	-.15	-.07	- .39**	-.34**
11S	-.16**	+.02	- .76**	-.31**

* significant at the 5% level

** significant at the 1% level

VI. CONCLUSIONS

In these studies shattering resistance and height were controlled by partial dominant gene action and seed size and maturity by additive gene action. In crosses between indeterminant types, inheritance of height appeared to be controlled by additive gene effects. In crosses between determinant and indeterminant types inheritance of height appeared to be controlled by partial dominance in the direction of tallness.

Broad sense estimates of heritability are high for all characters, however narrow sense estimates are low for all characters except height. The F_2 generation and its F_3 progenies are significantly correlated for all characters except seed weight. Correlations between characters were positive except for a negative correlation between seed weight and height. Selection for height can be practiced in early generations. Selection for the other characters may be practiced in early generations but success depends on the type of environment encountered.

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THE INHERITANCE AND INTERRELATIONSHIP OF POD DEHISCENCE AND SOME OTHER AGRONOMIC CHARACTERS IN SOYBEANS

by

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B. S., Kansas State University, 1971

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1973

An experiment was performed in Manhattan, Kansas in 1971 and 1972 to study the inheritance of shattering in soybeans and its relation to some other agronomic characters and also study the inheritance of maturity, height and seed weight and the relationship of these characters with each other.

Inheritances of shattering, maturity, height, and seed weight were studied in the F_1, F_2, and F_3 generations of the following soybean crosses: 'A100' x 'Goldsoy' (9S); 'A100' x 'Burwell' (10S); 'A100' x 'Giant Green' (11S). Data indicates that shatter resistance and tallness are controlled by partially dominant genes and seed size and maturity by additive gene action.

Broad sense estimates of heritability in all three crosses were high for all four characters while, except for height, narrow sense estimates of heritability were low. Except for seed weight, the F_2 generation and its F_3 progenies for the other three characters are significantly correlated. Based on F_3 population means shatter resistance and maturity are significantly positively correlated genotypically in the 9S and 10S crosses. Shatter resistance and seed weight are significantly positively correlated genotypically only in the 9S cross. Height and shatter resistance are significantly positively correlated both phenotypically and genotypically in the 9S and 11S crosses. In the 9S and 10S crosses there is a significant positive correlation between seed weight and maturity. There is a negative correlation between seed weight and height in the 10S and 11S crosses. Correlations between height and maturity vary between crosses with a significant positive correlation in the 11S cross, no correlation in the 10S cross, and a significant negative genotypic and positive phenotypic correlation in

the 9S cross. Genotypic correlations in most cases were larger than phenotypic correlations.