INHERITANCE OF TIME OF FLOWERING AND MATURITY AND THEIR ASSOCIATION WITH OTHER AGRONOMIC CHARACTERS IN SOYBEAN (GLYCINE MAX (L.) MERRILL)

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CHAPTER I

INTRODUCTION

The soybean, Glycine max (L.) Merr., is a member of the family Leguminoseae, subfamily Papilionoideae Hermann (11). Several hundred species have been assigned to the genus in the past, but Hermann now assigns only ten, including a few subspecies. The species are grouped in three subgenera. G. max and G. ussuriensis Regel and Maack comprise the subgenus Soja (Moench) F. J. Herm. G. max is said by Hermann to be "a derivative of G. ussuriensis or some Asiatic ancestor closely related to it."

The soybean, a native of eastern Asia, is one of the oldest crops of that area and is considered to be a vital grain. It provides human food, animal feed, and materials for many industrial uses. It also complements the contribution of most other major crops. The P.A.G. (Protein Advisory Group) of the United Nations System recommends urgent research attention to eight major species of food legumes: dry beans, pigeon peas, cow peas, chick peas, broad beans, peas, and the two leguminous oilseeds peanuts and soybeans.

To meet the growing world demand, the plant breeder then has the challenge to increase cereal legume crop yields, while meeting consumer acceptance qualities and priorities for genetic improvement of various nutritional factors. A better understanding of the mechanisms of inheritance for agronomic characters is essential if efficient and

directed improvements are to be achieved. Knowledge of the type of gene action involved in the expression of different characters would be useful in planning desired breeding programs of soybean cultivars.

The research problem reported herein was designed to detect the mode of inheritance of the flowering character and its association with maturity, plant height, grain yield/plant, and weight of 100 seed/plant in a soybean cross (Lee 74 x Bonus).

CHAPTER II

REVIEW OF LITERATURE

Maturity to Fit the Area of Production and Photoperiodism

Proper maturity is the most important factor in the adaptation of a soybean variety to a particular latitude. Parker and Borthwick (23) stated that the soybean plant is peculiarly sensitive to the number of hours of darkness to which it is subjected each day for the hours of darkness determine whether or not it will produce flowers. Plants of certain varieties are incapable of producing flowers unless they receive ten or more hours of darkness each day. Generally all varieties flower more quickly with dark periods of fourteen to sixteen hours than they do with shorter ones. This sensitivity to darkness determines the latitude where a variety may be adapted. Summer days in the northern states and Canada are known to be much longer and the period of darkness much shorter than the southern states. Varieties adapted to the northern latitudes express the capability of initiating flower buds with the short periods of darkness found there in midsummer. Varieties adapted to the southern states must have a long period of darkness to flower satisfactorily.

It is important to mention that when this phenomenon was first studied it was believed that the length of the period of light (day length) was the controlling factor. As a result varieties were

sometimes classified as long-day or short-day varieties. However, it has been learned that the length of the period of darkness rather than the length of the period of light determines when flowering is initiated. Poehlman (24) pointed out that from north to south, most varieties have a very narrow range in which they will mature properly and produce satisfactory yields. Varieties moved northward may not mature, whereas varieties moved southward flower early and develop seed while temperatures are still high. Thus, under the latter conditions seed yields will be low and seed will be inferior in quality.

It was also observed very early that the soybean varieties introduced into America from different latitudes in the Orient were always adapted to areas of about the same latitude in the United States. However, local testing of introduced varieties is needed to determine the appropriate varieties for each region. For convenience in testing, soybean varieties have been classified into ten maturity groups which range from very early-maturing varieties adapted to the short summers and long days of southern Canada and the northern states to very late, short-day varieties grown in the Gulf Coast region. The maturity groups are designated by Roman numerals, starting with 00 for the earliest-maturing group grown in the northern United States and Canada and ending with VIII for the latest-maturing group grown in the southernmost area of soybean production in the United States. Varieties from two or more maturity groups are often recommended in the same area to provide for early and late planting or to spread the period of harvest. For this reason, there is an overlapping of the areas where the various groups are grown.

The Genetic Nature of Characters in Soybean

Soybeans display two kinds of growth habit: The indeterminate type of growth habit (i.e., tall and the stem does not terminate in a cluster; the plant continues to form leaves at the stem apex while flowers are forming and pods are being set at lower nodes on the stem), and the determinate type of growth habit (i.e., short and terminates with a pronounced raceme having as many as 20 flowers; this type terminates its vegetative growth and then the stem apex is converted to a floral condition). Varieties adapted to the northern part of the United States are mostly indeterminate. Those adapted to the southern area are determinate.

Woodworth (36) described the difference between determinateness and indeterminateness as due to a single gene pair. Bernard (3) has extended the description to include additional growth types.

Smith and Circle (27) stated that soybean flowers are borne in the axillary position and are 6 to 7 mm in length. A dozen or more flowers may be borne at each node, but many of these will not result in pods and seeds. As a result, counting the number of flowers is not a reliable means of predicting yield, since the number of pods and seeds and weight of seeds are strongly influenced by environmental factors.

Soybeans are self-pollinated. Weber and Hanson (31) estimated that out-crossing under natural conditions is from 0.5 to 1 percent.

Johnson and Bernard (15) found that flowers are usually either purple or white, with purple being dominant. They also discussed some variation in intensity of color and other minor aspects. Soybean pods

may be black, brown, or tan at maturity. Bernard (4), in a study of the inheritance of pod color in soybeans, pointed out that two gene pairs are involved in this character.

The soybean Glycine max (L.) Merr. is a short-day plant which flowers only when the daylength is less than some critical value. Varietal differences in critical daylength were recognized in soybeans by Garner and Allard (10); they observed differences in time of flowering with different daylengths obtained from dates of planting. Basnet et al. (2), in a study of the influence of altitude on seed yield and other characters of soybeans differing in maturity in Sikkim, Himalayan Kingdom, reported that soybean growth and development was retarded at the higher altitude, and plants were shorter, lodged less, and had fewer nodes. Seeds with better quality were produced at the higher altitude. Yield of most varieties was lower at the higher altitude. Basnet et al. also found that the higher altitude prolonged the intervals from planting to first flowering 3 to 13 days, and planting to maturity 2 to 24 days. Dates of first flowering and maturity of groups V through VII soybeans were delayed more than those of earlier maturing groups.

Fisher (9) observed considerable delay in time of flowering of 'Harosoy 63', 'Hawkeye', and 'Lincoln' soybean varieties under a 20-hour daylength in growth cabinets. Where varieties were grown under an extended daylength of 20 hours in the greenhouse, Harosoy 63 was delayed in flowering as expected, but the flowering of 'Blackhawk' was not delayed. Under field conditions, Blackhawk flowers and matures only a few days earlier than Harosoy 63.

Although there has been considerable research since then on the physiology and ecology of flowering in soybeans, very little is known about the genetics of the control mechanisms of flowering. Buzzell, (6) studied the inheritance of flowering time in the short-day soybean, Glycine max (L.) Merr., under long-day conditions in the greenhouse using natural daylength extended to 20 hours with cool-white fluorescent light. A single major gene with two alleles was found to control the flowering response. The dominant allele which gave a fluorescent-sensitive response of delayed flowering also resulted in later field maturity whereas the recessive allele which gave an insensitive response resulted in earlier maturity. The maturity symbols E_3 and e_3 were proposed for these alleles. Isolines have also been developed.

In general, the time of flowering and the time of maturity (i.e., pod ripening) have been considered to be quantitatively inherited, and the continuous variation usually observed justified this conclusion. However, in 1923, Woodworth (36) reported evidence for a gene pair (Ss) affecting plant height and maturity with tall and late dominant to short and early. The population he studied was the progeny of a single plant of probable outcross origin, and the population has since been discarded according to C. M. Woodworth. The described effects on plant growth cannot be identified though, since the original lines were lost.

Bernard (5), in a study of the gene model of flowering and maturity in soybeans, supported the hypothesis of two major genes affecting time of flowering and maturity. The procedure was to transfer E_1, a gene for lateness linked to pubescence color (Tt), from strain T175, and e_2, a gene for earliness, from strain T245. The late

allele at each locus was described to be partially dominant in most combinations. These qualitative characters were described similarly to what was discussed by Woodworth previously except for the reported complete dominance of S.

In 1927, Owen (22) studied maturity in the cross between 'Black Eyebrow' (introduced from Manchuria) and a glabrous Japanese variety, 'J5'. Based on the high correlation that he found between late maturity (apparently measured by the time of flowering) and gray pubescence (t), he concluded that a major gene pair, which he designated Ee, affected time of maturity. However, there were no clear-cut maturity classes or 3:1 ratio. Owen found, among the 64 gray-pubescent segregates, four definitely early plants and four borderline ones and estimated either 3 or 6 percent crossing over.

Bernard (5), in crosses with 'Clark', observed that the E_1 allele occurred in all Japanese-Korean determinate varieties tested, but not in Black Eyebrow, which presumably carries the early allele e_1. Bernard thought that the description of earliness as dominant given by Owen may be simply a function of the arbitrary date chosen to distinguish early from late in his classification of the majority of F_2 plants.

Based on Owen, Woodworth assigned the T-E linkage to linkage group I, and this designation has been followed in review articles since that time by Morse and Cartter (20), Woodworth and Williams (39), Weiss (33), Johnson (14), and Johnson and Bernard (15). Bernard has used the symbols E_1 e_1, but indicated lateness dominant to earliness.

Van Schaik and Probst (28), in a study of inflorescence type, presented F_2 data showing ratios of three late-maturing plants to one

early in crosses of 'Mukden' and T109 with 'Midwest' and P.I. 196 176. They do not mention linkage with pubescence color, but their data are probably due to E_1 e_1 segregation, since Mukden and T109 are e_1 and Midwest and P.I. 196 176 have appeared to contribute E_1 to hybrid populations that Bernard observed.

Hague (11) investigated, in a 'Ralsoy' x L 6-2132A14 soybean cross, the mode of inheritance of the lateness versus earliness character. He reported that the material was segregating for lateness (S) versus earliness (s) and the two alleles account for about two weeks difference in maturity, but due to the effect of other segregating loci the late versus early segregation is not clearcut. Hague did not explain his use of (Ss) nor refer to Woodworth's work mentioned previously. Bernard said, "it is likely that Hague was observing E_1 e_1 segregation, since L 6-2132A14 is nearly identical to the variety Clark (from the same F_4 plant) and Ralsoy is a late determinate variety introduced from Korea."

In 1970, Weiss (34) reported a crossover value of $3.9 \pm 0.5\%$ between E_1 e_1 and Tt. Hawkeye, a Manchurian derived variety, was the source of the e_1 allele and 'Lee', a determinate southern U.S. variety, was the source of E_1.

Moshkov et al. (21), in their experiment of the determination of the model of the photoperiodic mechanism in plants, discussed the nature of the genetic principles of the photoperiodic reaction. A proposed model scheme was concretized according to two groups of plants: nyctophilic plants including short-day and stenophotoperiodic species, and nyctophobic plants representing long-day, neutral, and amphiphotoperiodic species. Moshkov et al. mentioned that, in the case of

photoperiodism, more complex phenomena are involved than in a study of phages. An important role in photoperiodism is played by the time organization (diurnal rhythm), and many photoreceptor systems exist in the plant which interact complexly with one another. Moshkov et al. stated that the scheme of Jacob and Monod (13) in the pure form cannot be extended to plants, although some of its vital elements can be used in the construction of a model of photoperiodism. They concluded that for the transition to development both of short-day and of long-day plants, some minimum time is required, during which the operator should be induced. This time is approximately the same for both types of plants (about 12-14 hours) and corresponds to the critical day length. Moreover, a mutation of the operator gene can convert the plant from a long-day form to a short-day form, and conversely. Mutations that bring the operator gene out of obedience solely to certain regulators may also be possible. Moshkov et al. found that some of these forms are nonviable, whereas others are phenotypically indistinguishable. They noted that, in work with Arabidopsis thaliana, an herb in which gene dosage and interaction have been studied extensively, the transition of a plant from one photoperiodic type to another under the action of a single mutation was demonstrated. Optimum temperature is also one of the parameters that affects the transition to reproduction.

The question of whether the transition of plants to reproduction is the result of the action of the flowering-hormone or the result of the action of a flowering-inhibitor is still in dispute according to Salisbury (26).

Quinby (25), in a broad and recent genetic review of sorghum improvement, mentioned that the maturity genes control time of floral

initiation and they control duration of growth, which is an important part of adaptation.

Heritability of Characters

The coefficient of heritability is widely used at the present time in plant and animal genetics and breeding. It is beginning to occupy a large place for characterizing the genetic structure of populations, varieties of plants, and breeds of animals according to different attributes. It can serve along with certain other indices for predicting the results of selection and even for evaluating hybrid vigor and predicting the results of the selection in crossbred hybrids. However, it must be noted that in various genetic and breeding works there is a great diversity as to the nature of this genetic parameter and the significance of different methods of its determination.

In understanding the coefficient of heritability it is necessary to adhere to its classical definition, which goes back to the early works of Wright (40) and Lush (18): it expresses the fraction of genetic variation in the overall phenotypic variation for a given characteristic in a population. Thus, it pertains only to populations and not to individuals. Then, it is of interest to differentiate between "heritability" and heredity, which can be found in one parent-progeny pair. Furthermore, heritability cannot be considered simply as an index of the genetic diversity of a population, since it evaluates only the fraction of genetic diversity in the overall phenotypic variation and therefore is a relative value.

The division of heritability into two types was essentially introduced by Lush: heritability in the broad and narrow sense of the

word. In the first case

$$h^2 = \frac{\sigma^2_G}{\sigma^2_P}$$

while in the second

$$h^2 = \frac{\sigma^2_A}{\sigma^2_P}, \text{ where}$$

σ^2_G is the overall genetic variance and σ^2_A is the fraction of it which depends on genes with an additive effect, and σ^2_P is the phenotypic variance. The role of allelic (dominance) and non-allelic (epistasis) interaction is not taken into account in the index of heritability in the narrow sense.

Heritability estimates and gene effects for agronomic characters in soybeans are used for determining the importance of the character as a means of selecting for yield. Genotype by environmental interaction effects for grain yield, plant height, maturity, days from flowering to maturity, time of flowering, pod dehiscence, seed weight, lodging, oil and protein content, and others were investigated in different studies by Johnson et al. (17), Mahmud and Kramer (19), Weber (30), and Caviness (7). Broad sense estimates for pod dehiscence, date of flowering, date of maturity, days from flowering to maturity, and seed size were determined by Caviness in four soybean crosses. In most cases, with the exception of seed size, estimates were above 90 percent with only minor variations between the different crosses. Broad-sense heritability estimates for seed size varied from 40 percent in a cross

involving the largest and smallest seed parents ('Rokusun' x 'Wild') to 69 percent in a cross involving parents with the smallest seeds ('Lee' x 'Wild'). Caviness stated that the date of flowering, date of maturity, and days from flowering to maturity are highly heritable, and selection is effective for these characters in early generations whereas seed size is considerably influenced by environment.

The persistence of a character in a subsequent generation is a good measure of heritability as pointed out by Warner (29). Regression coefficients between the same character for F_2 plants and mean values for their F_3 progenies in the four crosses discussed by Caviness showed a strong tendency to persist for pod dehiscence reaction, date of flowering, date of maturity, and seed size.

Weiss et al. (35) reported significant positive correlations among the means of five varieties for the following characters: large seed and low iodine number of the oil; lateness of maturity and high oil content; lateness and low protein content; high oil content and low iodine number; and high protein content and low oil content. They also found that the correlations did not vary significantly among years, locations, or locations by years.

In 1952, Weber and Moorthy (32) estimated genotypic and phenotypic correlations between all possible pairs of seven characters measured in $3F_2$ populations of soybeans. They found that, in general, the genotypic correlations were higher than the phenotypic. They obtained positive genotypic correlations between flowering time and maturity date, yield and maturity date, yield and plant height, and yield and seed weight. Negative genotypic correlations were obtained between

flowering time and period from flowering to maturity, maturity date and oil percentage, and seed weight and oil percentage.

CHAPTER III

MATERIALS AND METHODS

The soybean material used in this study was grown on a Teller loam at the Agronomy Research Station, Perkins, Oklahoma in 1975. All entries were space-planted 75 cm apart using a hand planter.

A preplant application of fertilizer (100 lbs. of 18-46-0/A) was broadcast on the experimental area. All cultural practices such as cultivation, irrigation, weed and insect control were conducted as required.

The soybean parental lines, F_1's and F_2's used in this study were obtained from Dr. Charles Caviness, Department of Agronomy, University of Arkansas. Some descriptive data for the two parental lines are given below.

Variety	Stem Type	Maturity Group	Fruiting Character
Lee 74	Determinate	VI	Late
Bonus	Indeterminate	IV	Early

Care was taken to provide optimum environment for plant growth; however, failure to germinate, stem breakage, and probably other environmental effects caused the loss of 632 entries. All data were collected on a single plant basis.

The soybean entries utilized in this study were as follows:

Entries	Number of Seeds Planted	Number of Plants Surviving
Lee 74	111	80
Bonus	110	76
F_1	10	4
F_2	1065	504

F_2 seeds were in 38 sacks and each sack contained seeds from an individual F_1 plant.

The field layout corresponded to a completely randomized design. The experimental units consisted of single plants spaced 75 cm apart. Planting was made on June 12, 1975. All the plants were checked daily and measurements were recorded for the following characters:

Flowering date. Number of days from June 12, 1975, to the date when the petals of the first flower had expanded beyond the sepals.

Maturity date. Number of days from June 12, 1975, to the date when approximately 95% of the pods were ripe.

Plant height. The length of the distance in centimeters between the ground surface and the tip of the main stem.

Grain yield/plant. Yield per plant was determined by threshed grain weight in grams.

Weight of 100 seed. Weight was recorded as grams per 100 seed.

Analytical Procedures

An analysis of variance including all entries was conducted for each of the above characters to determine whether any differences existed among these entries. Separate analyses for F_2 population, and for Lee 74 parent, Bonus parent, and F_1 populations were also performed to determine genotypic and environmental variances.

The minimum number of genes (K) controlling inheritance of each character was estimated by the following formula.

$$K = \frac{1}{8} \frac{(\bar{P}_1 - \bar{P}_2)^2}{\sigma^2_G}$$

where $\bar{P}_1$ = mean of the Lee 74 parent, $\bar{P}_2$ = mean of the Bonus parent, and σ^2_G = genetic variance. Assumptions are equal gene effect, no dominance, no epistasis, and no linkage involved (8).

Phenotypic correlations on a plant basis (r_p) were calculated as:

$$r_p = \frac{\text{cov}(x,y)_{F_2}}{\left[(\text{Var } x)_{F_2} (\text{Var } y)_{F_2}\right]^{\frac{1}{2}}}$$

where $\text{cov}(x,y)_{F_2}$ represents the covariance between the characters x and y, and $(\text{Var } x)_{F_2}$ and $(\text{Var } y)_{F_2}$ denote the variances of x and y, respectively. Variances and covariances were based on measurements taken on individual plants of the F_2 population, and were estimated by the within-F_2 mean squares and mean products, respectively.

Environmental correlations on a plant basis (r_e) were calculated as:

$$r_e = \frac{\text{cov}(x,y)_e}{\left[(\text{Var } x)_e \ (\text{Var } y)_e\right]^{\frac{1}{2}}}$$

where $\text{cov}(x,y)_e$ = cov(Lee 74 Parent, Bonus Parent, and F_1), assuming that the environmental variability in each parental line and F_1 is the same.

Genotypic correlations on an individual plant basis (r_g) were calculated as:

$$r_g = \frac{\text{cov } (x,y)_{F_2} - \text{cov } (x,y)_e}{\left[(\text{Var } x)_{F_2} - (\text{Var } x)_e\right]^{\frac{1}{2}} \left[(\text{Var } y)_{F_2} - (\text{Var } y)_e\right]^{\frac{1}{2}}}$$

While significance of the phenotypic and environmental correlation coefficients can be determined in the usual way, no test is as yet available for evaluating the significance of the genotypic correlation coefficient calculated as above. Nevertheless, the relative magnitude of that coefficient will reflect the degree of genotypic association between two given characters.

Expected F_1 relative frequencies were also determined for both flowering and maturity characters assuming one effective single pair of alleles operating for each of these two characters and using the following formula:

$$F_1 = 2F_2 - \tfrac{1}{2}P_1 - \tfrac{1}{2}P_2$$

Expected F_1 relative frequency distributions were truncated beyond negative values.

CHAPTER IV

RESULTS AND DISCUSSION

Means and Variances

Analyses of variance presented in Tables I, II, III, IV, and V indicated significant differences among parental lines, F_1's, and F_2's for flowering, maturity, plant height, and weight of 100 seed characters. No significant differences among entries were detected for yield. Means and variances for parental lines, F_1's, and F_2's are presented in Tables VI, VII, VIII, and IX. Unless otherwise stated, further reference to P_1 and P_2 will indicate Lee 74 parent and Bonus parent, respectively. P_1 was later in flowering and maturity, shorter in height, yielded less, and had lighter seeds than P_2. In plant height, the F_1 was taller than either parent indicating heterosis.

Variances for flowering, maturity, and plant height were considerably larger for the F_2 generation than for the non-segregating generations. This is evidence of genetic diversity for these characters.

Inheritance of Flowering and Maturity

The minimum number of genes (K_f, K_m) controlling flowering and maturity, respectively, were determined in this study as follows:

TABLE I

ANALYSIS OF VARIANCE OF DATA FROM PARENTS, F_1, AND F_2 FOR FLOWERING

Source	d.f.	M.S.S.
Entry	3	5406.96**
Sack (entry)	37	64.22**
Residual	623	39.93
Corrected Total	663	65.57

**Significantly greater than the error mean square at P = 0.01.

TABLE II

ANALYSIS OF VARIANCE OF DATA FROM PARENTS, F_1, AND F_2 FOR MATURITY

Source	d.f.	M.S.S.
Entry	3	9227.34**
Sack (entry)	37	91.64
Residual	622	65.50
Corrected Total	662	108.48

**Significantly greater than the error mean square at P = 0.01.

TABLE III

ANALYSIS OF VARIANCE OF DATA FROM PARENTS, F_1, AND F_2 FOR HEIGHT

Source	d.f.	M.S.S.
Entry	3	9426.31**
Sack (entry)	37	1195.09**
Residual	482	620.53
Corrected Total	522	711.86

**Significantly greater than the error mean square at P = 0.01.

TABLE IV

ANALYSIS OF VARIANCE OF DATA FROM PARENTS, F_1, AND F_2 FOR YIELD

Source	d.f.	M.S.S.
Entry	3	3371.75
Sack (entry)	37	1513.83
Residual	572	1713.65
Corrected Total	612	1709.70

TABLE V

ANALYSIS OF VARIANCE OF DATA FROM PARENTS, F_1, AND F_2 FOR WEIGHT OF 100 SEED

Source	d.f.	M.S.S.
Entry	3	265.79**
Sack (entry)	37	8.51
Residual	572	7.24
Corrected Total	612	8.59

**Significantly greater than the error mean square at P = 0.01.

TABLE VI

MEANS AND VARIANCES FOR F_1

Variable	Mean	Variance
FLWR	58.50	1.66
MATUR	137.75	2.91
HT	84.25	222.91
YIELD	81.75	450.91
W100SD	17.25	0.25

TABLE VII

MEANS AND VARIANCES FOR F_2

Variable	Mean	Variance
FLWR	50.05	53.31
MATUR	124.58	85.90
HT	66.45	888.73
YIELD	71.99	1859.64
W100SD	17.56	8.41

TABLE VIII

MEANS AND VARIANCES FOR P_1 (LEE 74)

Variable	Mean	Variance
FLWR	60.57	4.19
MATUR	138.01	9.40
HT	46.12	70.16
YIELD	70.44	1180.64
W100SD	15.77	1.09

TABLE IX

MEANS AND VARIANCES FOR P_2 (BONUS)

Variable	Mean	Variance
FLWR	40.38	1.35
MATUR	111.71	3.46
HT	61.39	172.37
YIELD	83.82	1320.06
W100SD	20.27	7.32

$$K_f = \frac{(60.57 - 40.38)^2}{8 \times 49} = 1.02$$

$$K_m = \frac{(138.01 - 111.71)^2}{8 \times 79} = 1.09$$

These results indicated that the flowering and maturity characteristics each seemed to be regulated by a single gene. Data presented in Tables X and XI and Figures 1 to 4 indicate that there was a degree of phenotypic dominance toward lateness for both flowering and maturity. This is evident from relative frequency distributions of the F_2, and expected F_1 generations. Expected F_1 frequency distributions for flowering and maturity were slightly skewed toward the late cultivar P_1 indicating dominance of lateness over earliness. A clear tendency for higher frequencies in the late-flowering, late-maturing classes intermediate to the parental distributions can also be seen. Distributions for the F_2 generation were bimodal for these characters and individuals appeared to fall into discrete classes. Our results are consistent with those reported by Bernard (5) and Buzzell (6). Bernard described the late alleles, E_1 and E_2, to be partially dominant, since in most cases the heterozygotes flowered and matured more closely to the late homozygote. Flowering and maturity were delayed in the parent P_1 20 and 27 days, respectively. The F_1 hybrid generation flowered 18 days and matured 26 days later than the P_2 parent.

TABLE X

OBSERVED AND EXPECTED RELATIVE FREQUENCIES FOR FLOWERING CHARACTER

Classes in Days	F_2 Observed	F_2 Observed Relative Frequency in %	F_1 Expected Relative Frequency in %	P_1 (Lee 74) Observed	P_1 (Lee 74) Observed Relative Frequency in %	P_2 (Bonus) Observed	P_2 (Bonus) Observed Relative Frequency in %
39 - 40	113	22.42	2.74			64	84.2
41 - 42	20	3.96	3.32			7	9.2
43 - 44	1	0.19	-2.27			4	5.3
45 - 46	2	0.39	0.78			0	0
47 - 48	79	15.67	30.69			1	1.3
49 - 50	43	8.53	17.06				
51 - 52	52	10.31	20.62				
53 - 54	35	6.94	12.63	2	2.5		
55 - 56	34	6.74	12.85	1	1.25		
57 - 58	47	9.32	15.51	5	6.25		
59 - 60	49	9.72	1.31	29	36.25		
61 - 62	21	4.16	-11.05	31	38.75		
63 - 64	5	.99	- 4.27	10	12.5		
65 - 66	3	0.59	- 0.07	2	2.5		
Totals	504	99.93	99.86	80	100.00	76	100.00

TABLE XI

OBSERVED AND EXPECTED RELATIVE FREQUENCIES FOR MATURITY CHARACTER

Classes In Days	F_2 Observed	F_2 Observed Relative Frequency in %	F_1 Expected Relative Frequency in %	P_1 (Lee 74) Observed	P_1 (Lee 74) Observed Relative Frequency in %	P_2 (Bonus) Observed	P_2 (Bonus) Observed Relative Frequency in %
105-107	3	.595	1.190			-	-
108-110	19	3.769	-15.488			35	46.052
111-113	31	6.150	- 4.805			26	34.210
114-116	110	21.825	34.439			14	18.421
117-119	19	3.769	6.880			1	1.315
120-122	18	3.571	7.142				
123-125	52	10.317	20.634				
126-128	59	11.706	23.412				
129-131	50	9.920	17.340	4	5.00		
132-134	60	11.904	20.058	6	7.50		
135-137	36	7.142	5.534	14	17.50		
138-140	33	6.547	-12.531	41	51.25		
141-143	14	2.777	- 3.821	15	18.75		
Totals	504	99.992	99.985	80	100.00	76	99.998

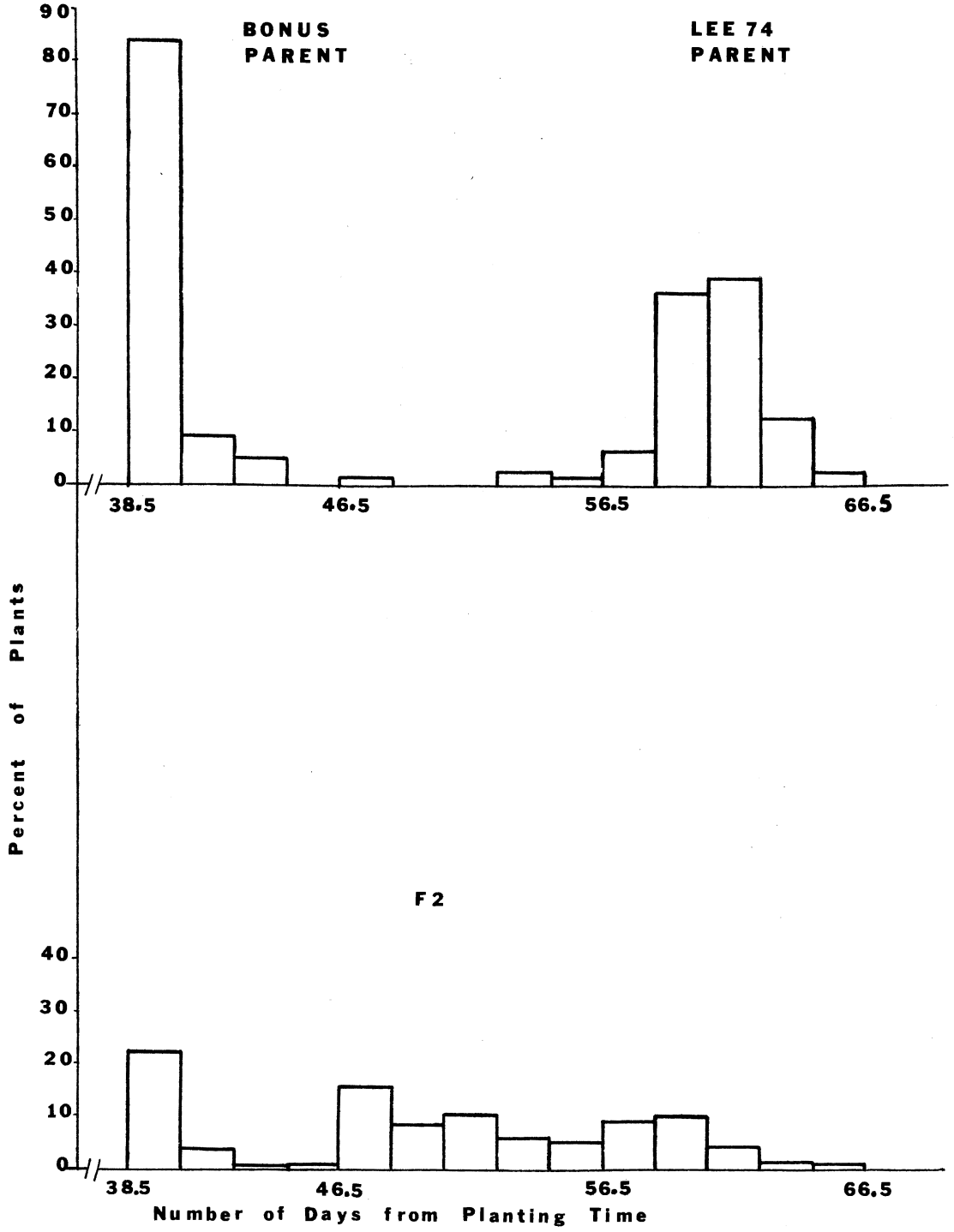

Figure 1. Frequency Distributions of Parental and F_2 Populations for Flowering

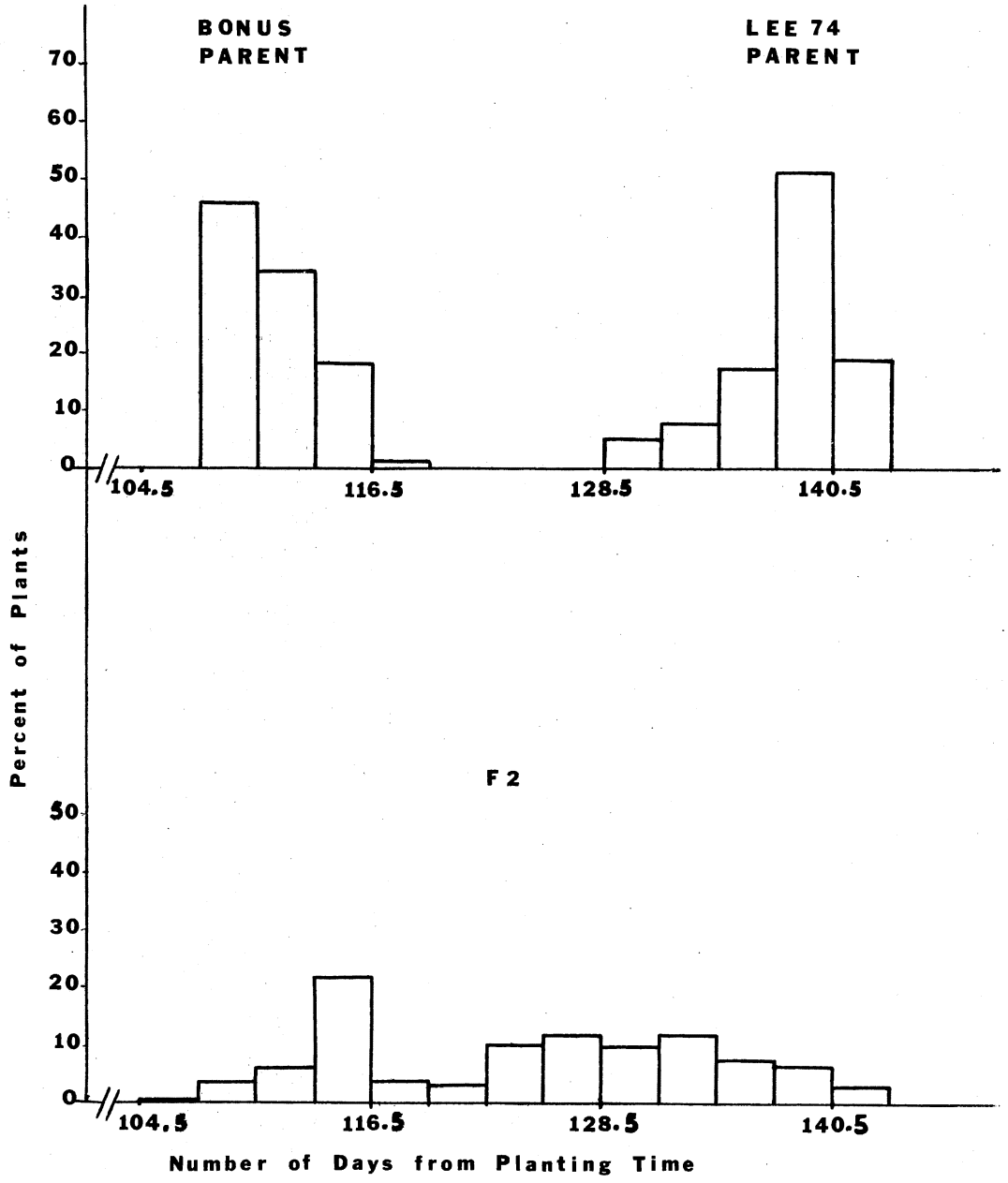

Figure 2. Frequency Distributions of Parental and F_2 Populations for Maturity

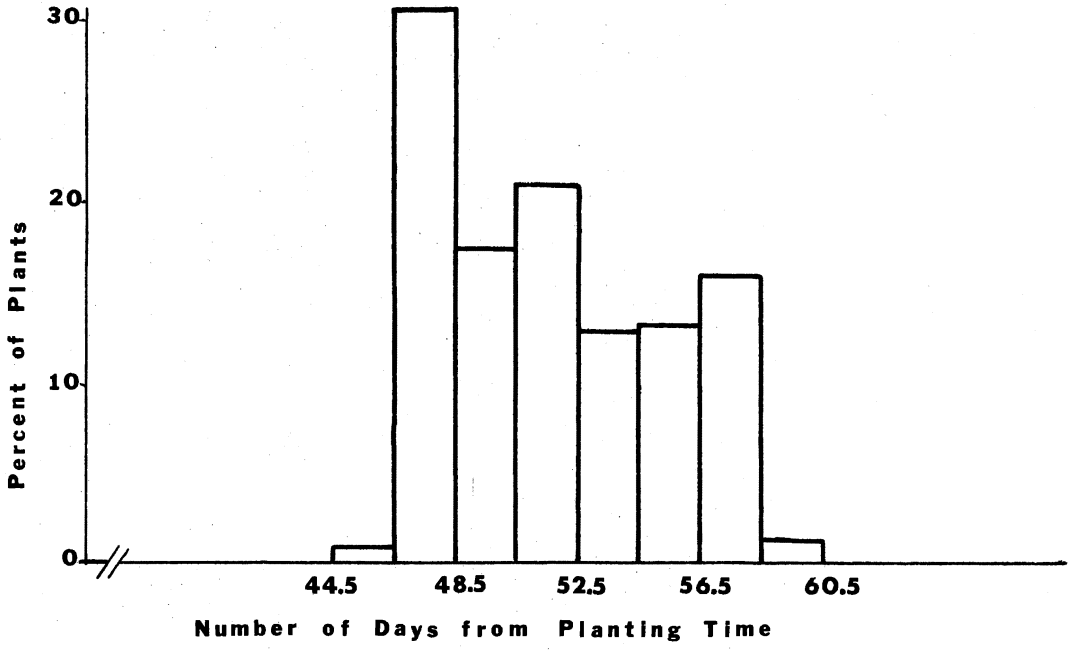

Figure 3. Expected F_1 Relative Frequency Distribution for Flowering

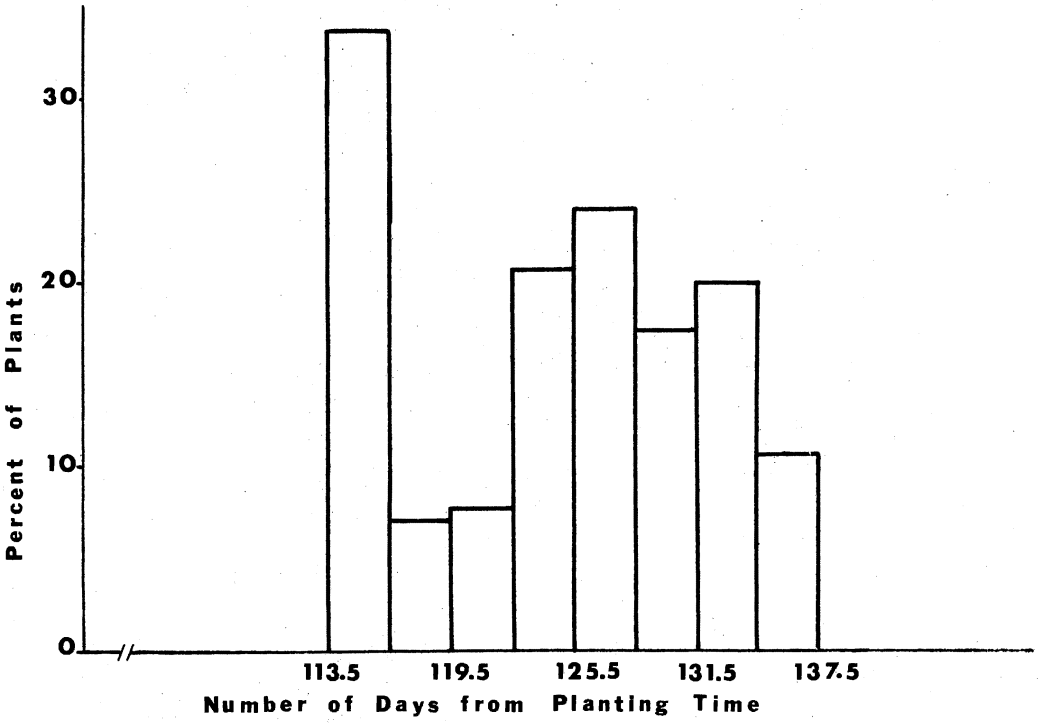

Figure 4. Expected F_1 Relative Frequency Distribution for Maturity

Correlations

Coefficients of linear correlations among the various traits in all combinations are displayed in Table XII. Genotypic correlations were of greater magnitude than phenotypic or environmental correlations which indicated that these associations were primarily genetic. Phenotypic and genotypic correlations agreed in sign. Flowering time was positively correlated with maturity time and plant height indicating that early flowering genotypes were shorter and matured earlier. Earlier maturing plants in this material also tended to have heavier seeds. Highly significant positive correlations were anticipated and indeed obtained between yield and height. These results suggest that selection for taller plants would be beneficial through a correlated response for yield. The positive correlations of flowering and maturity and of yield and plant stature are corroborated by similar findings of Weber and Moorthy (32). Although highly statistically significant at the phenotypic level, the magnitude of genotypic correlation between maturity and height is relatively low. Woodworth (36) reported evidence for a gene pair affecting plant height and maturity with tall and late dominant to short and early. Highly significant negative correlations were observed between weight of 100 seed and flowering, maturity, plant height, and yield.

It is realized, of course, that the material in this study was space-planted; therefore, extrapolation of the results to other planting conditions cannot be made without caution. Correlation coefficients are used to characterize the intensity of association between two traits without regard to causation.

TABLE XII

COEFFICIENTS OF PHENOTYPIC (P), ENVIRONMENTAL (E), AND GENOTYPIC (G) CORRELATIONS AMONG FIVE AGRONOMIC TRAITS IN A SOYBEAN CROSS

Trait		Flowering	Maturity	Height	Yield	Weight of 100 Seeds
Flowering	P		0.8303**	0.3734**	0.1950**	-0.3980**
	E		0.0935	-0.2546**	-0.0365	0.0512
	G		0.8803	0.4524	0.3542	-0.5880
Maturity	P			0.3045**	0.1473**	-0.2811**
	E			-0.0921	0.0022	0.2683**
	G			0.3655	0.2633	-0.4910
Height	P				0.5554**	-0.4632**
	E				0.2244**	-0.0480
	G				0.9470	-0.7132
Yield	P					-0.2011**
	E					0.1631
	G					-0.6961

**Significantly different from zero at P = 0.01. No test of significance is available for genetic correlations.

CHAPTER V

SUMMARY AND CONCLUSIONS

The objective of this study was devoted to evaluating the gene action involved in the expression of flowering and maturity and their association with other agronomic characters in a soybean cross Lee 74 x Bonus. Lee 74 is a late-maturing parent and Bonus is an early-maturing parent. Parents, F_1, and F_2 generations were utilized to study the nature of inheritance of flowering and maturity characters.

Collected data, computed from parents, F_1, and F_2 generations indicated that the two parents utilized in this study differed by a single gene each for flowering and maturity.

Frequency distributions for these two characters were skewed toward the late-maturing cultivar. Minimum number of genes controlling the flowering and maturity characters were calculated and were equal to 1.02 and 1.09, respectively.

Correlation coefficients were determined from parental, F_1, and F_2 data of the previously described Lee 74 x Bonus cross to assess the possibility of combining desirable characters from the parents. The results from this study indicated that flowering was positively correlated with maturity, plant height, and yield indicating the difficulty of selecting from this cross higher yielding varieties that are earlier and shorter. Significant negative correlations were

observed between weight of 100 seed and yield, plant height, maturity, and flowering.

Further information on the genetic systems controlling the length of flowering and its association with maturity, and the position on the plant where the first flower occurs would be of much interest to counter-balance the most prevalent factors determining the extent of losses caused by combine-harvesting.

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APPENDIX

TABLE XIII

ANALYSES OF VARIANCE OF DATA FROM PARENTS AND F_1 FOR FLOWERING AND MATURITY

Source	d.f.	M.S.S. for	
		Flowering	Maturity
Entry	2	8063.87**	13788.30**
Plant (entry)	157	2.79	6.44
Corrected Total	159	104.19	179.79

**Significantly greater than the error mean square at P = 0.01.

TABLE XIV

ANALYSES OF VARIANCE OF DATA FROM PARENTS AND F_1 FOR PLANT HEIGHT, YIELD, AND WEIGHT OF 100 SEED

Source	d.f.	M.S.S. for		
		Height	Yield	W100S
Entry	2	6273.81**	3469.77	387.89**
Plant (entry)	154	122.91	1234.32	4.11
Corrected Total	156	201.77	1262.98	9.03

**Significantly greater than the error mean square at P = 0.01.

TABLE XV

ANALYSIS OF VARIANCE OF DATA FROM F_2 FOR FLOWERING

Source	d.f.	M.S.S.
Sack (entry)	37	64.22
Residual	466	52.45
Corrected Total	503	53.31

TABLE XVI

ANALYSIS OF VARIANCE OF DATA FROM F_2 FOR MATURITY

Source	d.f.	M.S.S.
Sack (entry)	37	91.65
Residual	465	85.44
Corrected Total	502	85.90

TABLE XVII

ANALYSIS OF VARIANCE OF DATA FROM F_2 FOR PLANT HEIGHT

Source	d.f.	M.S.S.
Sack (entry)	37	1195.09
Residual	328	854.17
Corrected Total	365	888.73

TABLE XVIII

ANALYSES OF VARIANCE OF DATA FROM F_2 FOR YIELD AND WEIGHT OF 100 SEED

Source	d.f.	M.S.S.	
		Yield	W100S
Sack (entry)	37	1513.83	8.51
Residual	418	1890.25	8.40
Corrected Total	455	1859.64	8.41

VITA

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