INHERITANCE OF POD SIZE, SHELL THICKNESS AND SEED MATURITY IN PEANUTS, ARACHIS HYPOGAEA, L.

By

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CHAPTER I

INTRODUCTION

Recognition of world protein requirements has placed new emphasis on developing high yielding varieties of protein rich crops. At present, the population of many developing countries of the world is facing a serious problem of malnourishment. Statistics for the last few years show that 60 percent of the people in the developing world do not receive balanced nutrition. Although the outcomings of the green revolution seem to place a solution within man's reach, the problem of food quality still remains a great challenge to mankind (39).

Peanuts (Arachis hypogaea L.), a native South American legume, are rich in protein (25 to 30 percent) and oil (45 to 50 percent), and are considered an important source of protein and oil for many people of the world. Three-fourths of all peanuts in the world are produced by India, mainland China, Nigeria, the United States, and Senegal. In the United States, the peanut is largely cultivated in the southern states, and is considered an important cash crop (18).

To accomplish a goal of feeding a balanced nutrition to the ever-increasing population of the world, peanut breeders have an important role in the future. Development of new varieties is a never ending goal for plant breeders, and, in this concern, the search for desirable germplasm is always continuing. Though many improved varieties of peanuts have been developed in recent years, there is still a need to search for high yielding, protein rich, and broadly adaptable varieties. Peanut research assumes greater importance in view of world-wide increased production of the crop in coming years.

In a breeding program, estimates of genetic components provide useful guidelines for developing an appropriate variety. The purpose of the present study was to evaluate the genetic potential for pod size, shell thickness and seed maturity of eight lines of peanuts for their possible use in future peanut research. Knowledge of the type of gene action involved in the expression of characters such as pod size and pod number would be useful in breeding programs, designed to improve the yielding potential of peanut cultivars. A better understanding of the mechanisms of inheritance for agronomically important traits is essential if further improvements are to be accomplished. Inheritance studies for pod size, pod number, shell thickness, and seed maturity were carried out to provide an insight of the genetic variation available to a breeder for possible incorporation of desired traits in our present commercial varieties.

CHAPTER II

LITERATURE REVIEW

Most peanut breeding at present is focused upon maximum yield of seed or oil, shelling grade, milling proerties and quality of end-use products. Many of these characters are influenced by multiple gene action. Inheritance of these characters, either dominant or recessive has been recorded in peanuts, beginning with the work of Van der Stok in 1910 (46). The findings of both simple and complex genetic ratios is not unexpected in an alloploid species like peanuts.

Pod Size Inheritance

Van der Stok (46) was the first to report a multigenic inheritance for pod size. He crossed a variety having small thin pods with another having large thick pods, and observed a greater ratio than 3:1.

Badami (2), in his work on hybridization in groundnuts, claimed that large sized pods were dominant with three factors governing inheritance.

Hassan (19) reported dominance of large size pods over the small ones in crosses among four varieties of groundnut viz. Ak_{12} - 24A, Early Runner, K_{17}, and Big Japan, representing bunch and spreading type of peanut varieties.

Patil (35), in his induced mutation studies on peanuts, reported dominance of big pods over small pods, since the frequency curves of segregating populations were skewed towards big pods.

Ilieff (24) observed binomial F_2 distribution in his peanut crosses, suggesting fruit size being controlled by multiple factors.

Wynne, et al. (47), in their study of heterosis and combining ability in peanuts, suggested additive gene action for fruit size, since general combining ability estimates for fruit length were high.

Genetics of some other pod characters have also been studied by peanut breeders. Badami (3) studied the inheritance of pod constriction, and proposed that the absence of pod constriction was dominant to its presence. He described four groups on the basis of depth of constriction, and concluded that two factors were involved, with the cylindrical type being the double dominant. Hassan (19) confirmed the dominance of shallow constriction to deep constriction. However, he proposed a trigenic complementary model with an F_2 phenotypic ratio of 45:19. He explained these results by assuming that A is a basic gene with B and C complementary to A but not to each other. Shallow constriction appears when A is present together with B or C or both. Recent reports by Mouboussin (Unpublished) as cited by Hammons (18) suggest dominance for presence of pod constriction to the absence of pod constriction.

Coffelt and Hammons (11) studied the inheritance of pod constriction in a cross between 'Argentine' (unconstricted) and 'Early Runner' (constricted). Their results indicate that the two peanut cultivars differ at three unlinked nuclear loci and one cytoplasmic factor. Three dominant alleles, one at each of any three of the four factors, are required for the presence of pod constriction. Any two homozygous recessive factors result in unconstricted pods. Constricted pod is dominant to unconstricted pod. They proposed the genetic formulae for Argentine as $pc_1pc_1pc_2pc_2pc_3pc_3$ for the nuclear loci and 'a' for the cytoplasmic factor, and for Early Runner as $Pc_1Pc_1Pc_2Pc_2Pc_3Pc_3$ for the nuclear loci and 'A' for the cytoplasmic factor. Phenotypic ratios of F_2 reciprocal populations were 27:37 and 54:10, using Argentine and Early Runner as female, respectively. Their assumption of a cytoplasmic factor is also supported by Ashri (1), who has reported the growth habit trait in peanuts to be under partial cytoplasmic control. He has shown that at least two plasmons and two nuclear genes interact to produce the growth habit in peanuts, either spreading or bunch.

Nguyen and Norden (33) have reported pod pubescence inheritance to be controlled by two loci segregating independently and acting additively.

Hayes' (20) work on the inheritance of growth habit and length of pod indicates the difference of two factors in each trait. After grouping long and intermediate pods together, the ratio obtained was 15:1, which fit the difference of two loci with long being dominant over short.

Badami (3) also reported the mode of inheritance for deep reticulation on the pods. He has shown at least four factors responsible for the trait, with deep reticulation being dominant to shallow. However, Patil (36) found a ratio of 3:1 in F_2 progenies indicating the pattern of reticulation to be controlled by one gene pair, with deep reticulation being dominant over shallow.

Inheritance of number of seeds in a pod was also studied by Badami (3). He suggested the presence of three factors, with three or more seeded pods dominant over fewer than 3-seeded pods. Results of Tahir (43) also revealed the dominance of pods with higher numbers of seeds.

Seed Maturity Inheritance

There are very few reports available on the inheritance of peanut seed maturity. Previous workers have reported maturity on the basis of pods. Badami (2), in his work on maturity, reported that late maturity was dominant to earliness. Patel, *et al*. (34) observed a ratio of 1:2:1 in F_2 plant populations of crosses involving early and late maturing varieties of peanuts. It is reported in their results that there is a single factor difference between early and late. If medium and late plants are grouped together, late type shows dominance over early and supports Badami's findings.

Genetic studies conducted by Hassan (19), in a cross between early and late varieties, indicated intermediate and mature plants in F_1, and the F_2 showed a monogenic segregation of 1 early: 2 medium: 1 late plant.

Shell Thickness Inheritance

Little work has been done on the genetics of shell thickness. Inheritance of shell thickness was first reported in Van der Stok's work (46). He studied two characters, pod size and shell thickness. In hybridization of a variety having small thin pods with another having large thick pods, Van der Stok observed a greater difference than a 3:1 ratio suggesting multigenic control of the thickness trait.

According to Seshadri (40), thin pericarp is dominant and governed by five factors. He also reported a linkage between thin pericarp and pigmy seed but the method of determining the linkage was not stated.

Heritability and Correlation Studies

Lin (27) analyzed the inheritance of several quantitative characters in progenies of Spanish by Virginia crosses. He reported relatively small heritability values for number of pods per plant.

Bernard (8) investigated the magnitude of genetic and environmental variability in several crosses of peanut varieties. Of the ten traits investigated, all appeared to have sufficient genetic variability for appreciable changes to be possible through selection. Of these, the percentage of immature seeds, the weight per seed, the shelling percentage and the leaf spot score were more highly heritable than yield.

Gupton (16), in his work on the heritability of maturation indices associated with specific growth periods in Virginia type peanuts, reported estimates of heritability of kernel maturity remarkably high. In the third pegging group the heritability estimates were .95 and .94 when calculated from variance components and parent-progeny regressions, respectively. The percent gain in maturity from hypothetical selection increased with successive pegging groups, resulting in more than twice as much gain from selection in the third group as in the first group.

High heritability estimates and great expectations of genetic advance were obtained by Kulkarni and Albuquerque (26) for number of developed pods, number of undeveloped pods, number of branches, and height of the main shoot. They studied the variation in five quantitative characters of nine strains of groundnut, evolved at Raichur, India. The heritability for total number of pods was reported not so high when compared to other characters.

Basu and Ashoka Raj (6), however, calculated high heritability for number of pods per plant in their material. Since the genetic coefficient of variance was high for the number of pods per plant, they concluded that selection may be based on phenotypic performance.

Majumdar, _et al_. (29) in Bihar, India, observed a wide range of phenotypic variation for 11 of 17 quantitative characters measured in a collection of 45 peanut varieties. Broad-sense heritability estimates were high for pod size, and low for number of pods and number of mature pods.

Sangha and Sandhu (38) observed low genotypic coefficient of variation and little genetic advance for number of pods in their study of yield components of 54 varieties of peanuts in Punjab, India.

Patil (35), in his work of induced mutations for improving quantitative characters in peanuts, observed high heritability estimates for number of mature kernels, and pod size. Though the heritability for number of pods was relatively small, he was optimistic for appreciable changes through selection, due to transgressive segregation.

A number of reports have been published pertaining to correlation studies among various qualitative and quantitative traits in different varieties of peanuts.

Nevano (32) observed very close correlations between dry pod weight and the total number of pods, in different peanut varieties, as early as 1924 in Italy. He concluded that yield could be increased by choosing the heaviest plants.

Stokes and Hull (41) reported positive correlations among pod weight, number of pods, seed weight, and seed number.

Hayes (20) observed close relationship between length of leaf and width of leaf, length of sheath and number of seeds, length of rachis and hairs on petiole, and length of petiole and corrolla color.

Maralihalli (30) showed a positive correlation among number of branches, number of pods, number of flowers on the branch, and number of seeds in a study of crosses involving Spanish and Japanese peanut varieties.

During the 1950's, Lin (27), in Taiwan, studied correlations among various characters in 60 peanut varieties of Spanish type. He obtained highly significant correlations among each other for number of pods, weight of pods, number of seeds, and weight of seeds within each plant.

Bernard (8) observed some relationship of number of pods per plot, percentage of immature seeds, number of seeds per hundred segments, and weight per seed with seed yield in crosses of various peanut varieties.

Chaudri (10) used regression analysis over two seasons at Ludhiana, India, and reported a positive correlation between number of pods and yield.

Chandra Mohan, *et al*. (9) have shown a highly significant relationship between yield and number of mature pods.

Positive correlations were reported by Jaswal and Gupta (25) for number of mature pods, total number of pegs, and pod yield in 73 varieties of spreading type peanuts.

Badwal and Singh (5) studied the effect of growth habit on correlations of various traits in 60 varieties of peanuts. They observed positive correlations between number of mature pods and number of pods per plant in all the varieties, regardless of growth habit.

CHAPTER III

MATERIALS AND METHODS

The present study utilizes genetic material left from a study of the inheritance of oleic to linoleic fatty acid ratio in peanuts (44). The materials selected are listed in Table I. Eight peanut cultivars were used to study the inheritance of pod size, pod number, shell thickness, and seed maturity. They represent two types of peanuts, i.e. Spanish and Jumbo.

Hand crosses were made, utilizing a greenhouse and a growth chamber, to obtain F_1 seeds in 1969. The F_1 seeds were planted in the greenhouse in the early spring of 1970, and F_2 seeds were obtained that year. F_2 seeds and parental seeds were planted at the Perkins Agronomy Research Station in May, 1971. The F_2 plants were harvested in October, and data for parental, F_1, and F_2 plants were recorded for the present study.

Studies on Pod Characters

Pod size was determined for each pod of every plant of parental and F_2 populations. A series of holes graduated in sixteenths of an inch were used to measure the pod diameter at its largest point. Pods were dropped through the smallest hole that would allow them to pass. The number of pods going through each hole was recorded. Means of

TABLE I

EIGHT PEANUT CULTIVARS CHOSEN FOR GENETIC STUDIES

Oklahoma P-No.	Cultivar	Market Type
0002	Argentine	Spanish
0006	Starr	Spanish
0074	Argentine Selection	Spanish
0112	Spanhoma	Spanish
0963	Newberry	Jumbo
1616	Newberry	Jumbo
1617	Bleckley	Jumbo
1618	Korean	Jumbo

every class were calculated, and frequency distributions were determined for parents and F_2 populations.

For clarification and discussion of the data, pods have been placed into three categories of small, medium, and large, based on the following size ranges in diameter.

Small = Pod Size Class 7 - 9 (7/16" - 9/16")
Medium = Pod Size Class 10 - 12
Large = Pod Size Class 13 - 16

The number of pods on each plant were also counted and frequency distributions for F_2 plants were determined.

Studies on Seed Characters

After all pods were sized, shelling was done by hand and the pods and seeds were classified as mature, intermediate, or immature, according to the color of the interior surface of the pericarp. Seeds were counted and recorded in each maturity class. Parents P-0002, P-0006, P-0074, and P-0112 are known to yield more mature kernels, and parents P-1616, P-1617, and P-1618 produce more immature kernels under Oklahoma growing conditions (44). Maturity percentages for parents and F_2 plants were calculated and frequency distributions of F_2 populations are reported. The number of seeds on each plant were counted and means and ranges for parental lines and F_2 populations were computed.

Studies on Shell Thickness

In the present study, five good shells from the mature class were saved from each plant for measurement of shell thickness. If a plant had no mature pods then the five most mature pods were measured. A caliper, graduated in thousandths of an inch was used to measure the shell thickness at two different positions (T_1 and T_2) on one half of each pod after Beavers (7). The two different positions of shell thickness measurement are shown in Figure 1. The mean shell thickness of parental and F_2 plants were calculated and placed in various classes. Frequency distributions were determined.

Shell thickness measurements of the material used in this study have also been classified as thin, medium, and thick based on the following scale.

Thin = Shell Thickness Class 15 - 35 (.015" - .035")

Medium = Shell Thickness Class 45 - 75

Thick = Shell Thickness Class 85 - 115

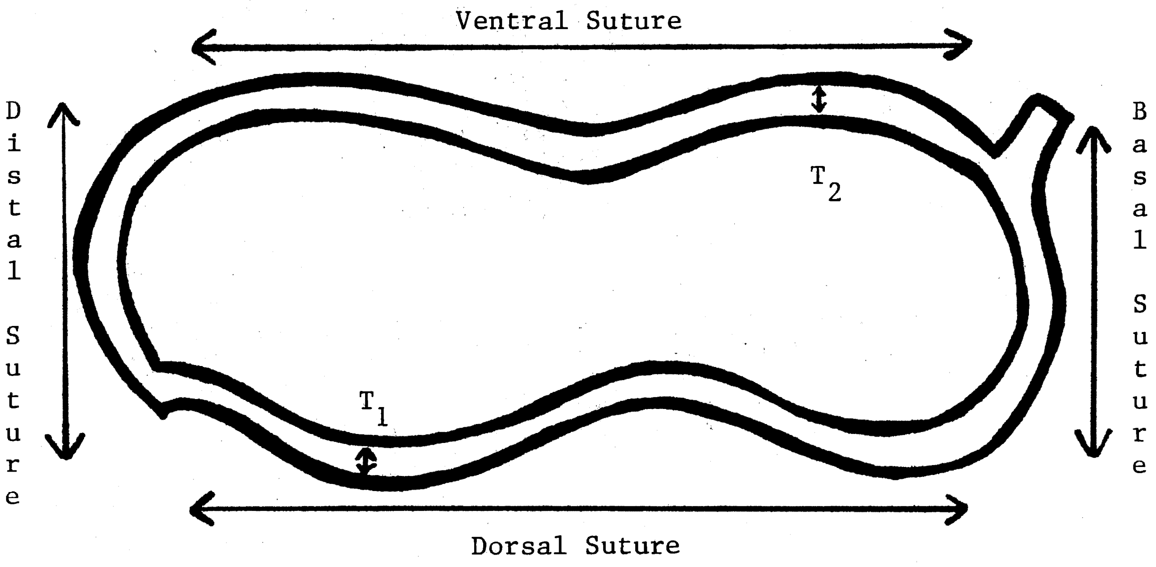

Figure 1. Longitudinal Sketch of the Peanut Pod Showing Positions (T_1 and T_2) Where Shell Thickness Determinations Were Made.

Studies on Heritability and Correlation

To make effective and efficient use of genotypes in advanced generations through selection, estimates of broad sense heritability, expected genetic advance with a selection intensity of five percent, minimum number of genes involved, and correlations have been computed for the following traits.

1. Number of pods - This was determined as the total number of pods per plant in individual crosses. Means and ranges for parental and F_2 populations were calculated.
2. Average Pod Size - This was presented by calculating the average pod size per plant, and getting a mean and range for every cross.
3. Number of seeds - The total number of seeds including mature, intermediate, and immature were calculated for every plant. Means and ranges of all the plants in parental and F_2 populations were computed.
4. Seed Maturity - This was determined by calculating the percentage of mature and intermediate seeds, grouped together, per plant. Mean maturity and range of each population was computed.
5. Shell Thickness - Shell thickness represents the average of two locations, T_1 and T_2, per plant. Means and ranges for parental and F_2 populations were calculated.

The broad sense heritability (h) of a character can be estimated by the following formula.

$$h = \frac{VF_2 - (VP_1 + VP_2)/2}{VF_2} \times 100$$

Where; VF_2 = variance of F_2 population, and VP_1 and VP_2 are the variances of the two parental populations.

Genetic advance measures the difference between mean genotypic value of the population produced by selected lines and mean genotypic value of original population. Expected genetic advance (GA) can be computed by the following formula.

$$GA = (k)\ (\sigma p)\ (H)$$

Where; σp = phenotypic standard deviation of the mean performance of original lines, H = heritability coefficient, and k = constant for selection differential.

The minimum number of genes (k) controlling inheritance of a character can be estimated by the following formula.

$$k = \frac{1}{8}\,\frac{(\overline{P}_1 - \overline{P}_2)^2}{\sigma_G^2}$$

Where; σ_G^2 = genetic variance of F_2, $\overline{P}_1$ = mean of the smaller parent, and $\overline{P}_2$ = mean of the larger parent. Assumptions are equal gene effect, no dominance, and no linkage involved (14).

CHAPTER IV

RESULTS AND DISCUSSION

Studies on Pod Characters

Inheritance of Pod Size

The parental cultivars used in this study represent two distinct categories of pod size. According to our scale given in Chapter III, parents P-0002, P-0006, P-0074, and P-0112 are classified as cultivars of small pod size. Parental lines P-0963, P-1616, P-1617, and P-1618 are classified as large pod size parents (Table II). Hereafter, small pod size parents will be referred to as group I and large pod size parents as group II. The mean and range for average pod size of parental lines are given in Table II. P-1616 of group II had the largest average pod size of 14.1, and ranged from 13.3 to 15.0. P-1618 was the smallest of group II with an average 13.3 pod size, and ranged from 12.4 to 14.0. P-0002 was the smallest in group I with an average pod size of 7.6, and a range from 7.4 to 7.7. P-0006 and P-0112 were the largest in group I, each with an average pod size of 8.0. Population means and ranges for each F_2 are shown in Table III. Many of the crosses exhibited small average pod size except those involving parent P-0074, where medium pod size was observed.

Frequency distributions of F_2 pod populations are shown in Figures 2, 3, and 4. Figure 2 shows that a majority of the pods, in crosses involving parent P-0006, had small size. The same trend was noticed in crosses involving parent P-0002 in Figure 4. However, in crosses of parent P-0074 in Figures 3 and 4, a majority of the pods were medium in size.

Frequency histograms of F_2 plant populations are shown in Figures 5 and 6. All F_2 populations approached normal distribution for pod size, however, most of these were slightly skewed toward small pod size indicating apparent dominance of smaller pods over larger ones. A possible explanation to this trend may be the short crop season in Oklahoma in which some of the genotypes did not have enough time to express their full genetic potential. The widest range of 8.6 to 13.2 average pod size was shown by cross P-0074 x P-1617. No transgressive segregates were observed in either direction. The trend of the majority of F_2 populations toward small or medium pod size, though do not agree with previous findings of Van der Stok (46), Badami (2), Hassan (19), and Patil (35), gives sufficient reason to believe the presence of dominant factors for small pod size since 9 out of 12 crosses exhibited the above trend in their F_2 populations.

Continuous variation in the F_2 populations, as shown in Figures 5 and 6, suggests that pod size is inherited quantitatively. These results agree with previous findings reported by Van der Stok (46), Badami (2), Ilieff (24), and Wynne, et al. (47).

Results shown in Table IV reveal low to medium heritability for pod size. Expected genetic advances were very low ranging from 0.24 to 1.16. The above data indicate that the character could be transmitted to future generations, however, no significant gains could be achieved through selection in early generations. The estimates of the minimum number of genes controlling pod size ranged from 7 to 55, suggesting complex gene action.

Inheritance of Number of Pods

Mean number of pods per plant for the parents are shown in Table II. P-0002 and P-1616 had the highest number of pods in groups I and II, respectively. Means and ranges for the F_2 populations are given in Table III. Considerable variation was observed both within and among F_2 populations, indicating possible genetic diversity. Cross P-0112 x P-1617 out-numbered all other crosses by producing a mean of 63.9 pods per plant. Other crosses with significant numbers of pods were those involving P-0002 and P-0006. Parent P-0002 was apparently able to transmit its superiority for number of pods to its F_2 progeny.

Frequency distributions for number of pods per plant are shown in Figures 7, 8, and 9. A considerable number of transgressive segregates were observed in many F_2 populations. Crosses like P-0002 x P-1616, P-0002 x P-1618, P-0006 x P-0963, P-0006 x P-1616, P-0006 x P-1617, and P-0112 x P-1617 had F_2 plants with more pods than either of their respective parents. The widest range in number of pods, 5 to 198, was exhibited by the F_2 plants of P-0006 x P-1616. The presence of transgressive segregates indicates a valuable genetic potential in these crosses, which could possibly be exploited for the improvement of yield in peanut cultivars.

The F_2 population of almost every cross approached a normal distribution, suggesting multigenic control of the trait. Since heritability and expected genetic advance for number of pods are quite high as shown in Table V, significant gains could be achieved through

TABLE II

MEAN AND RANGE FOR AVERAGE POD SIZE AND NUMBER OF PODS FOR PARENTAL LINES

	Average Pod Size* per Plant		Number of Pods per Plant	
Parent	Mean	Range	Mean	Range
P-0002	7.6	7.4 - 7.7	32.3	20 - 40
P-0006	8.0	7.8 - 8.0	13.0	12 - 14
P-0074	7.7	7.6 - 7.7	23.6	20 - 27
P-0112	8.0	7.7 - 8.1	18.6	9 - 31
P-0963	13.6	12.7 - 14.3	16.6	16 - 18
P-1616	14.1	13.3 - 15.0	19.6	13 - 23
P-1617	13.5	13.2 - 13.8	16.0	8 - 22
P-1618	13.3	12.4 - 14.0	15.0	9 - 20

*Largest diameter of pods in sixteenths of an inch.

TABLE III

MEAN AND RANGE FOR AVERAGE POD SIZE AND NUMBER OF PODS FOR F_2 POPULATIONS

F_2 Population	Average Pod Size* per Plant		Number of Pods per Plant	
	Mean	Range	Mean	Range
P-0002 x P-1616	9.6	8.1 - 11.6	53.3	6 - 186
P-0002 x P-1618	9.5	7.9 - 11.8	59.4	14 - 153
P-0006 x P-0963	9.2	7.0 - 11.5	54.0	2 - 141
P-0006 x P-1616	9.0	7.3 - 11.4	55.4	5 - 198
P-0006 x P-1617	8.4	7.0 - 11.3	57.6	4 - 179
P-0006 x P-1618	9.3	7.6 - 11.2	46.1	7 - 94
P-0074 x P-0963	10.1	7.7 - 12.1	37.7	5 - 96
P-0074 x P-1616	10.1	8.3 - 12.7	39.7	9 - 83
P-0074 x P-1617	10.3	8.6 - 13.2	31.4	6 - 66
P-0112 x P-0963	9.7	8.1 - 12.1	38.1	10 - 73
P-0112 x P-1616	9.4	7.9 - 12.3	55.4	10 - 122
P-0112 x P-1617	9.4	8.2 - 11.3	63.9	7 - 161

*Largest diameter of pods in sixteenths of an inch.

TABLE IV

ESTIMATES OF HERITABILITY, EXPECTED GENETIC ADVANCE WITH SELECTION INTENSITY (K)* OF FIVE PERCENT, AND THE MINIMUM NUMBER OF GENES FOR AVERAGE POD SIZE FROM VARIOUS F_2 POPULATIONS

F_2 Population	Heritability (%)	Expected Genetic Advance	Minimum No. of Genes
P-0002 x P-1616	27.11	0.35	48
P-0002 x P-1618	49.18	0.77	14
P-0006 x P-0963	50.29	0.79	13
P-0006 x P-1616	40.82	0.59	22
P-0006 x P-1617	63.24	1.16	7
P-0006 x P-1618	45.40	0.68	14
P-0074 x P-0963	62.44	1.13	8
P-0074 x P-1616	58.15	1.00	12
P-0074 x P-1617	54.42	0.90	11
P-0112 x P-0963	19.46	0.24	55
P-0112 x P-1616	51.52	0.82	14
P-0112 x P-1617	38.22	0.54	20

*K = 5% = 2.06

TABLE V

ESTIMATES OF HERITABILITY, EXPECTED GENETIC ADVANCE WITH SELECTION INTENSITY (K)* OF FIVE PERCENT, AND THE MINIMUM NUMBER OF GENES FOR NUMBER OF PODS FROM VARIOUS F_2 POPULATIONS

F_2 Population	Heritability %	Expected Genetic Advance	Minimum No. of Genes
P-0002 x P-1616	94.20	55.09	0
P-0002 x P-1618	92.80	48.72	0
P-0006 x P-0963	92.67	48.22	0
P-0006 x P-1616	94.27	55.47	0
P-0006 x P-1617	95.29	61.86	0
P-0006 x P-1618	84.81	30.64	0
P-0074 x P-0963	81.91	27.11	0
P-0074 x P-1616	83.93	29.48	0
P-0074 x P-1617	66.26	16.06	0
P-0112 x P-0963	75.74	21.65	0
P-0112 x P-1616	90.02	40.13	0
P-0112 x P-1617	95.60	64.22	0

*K = 5% = 2.06

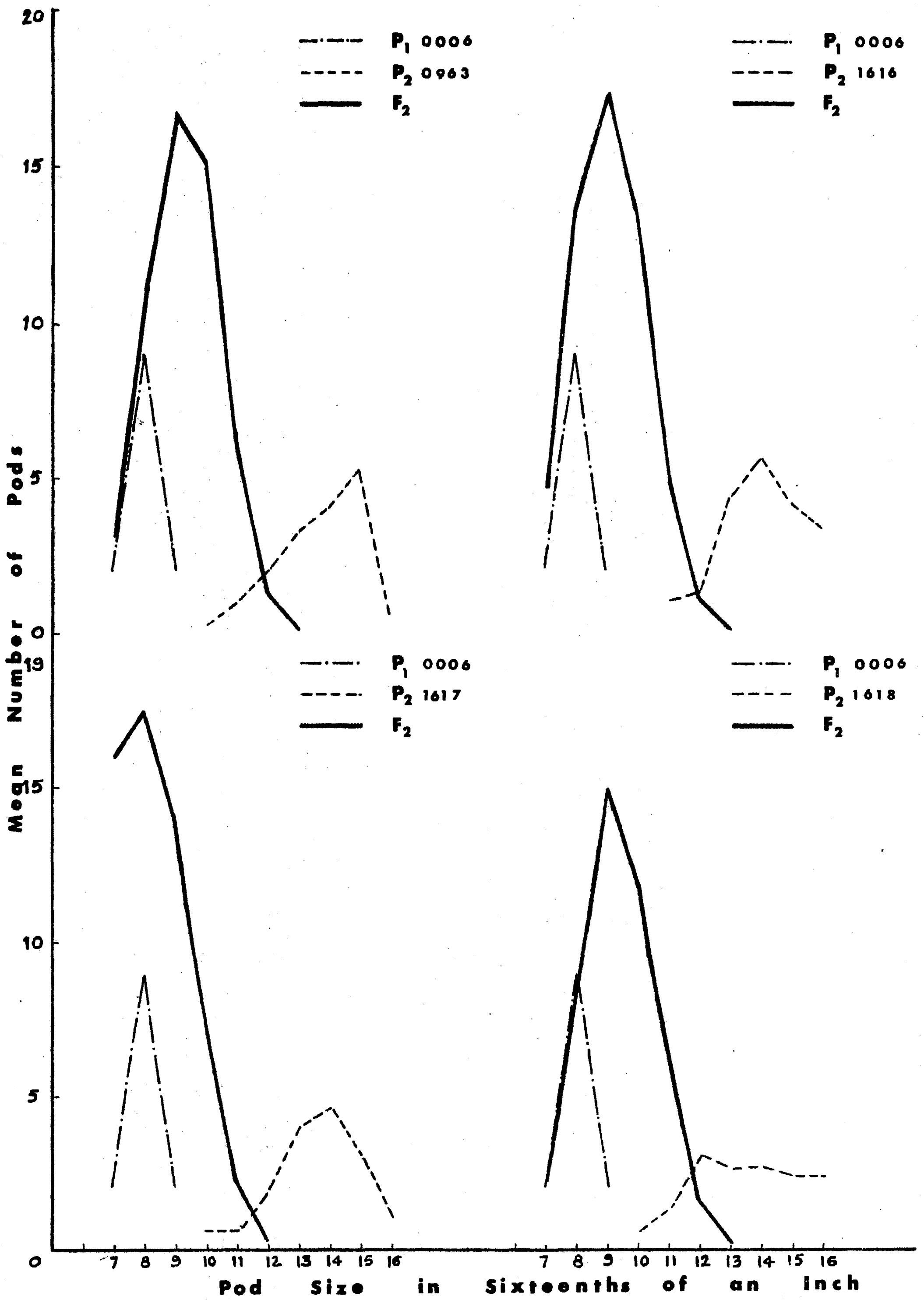

Figure 2. Pod Size Distribution for Parental and F_2 Plants of Crosses P-0006 x P-0963, P-0006 x P-1616, P-0006 x P-1617, and P-0006 x P-1618.

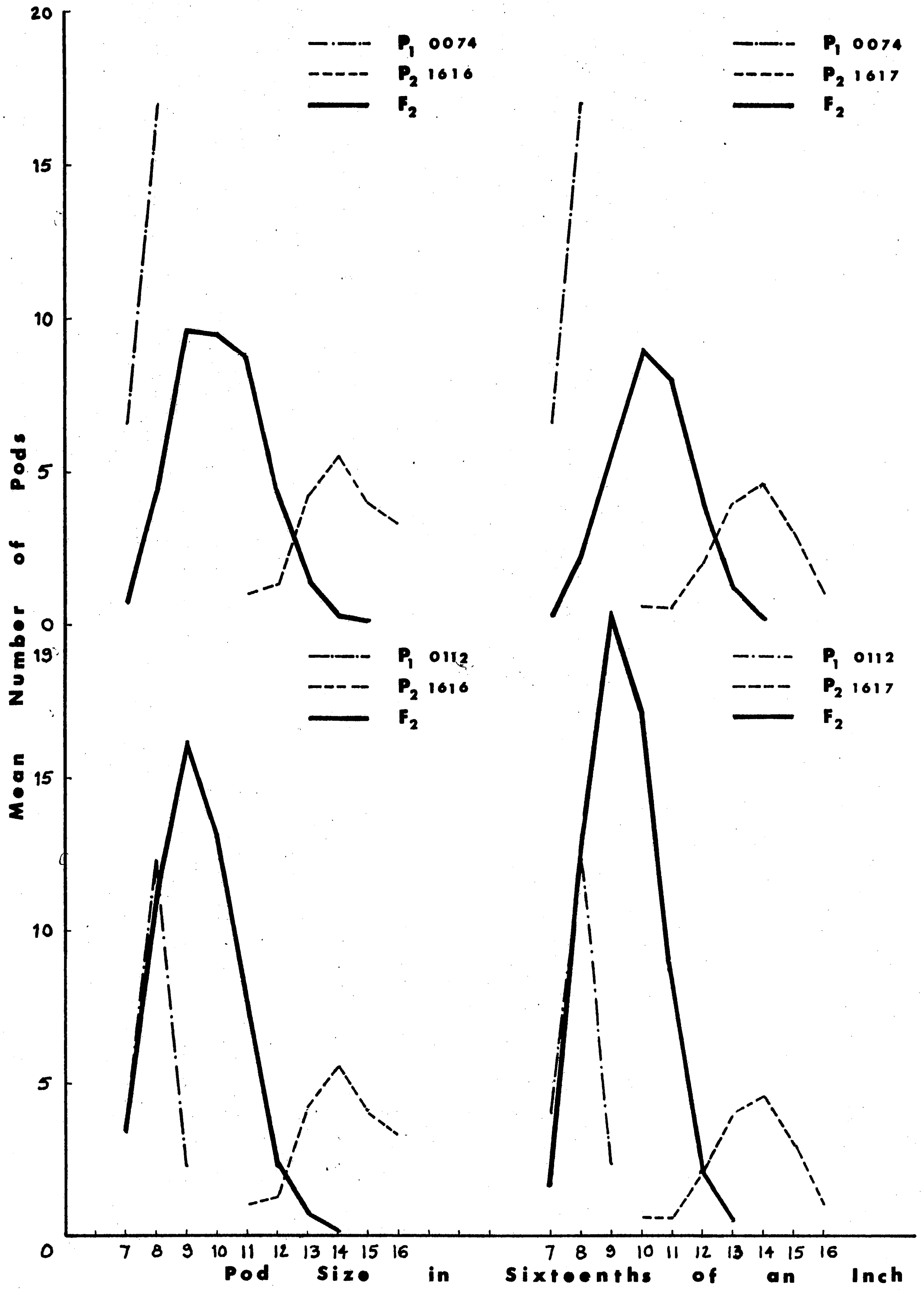

Figure 3. Pod Size Distribution for Parental and F_2 Plants of Crosses P-0074 x P-1616, P-0074 x P-1617, P-0112 x P-1616, and P-0112 x P-1617.

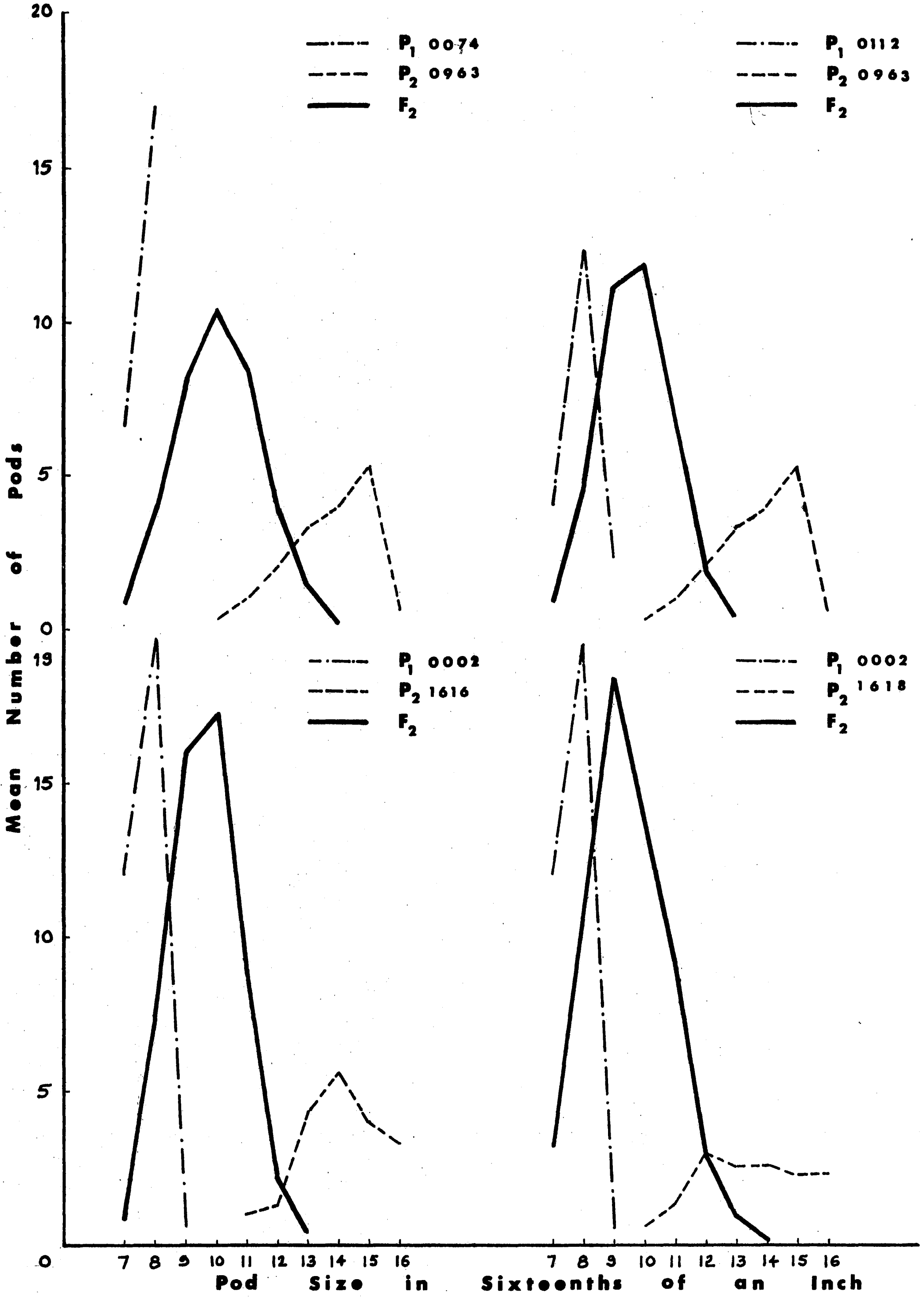

Figure 4. Pod Size Distribution for Parental and F_2 Plants of Crosses P-0074 x P-0963, P-0112 x P-0963, P-0002 x P-1616, and P-0002 x P-1618.

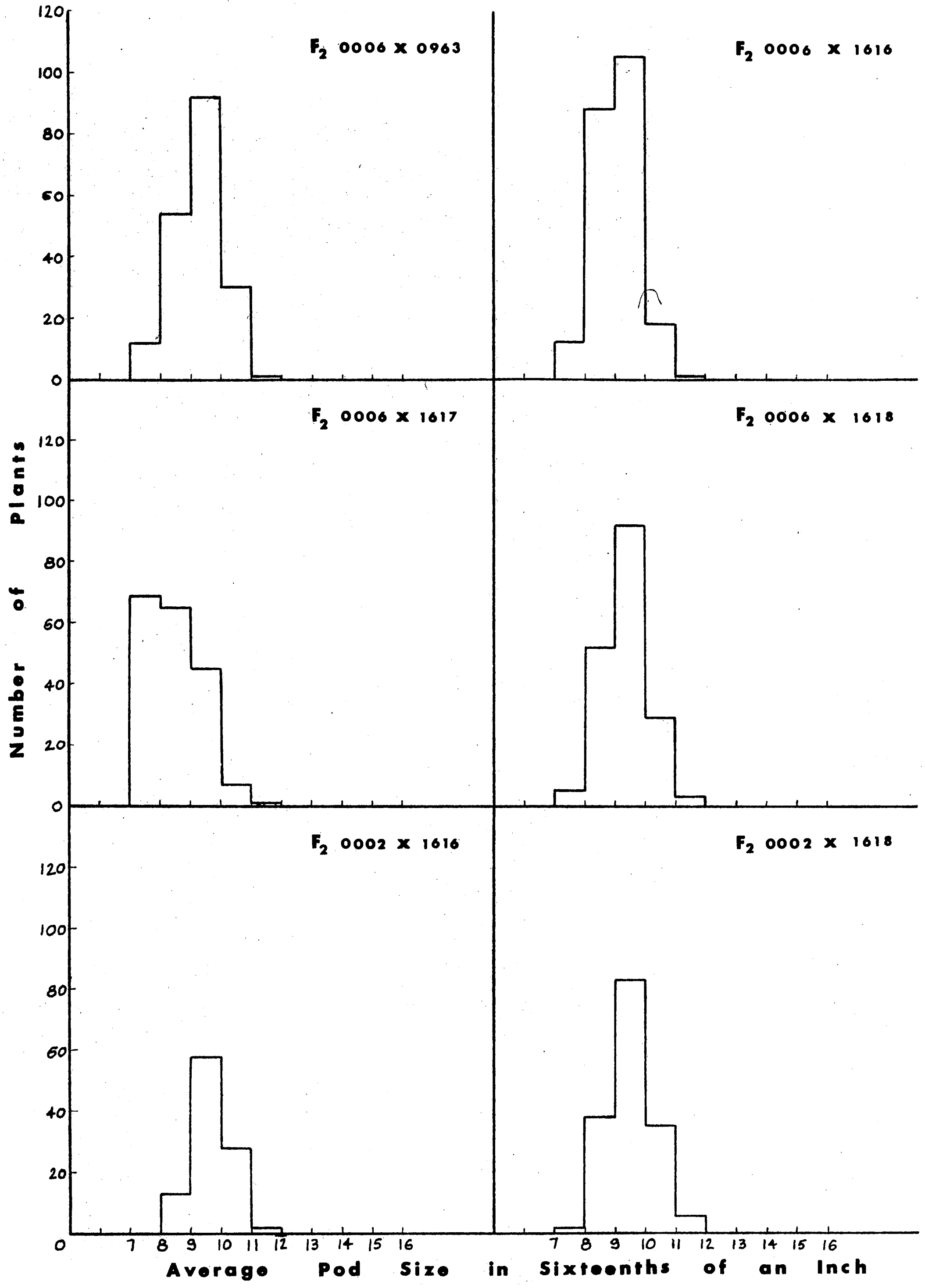

Figure 5. Frequency Histograms on Average Pod Size for F_2 Plants of Crosses P-0006 x P-0963, P-0006 x P-1616, P-0006 x P-1617, P-0006 x P-1618, P-0002 x P-1616, and P-0002 x P-1618.

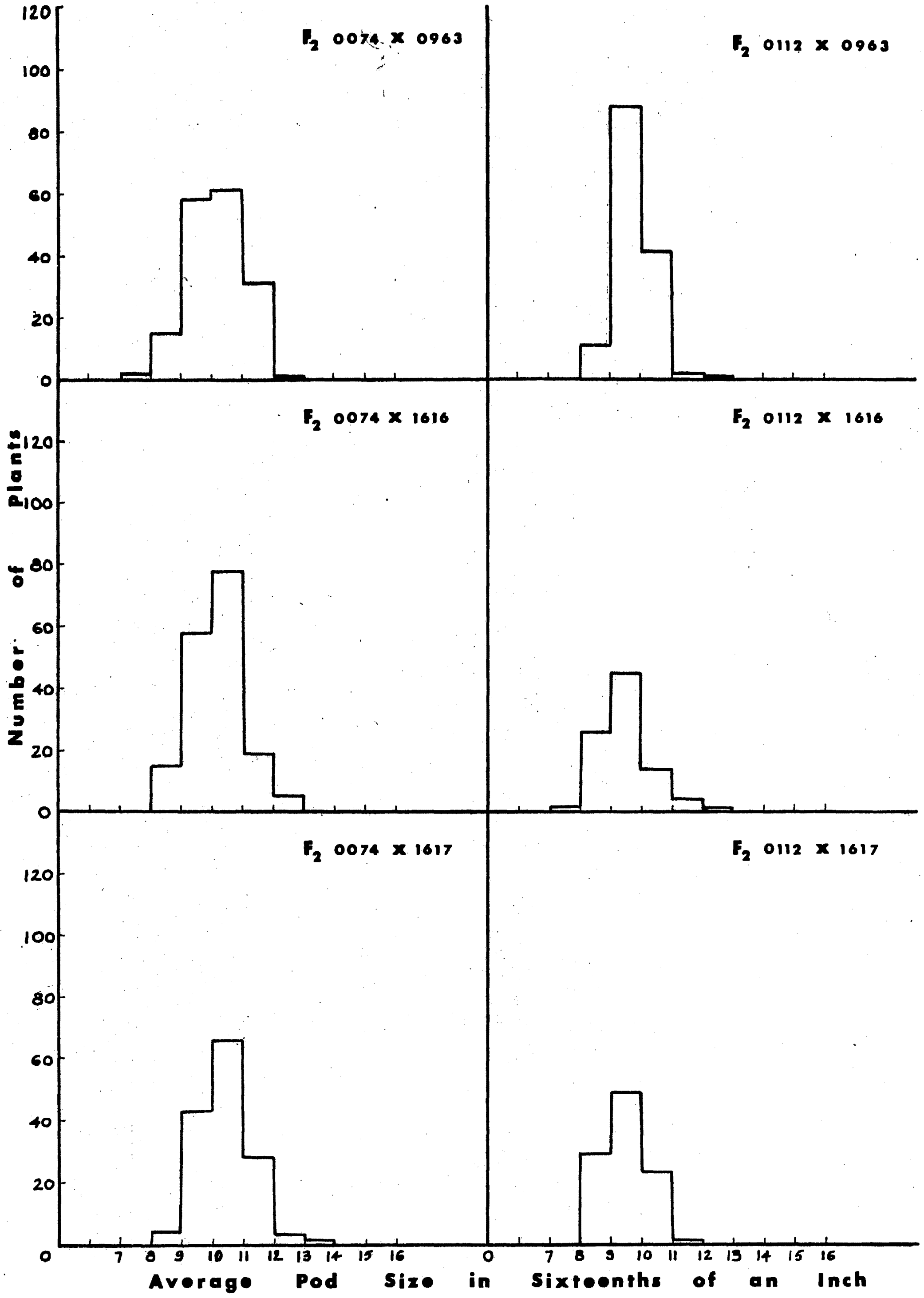

Figure 6. Frequency Histograms on Average Pod Size for F_2 Plants of Crosses P-0074 x P-0963, P-0112 x P-0963, P-0074 x P-1616, P-0112 x P-1616, P-0074 x P-1617, and P-0112 x P-1617.

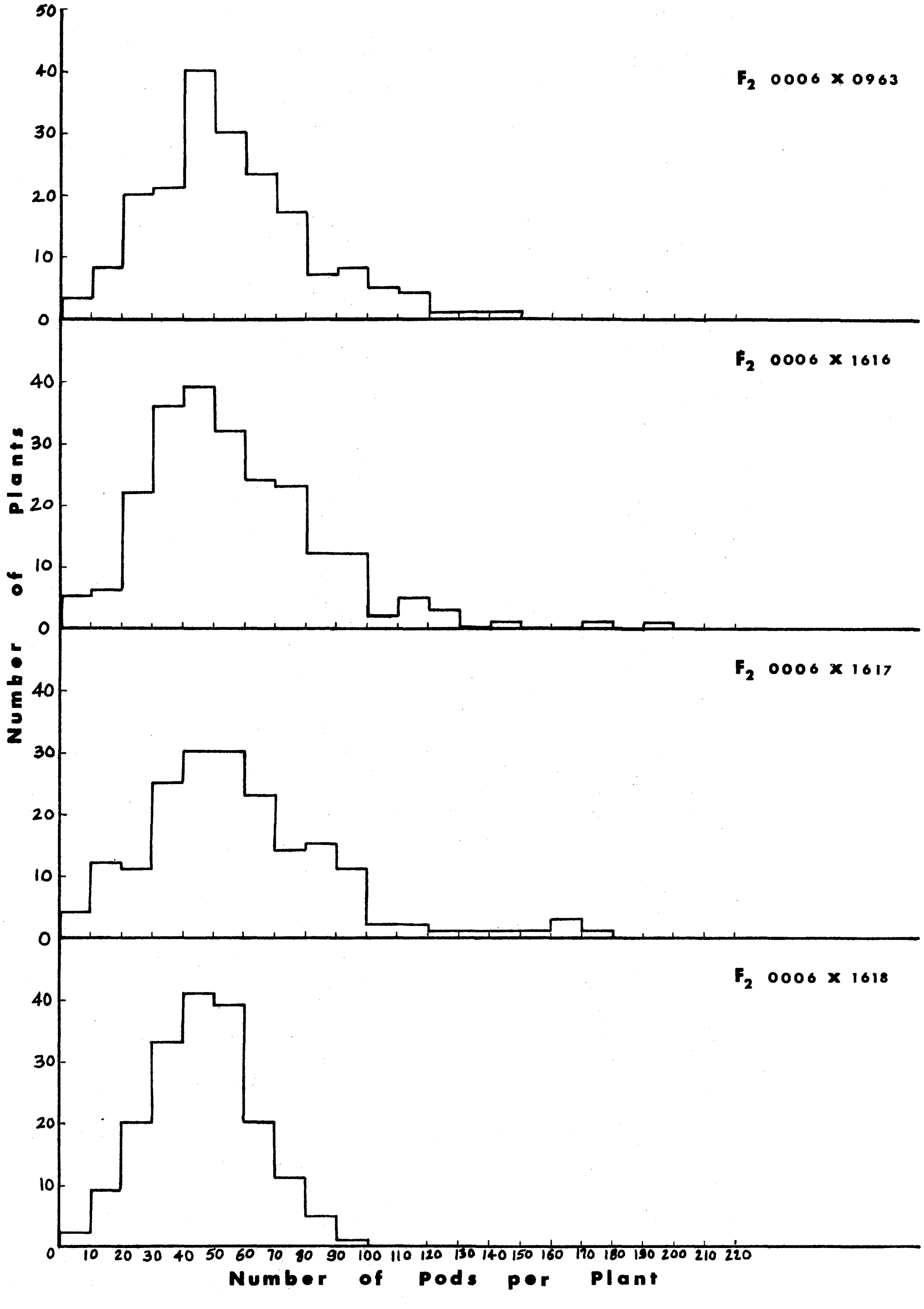

Figure 7. Frequency Histograms on Number of Pods Per Plant for F_2 Plants of Crosses P-0006 x P-0963, P-0006 x P-1616, P-0006 x P-1617, and P-0006 x P-1618.

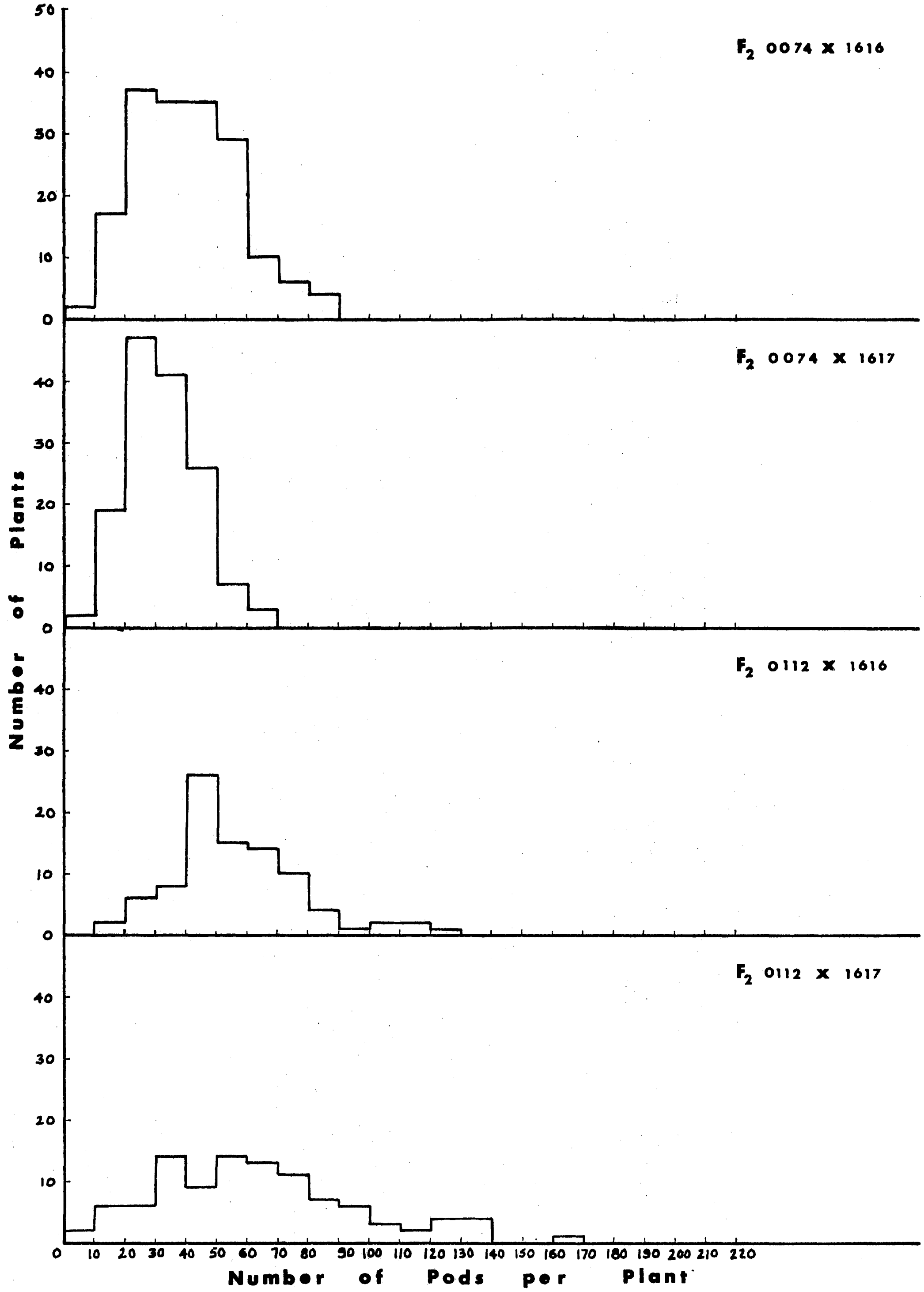

Figure 8. Frequency Histograms on Number of Pods Per Plant for F_2 Plants of Crosses P-0074 x P-1616, P-0074 x P-1617, P-0112 x P-1616, and P-0112 x P-1617.

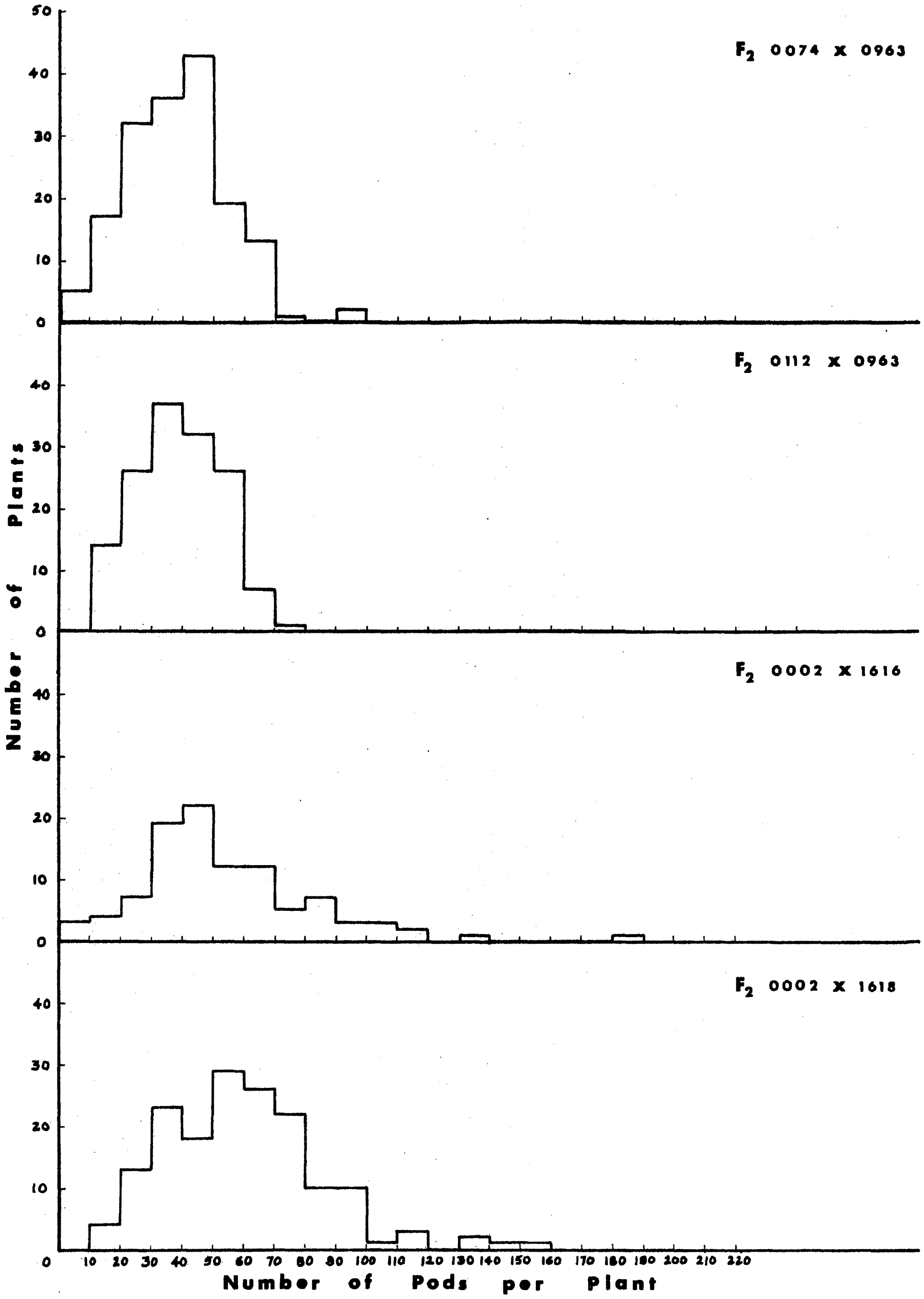

Figure 9. Frequency Histograms on Number of Pods Per Plant for F_2 Plants of Crosses P-0074 x P-0963, P-0112 x P-0963, P-0002 x P-1616, and P-0002 x P-1618.

selection in future generations. These results are in confirmation with Kulkarni and Albuquerque (26), Basu and Ashoka Raj (6), and Patil (35).

Estimates of minimum number of genes were zero as shown in Table V. A possible explanation for this would be that parental lines were phenotypically very similar for number of pods which would result in a very low estimate of number of genes. The formula used to calculate gene number gives the best estimate of number of genes when the parental lines are extremely different genetically. However, if the parental lines were phenotypically similar but in fact differed genetically by having offsetting positive and negative genes for control of the trait in question, this could account for high heritability values and large expected gain while still giving extremely low estimates for number of genes.

Studies on Seed Characters

Inheritance of Seed Maturity

Seed maturity has been classified into categories of mature, intermediate, or immature. Seed maturity as used in the present study is the percentage of mature + intermediate seeds per plant. Means and ranges for seed maturity of the parental lines are given in Table VI. According to this data, the eight peanut cultivars could be grouped into two distinct classes of seed maturity when grown in this area. The Spanish cultivars (P-0002, P-0006, P-0074, and P-0112) exhibited more than 90 percent seed maturity, and therefore are placed in the early or mature group. The Virginia jumbo peanuts (P-0963, P-1616, P-1617, and P-1618) showed less than 50 percent seed maturity and, therefore, are classified in the late or immature group. The highest seed maturity of 98.5 percent was observed for P-0002 in the early group. The lowest seed maturity of 6.9 percent was shown by P-1618 in the late group. Means and ranges for the F_2 populations are given in Table VII. The highest seed maturity was exhibited by cross P-0002 x P-1616. Parent P-0002 was apparently able to transmit its earliness to its F_2 progeny. Histograms for mean number of seeds of all F_2 populations are drawn in Figures 10 and 11. Seeds have been classified into mature, intermediate and immature classes. All F_2 populations had a majority of their seeds falling into the immature group except P-0002 x P-1616.

Frequency distributions for maturity percentage are shown in Figures 12 and 13. The F_2 plants showed a wide range of 0 to 100 percent maturity in almost every cross. Distributions in Figure 12 involving parent P-0006 were skewed toward late maturity and earliness about equally. The majority of the plants in the F_2 of P-0002 x P-1618 were immature while the F_2 of P-0002 x P-1616 had more mature plants. The F_2 populations of P-0074 x P-0963, P-0074 x P-1616, and P-0112 x P-1616 were all skewed toward immature or late maturity while the F_2's of P-0074 x P-1617, P-0112 x P-0963 and P-0112 x P-1617 were slightly skewed toward earlier maturity.

To further evaluate and understand seed maturity, heritability, minimum number of genes, and expected genetic advance estimates have been computed and are given in Table VIII. Cross P-0112 x P-1617 showed highest heritability of 93.1 percent among all F_2 populations. Considering the various heritability estimates from 10.05 to 93.1 percent and low to high genetic advance estimates from 3.07 to 50.01, one could expect a potential gain in early generations of selection in at least some of the populations. The above findings for high heritability estimates are in agreement with Gupton (16), Kulkarni and Albuquerque (26), and Patil (35).

Estimates of minimum number of genes varied from 1 to 24, which is not unexpected since the method of estimating gene number is highly variable depending upon various assumptions. However, fairly simple inheritance is indicated by 10 of the 12 crosses estimating 4 genes or less, controlling the seed maturity.

Inheritance of Number of Seeds

Since the number of seeds is a major component of yield, this character was also evaluated in the F_2 populations available. Means and ranges for number of seeds per plant for the parental lines are given in Table VI. P-0074 and P-1616 were the highest Spanish and jumbo types, respectively. Means and ranges of the F_2 populations are given in Table VII. Wide ranges were exhibited in all F_2 populations, indicating a possible genetic diversity. The highest mean number of seeds per plant was observed in the F_2 of P-0112 x P-1617 with a mean of 94.6 and a range of 6 to 225 seeds per plant. Transgressive segregates were frequently observed in both directions of low and high numbers of seeds. Those segregates which fell outside (above) the parental range would be especially important in a breeding program concerned with improved yield. Since heritability and expected genetic advance estimates for this trait are considerably high as given in Table IX, significant changes could be achieved through selection.

TABLE VI

MEAN AND RANGE FOR SEED MATURITY AND NUMBER OF SEEDS PER PLANT FOR PARENTAL LINES

	Seed Maturity (%)		Number of Seeds per Plant	
Parent	Mean	Range	Mean	Range
P-0002	98.5	95.5 - 100	77.0	68 - 82
P-0006	95.1	91.0 - 99.0	75.6	56 - 107
P-0074	92.8	78.6 - 100	81.6	61 - 120
P-0112	95.2	85.7 - 100	59.6	28 - 102
P-0963	29.1	5.8 - 65.9	37.6	32 - 47
P-1616	32.9	8.1 - 49.1	40.6	24 - 61
P-1617	13.1	0 - 22.2	31.3	23 - 36
P-1618	6.9	0 - 12.5	27.3	14 - 36

TABLE VII

MEAN AND RANGE FOR SEED MATURITY AND NUMBER OF SEEDS PER PLANT FOR F_2 POPULATIONS

F_2 Population	Seed Maturity (%)		No. of Seeds per Plant	
	Mean	Range	Mean	Range
P-0002 x P-1616	79.1	0 - 100	77.9	6 - 287
P-0002 x P-1618	38.4	0 - 100	87.9	11 - 239
P-0006 x P-0963	58.0	0 - 100	78.7	2 - 198
P-0006 x P-1616	37.4	0 - 90.9	79.4	6 - 264
P-0006 x P-1617	47.2	0 - 100	80.6	1 - 255
P-0006 x P-1618	58.2	0 - 100	68.4	5 - 131
P-0074 x P-0963	44.4	0 - 100	58.5	6 - 156
P-0074 x P-1616	38.8	0 - 100	60.0	13 - 139
P-0074 x P-1617	59.0	0 - 97	47.1	9 - 104
P-0112 x P-0963	61.8	10 - 100	58.8	12 - 115
P-0112 x P-1616	45.1	10 - 88.8	84.9	14 - 202
P-0112 x P-1617	64.2	0 - 100	94.6	6 - 255

TABLE VIII

ESTIMATES OF HERITABILITY, EXPECTED GENETIC ADVANCE WITH SELECTION INTENSITY (K)* OF FIVE PERCENT, AND THE MINIMUM NUMBER OF GENES FOR SEED MATURITY FROM VARIOUS F_2 POPULATIONS

F_2 Population	Heritability %	Expected Genetic Advance	Minimum No. of Genes
P-0002 x P-1616	10.05	3.07	24
P-0002 x P-1618	33.23	13.03	8
P-0006 x P-0963	61.33	31.60	1
P-0006 x P-1616	56.08	27.12	1
P-0006 x P-1617	59.54	29.99	2
P-0006 x P-1618	61.93	32.16	2
P-0074 x P-0963	62.36	32.57	1
P-0074 x P-1616	43.11	18.31	2
P-0074 x P-1617	52.02	24.07	3
P-0112 x P-0963	42.83	18.15	3
P-0112 x P-1616	30.34	11.65	4
P-0112 x P-1617	93.12	50.01	1

*K = 5% = 2.06

TABLE IX

ESTIMATES OF HERITABILITY AND EXPECTED GENETIC ADVANCE WITH SELECTION INTENSITY (K)* OF FIVE PERCENT AND THE MINIMUM NUMBER OF GENES FOR NUMBER OF SEEDS PER PLANT FROM VARIOUS F_2 POPULATIONS

F_2 Population	Heritability %	Expected Genetic Advance	Minimum No. of Genes
P-0002 x P-1616	75.44	69.95	0
P-0002 x P-1618	69.68	58.16	0
P-0006 x P-0963	70.99	60.57	0
P-0006 x P-1616	73.95	66.59	0
P-0006 x P-1617	78.55	77.95	0
P-0006 x P-1618	41.51	24.94	0
P-0074 x P-0963	42.86	26.05	0
P-0074 x P-1616	35.82	20.54	0
P-0074 x P-1617	11.87	5.15	0
P-0112 x P-0963	13.19	6.50	0
P-0112 x P-1616	60.91	44.77	0
P-0112 x P-1617	82.15	89.35	0

*K = 5% = 2.06

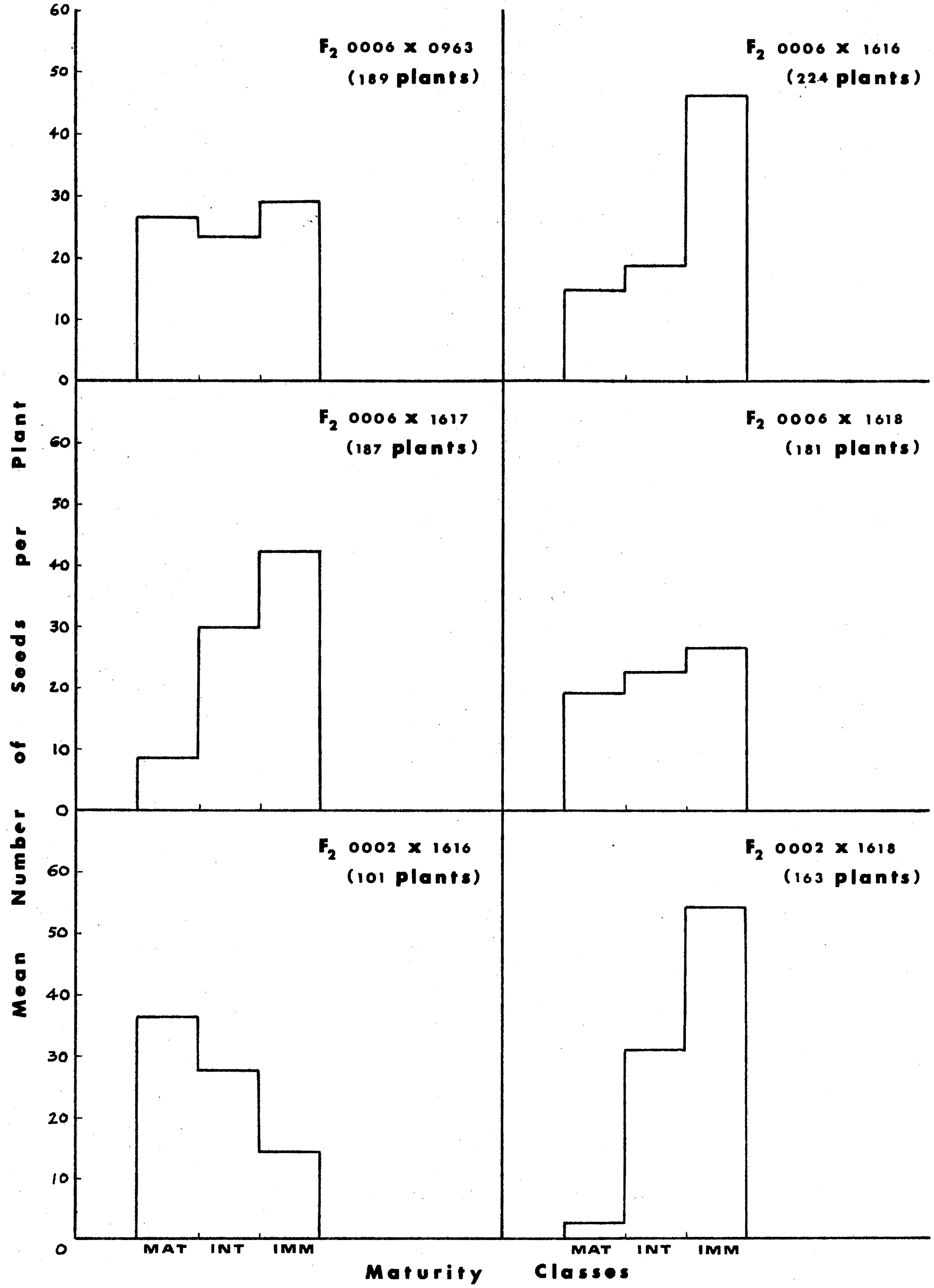

Figure 10. Seed Maturity Distribution for F_2 Plants of Crosses P-0006 x P-0963, P-0006 x P-1616, P-0006 x P-1617, P-0006 x P-1618, P-0002 x P-1616, and P-0002 x P-1618.

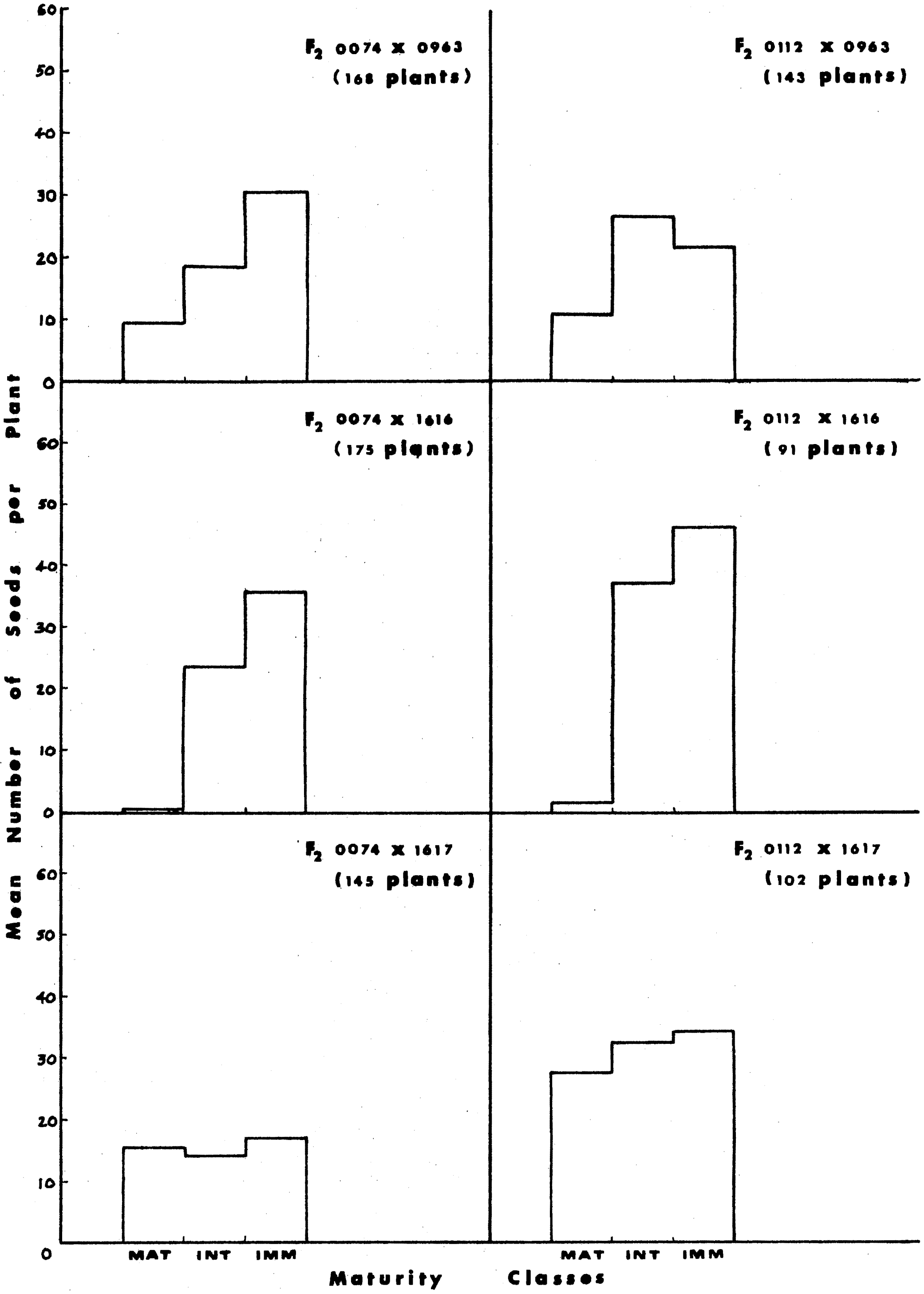

Figure 11. Seed Maturity Distribution for F_2 Plants of Crosses P-0074 x P-0963, P-0112 x P-0963, P-0074 x P-1616, P-0112 x P-1616, P-0074 x P-1617, and P-0112 x P-1617.

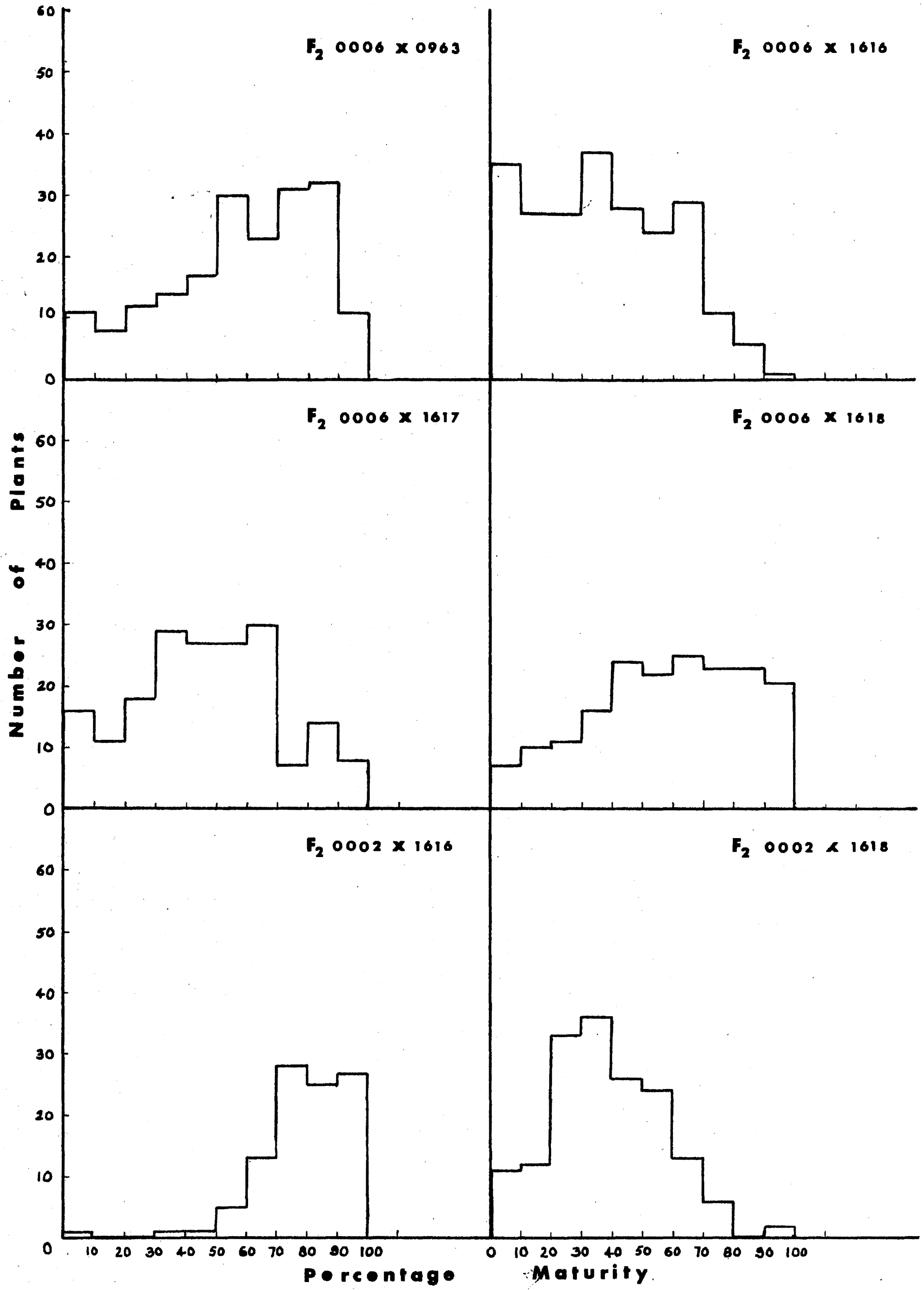

Figure 12. Frequency Histograms on Percentage Maturity for F_2 Plants of Crosses P-0006 x P-0963, P-0006 x P-1616, P-0006 x P-1617, P-0006 x P-1618, P-0002 x P-1616, and P-0002 x P-1618.

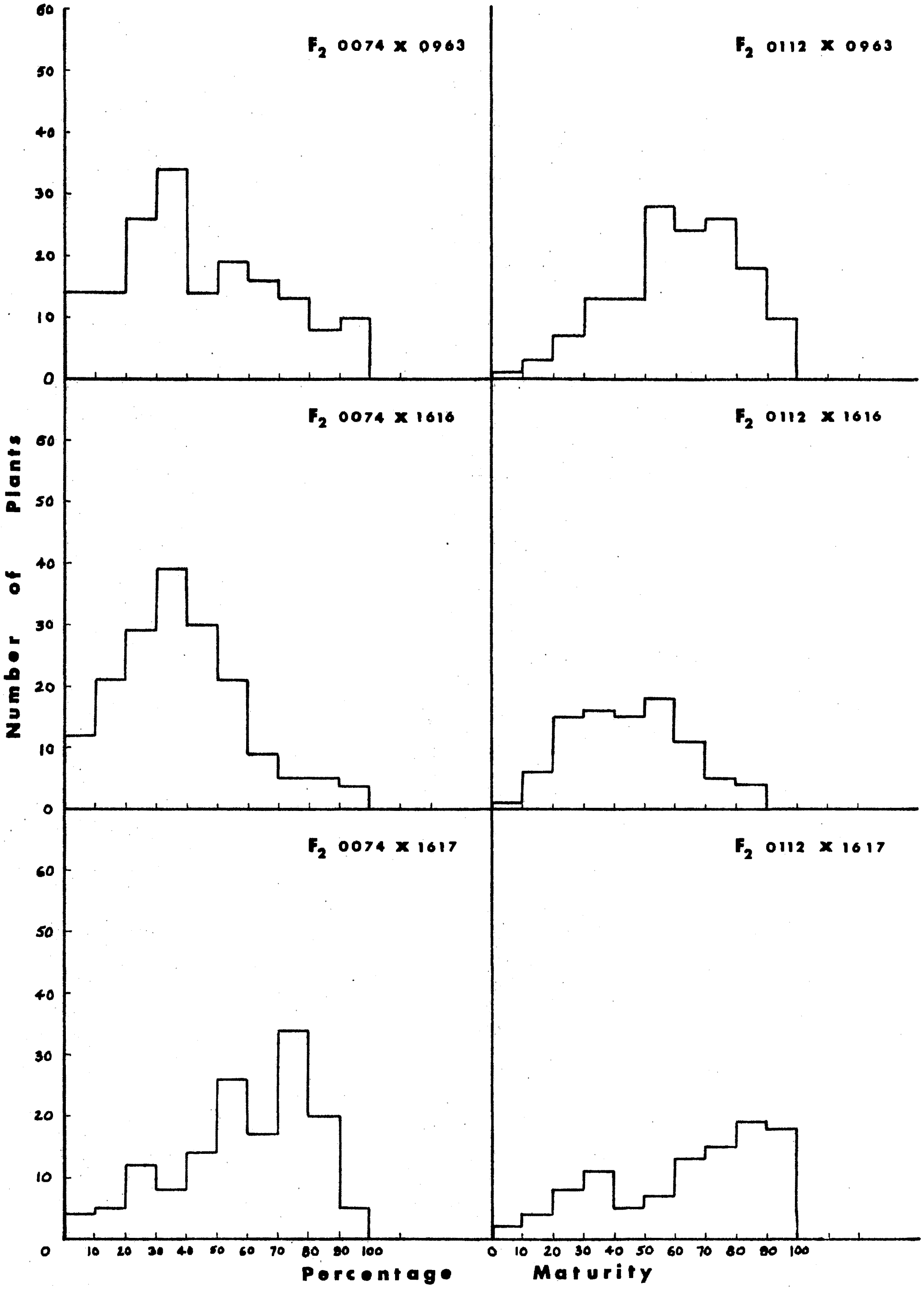

Figure 13. Frequency Histograms on Percentage Maturity for F_2 Plants of Crosses P-0074 x P-0963, P-0112 x P-0963, P-0074 x P-1616, P-0112 x P-1616, P-0074 x P-1617, and P-0112 x P-1617.

Estimates of minimum number of genes were zero as shown in Table IX. A possible explanation for this would be that formulae used to calculate gene number give the best estimate of number of genes when the parental lines are extremely different genetically. However, if the parental lines were phenotypically similar but in fact differed genetically by having offsetting positive and negative genes for control of the trait in question, this could account for high heritability values and large expected gain while still giving extremely low estimates for number of genes.

Inheritance of Shell Thickness

Shell thickness is an important factor in peanut breeding. Different criteria could be established depending upon the varieties grown in different areas and the machinery available for the shelling process. Genetic knowledge of this character will enhance the prospects of achieving an appropriate shell thickness in commercial varieties for resistance to insects or for resistance to mechanical damage in the digging, combining and shelling processes, and yet which will give satisfactory grade and shelling percentage.

Shell thickness, which is an average of two points of measurement (T_1 and T_2) on the shell, has been classified as thick, medium, or thin. Means and ranges of the parental lines for shell thickness are given in Table X. All four Spanish cultivars had relatively thin shells, P-0006 being the thinnest with a mean of .031 inches and a narrow range of .030 to .031 inches. The four jumbo parental lines can be classified in the thick shell category. P-1618 had the thickest shells with a mean thickness of 0.114 inches and a range from 0.092 to 0.129 inches.

Means and ranges for the F_2 populations are given in Table XI. Medium shell thicknesses with wide ranges were exhibited by all F_2 populations. Crosses involving parent P-0074 had the highest means and ranges. Transgressive segregates for both thin and thick shells were observed within the F_2 populations, indicating possible genetic diversity.

Frequency distributions of F_2 plants for shell thickness are shown in Figures 14, 15, and 16. All F_2 populations approached normal distribution with a few transgressive segregates in either direction. Continuous variation within the F_2 populations indicates the likelihood of the trait being controlled by multiple genes. The results are in confirmation with Van der Stok (46) and Seshadri (40). Further evaluation of the character was done by computing estimates of heritability, expected genetic advance, and the minimum number of genes involved. The results are given in Table XII. Estimates for the minimum number of genes varied from 3 to 30, again suggesting quantitative inheritance of the character. Heritability estimates of 23 to 96 percent, with expected genetic advance of .0045 to .0165 were obtained for this character.

Studies on Correlation

A knowledge of the relationship among agronomically important traits is very important to a plant breeder in planning a successful breeding program. Phenotypic correlation coefficients were estimated independently in each of the F_2 populations among the following

TABLE X

MEAN T_1, T_2, SHELL THICKNESS AND RANGE FOR SHELL THICKNESS FOR PARENTAL LINES

Parent	T_1 Mean (in)	T_2 Mean (in)	Shell Thickness Mean (in)	Shell Thickness Range (in)
P-0002	0.037	0.034	0.036	0.034 - 0.037
P-0006	0.029	0.033	0.031	0.030 - 0.031
P-0074	0.029	0.039	0.034	0.030 - 0.037
P-0112	0.031	0.039	0.035	0.032 - 0.036
P-0963	0.079	0.107	0.093	0.080 - 0.102
P-1616	0.083	0.128	0.106	0.102 - 0.111
P-1617	0.079	0.101	0.090	0.089 - 0.092
P-1618	0.104	0.124	0.114	0.090 - 0.129

TABLE XI

MEAN T_1, T_2, SHELL THICKNESS AND RANGE FOR SHELL THICKNESS FOR F_2 POPULATIONS

F_2 Population	T_1 Mean (in)	T_2 Mean (in)	Shell Thickness Mean (in)	Shell Thickness Range (in)
P-0002 x P-1616	0.048	0.065	0.056	0.032 - 0.087
P-0002 x P-1618	0.047	0.066	0.057	0.034 - 0.085
P-0006 x P-0963	0.040	0.057	0.049	0.019 - 0.084
P-0006 x P-1616	0.039	0.056	0.048	0.025 - 0.081
P-0006 x P-1617	0.031	0.045	0.038	0.017 - 0.067
P-0006 x P-1618	0.043	0.063	0.053	0.027 - 0.108
P-0074 x P-0963	0.050	0.082	0.066	0.040 - 0.097
P-0074 x P-1616	0.049	0.075	0.062	0.028 - 0.131
P-0074 x P-1617	0.048	0.077	0.062	0.027 - 0.126
P-0112 x P-0963	0.048	0.069	0.058	0.038 - 0.089
P-0112 x P-1616	0.044	0.066	0.055	0.037 - 0.084
P-0112 x P-1617	0.043	0.061	0.052	0.023 - 0.075

TABLE XII

ESTIMATES OF HERITABILITY, EXPECTED GENETIC ADVANCE WITH SELECTION INTENSITY (K)* OF FIVE PERCENT, AND THE MINIMUM NUMBER OF GENES FOR SHELL THICKNESS FROM VARIOUS F_2 POPULATIONS

F_2 Population	Heritability %	Expected Genetic Advance	Minimum No. of Genes
P-0002 x P-1616	23.53	0.0045	29
P-0002 x P-1618	41.37	0.0091	15
P-0006 x P-0963	49.25	0.0117	7
P-0006 x P-1616	25.27	0.0049	30
P-0006 x P-1617	30.61	0.0062	14
P-0006 x P-1618	49.25	0.0117	13
P-0074 x P-0963	57.50	0.0150	4
P-0074 x P-1616	58.02	0.0152	6
P-0074 x P-1617	60.91	0.0165	3
P-0112 x P-0963	30.61	0.0062	14
P-0112 x P-1616	41.37	0.0091	13
P-0112 x P-1617	96.87	0.0160	6

*K = 5% = 2.06

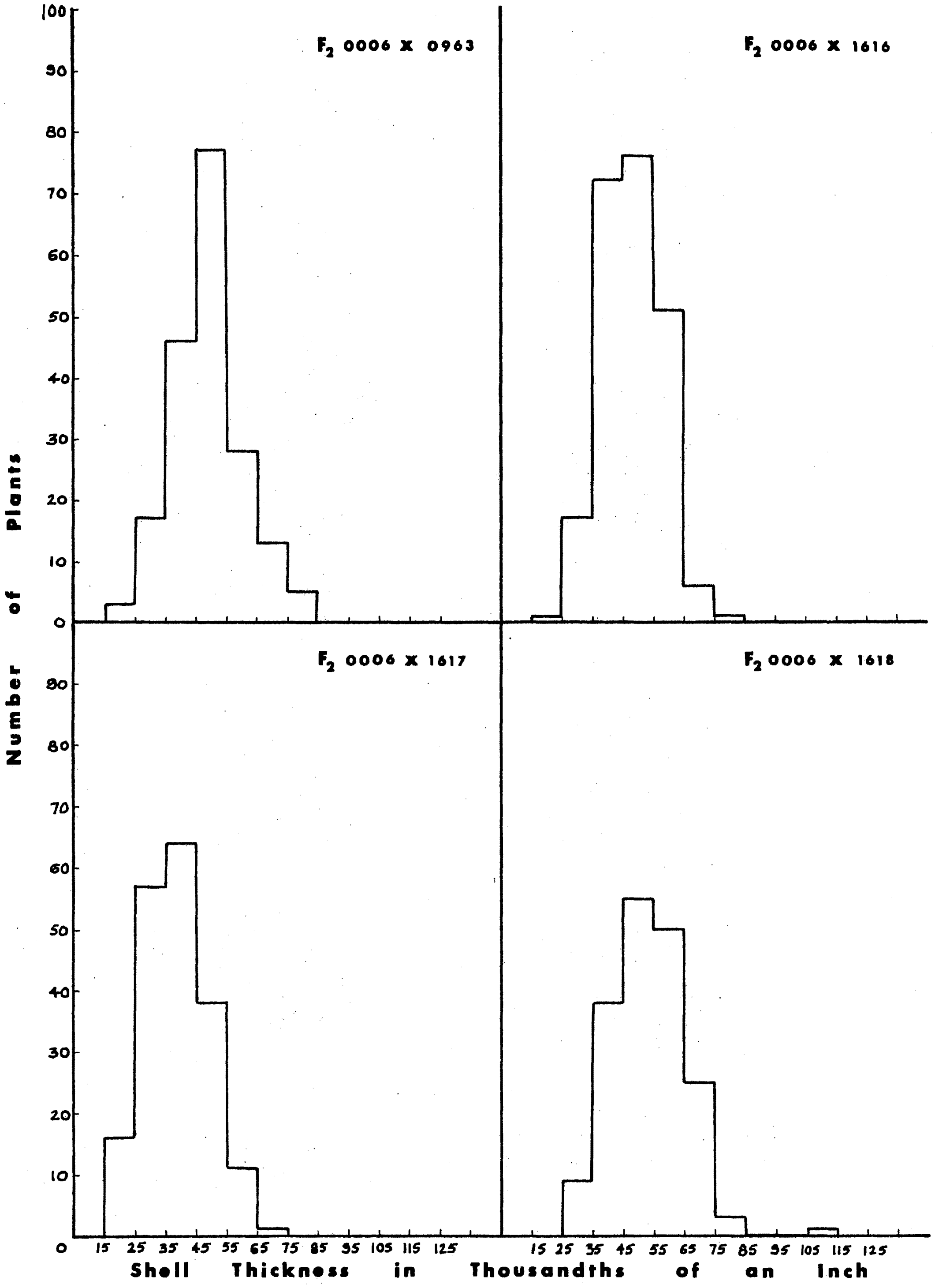

Figure 14. Frequency Histograms on Shell Thickness for F_2 Plants of Crosses P-0006 x P-0963, P-0006 x P-1616, P-0006 x P-1617, and P-0006 x P-1618.

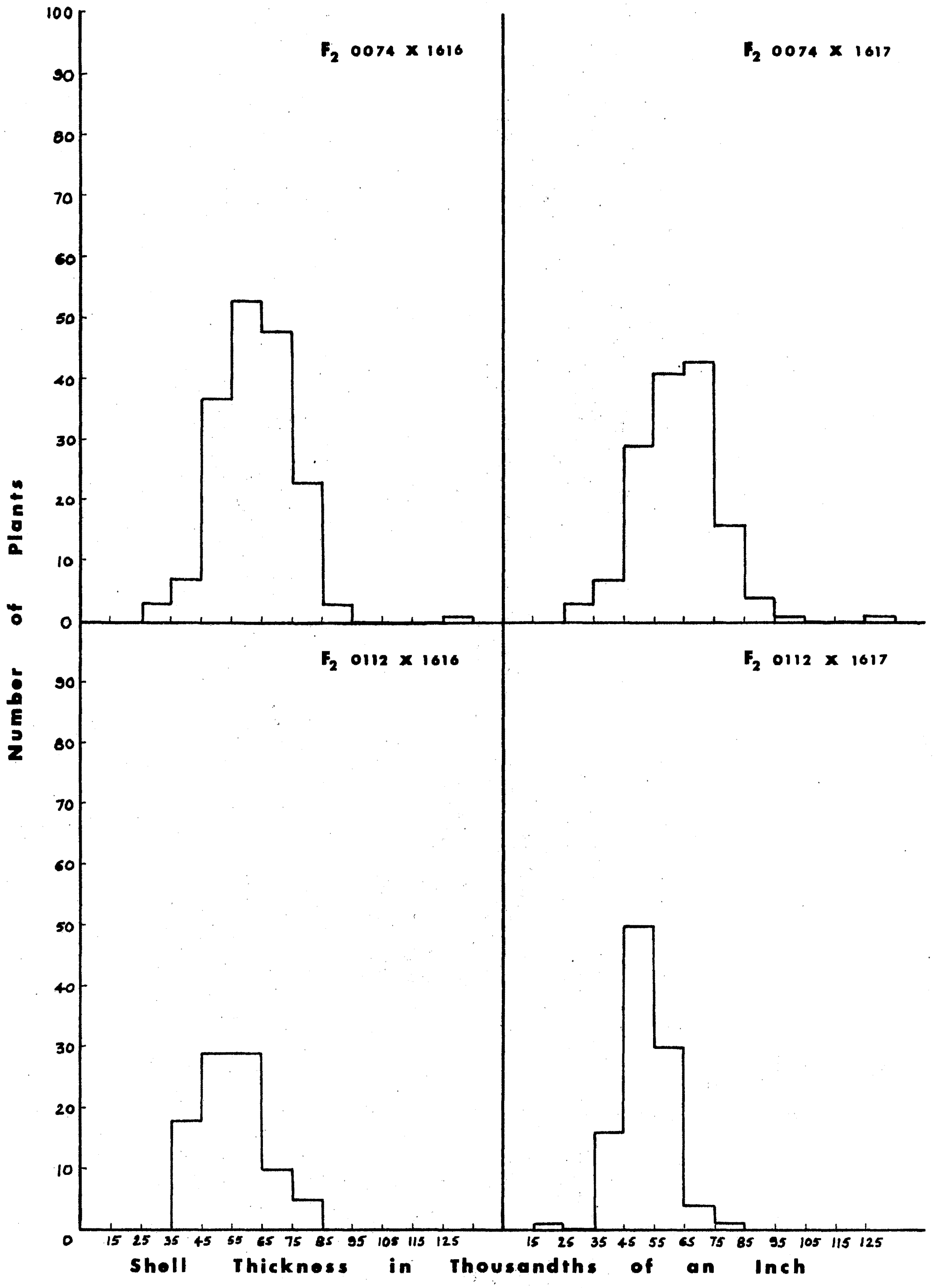

Figure 15. Frequency Histograms on Shell Thickness for F_2 Plants of Crosses P-0074 x P-1616, P-0074 x P-1617, P-0112 x P-1616, and P-0112 x P-1617.

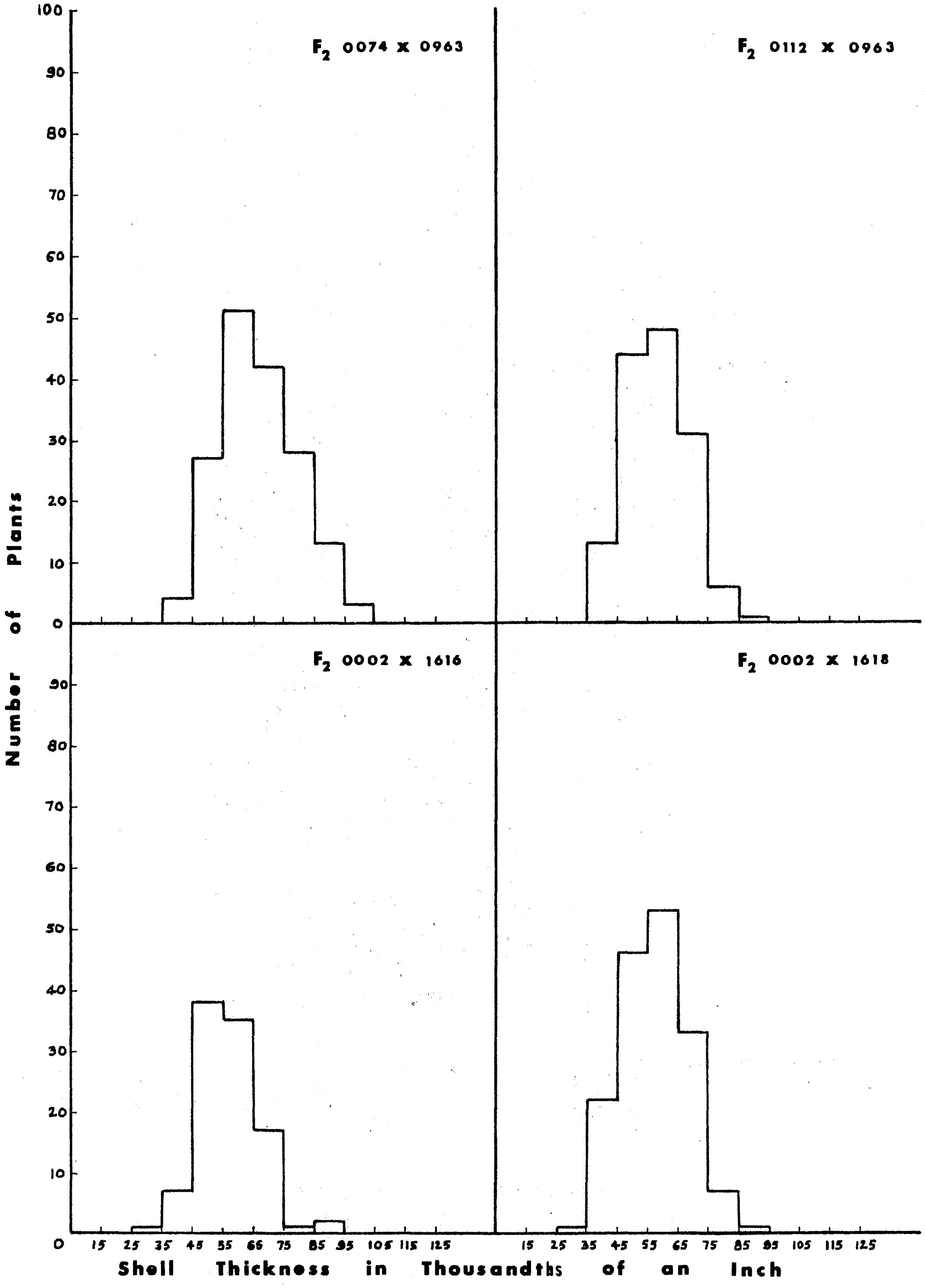

Figure 16. Frequency Histograms on Shell Thickness for F_2 Plants of Crosses P-0074 x P-0963, P-0112 x P-0963, P-0002 x P-1616, and P-0002 x P-1618.

five traits.

1. Pod Number
2. Average Pod Size
3. Seed Number
4. Seed Maturity
5. Shell Thickness

The results are given in Tables XIII through XVIII. The data presented in the above tables are summarized in Table XIX.

As expected, highly significant positive correlations were observed between pod number and seed number. Pod number was negatively correlated with average pod size. Significant positive correlations were observed between pod number and seed maturity in all F_2 populations except P-0002 x P-1618. The above relationship of smaller pods with high number of pods per plant and more seed maturity is typical of Spanish peanuts. Pod number was not significantly correlated with shell thickness with the exception of two crosses, P-0006 x P-1616 and P-0112 x P-1617 where positive correlations were observed.

Seed number, another important yield component, was negatively correlated with average pod size and positively related to seed maturity. Seed number showed a significant positive correlation with shell thickness in populations of P-0006 x P-0963, P-0006 x P-1616, and P-0112 x P-1617. Average pod size, as expected, was significantly related to shell thickness.

The relationship of seed maturity with pod number and seed number is important to a plant breeder, achieving higher yield goals with a good grade of peanuts.

The above correlation findings are in agreement with Badwal and

TABLE XIII

PHENOTYPIC CORRELATION COEFFICIENTS ESTIMATED FROM F_2 P-0002 x P-1616[a] AND F_2 P-0002 x P-1618[b] DATA

	Pod Number	Average Pod Size	Seed Number	Seed Maturity	Shell Thickness
Pod Number		-.061	.978**	.264**	-.052
Average Pod Size	-.180*		-.098	-.133	.085
Seed Number	.942**	-.159*		.314**	-.057
Seed Maturity	-.023	-.039	-.006		.040
Shell Thickness	-.034	.578**	-.016	-.053	

[a] P-0002 x P-1616 upper right-hand corner

[b] P-0002 x P-1618 lower left-hand corner

*,** Significantly different from zero at the .05 and .01 levels of probability, respectively (100 d.f. for $F_2{}^a$ and 162 d.f. for $F_2{}^b$).

TABLE XIV

PHENOTYPIC CORRELATION COEFFICIENTS ESTIMATED FROM F_2 P-0006 x P-0963[a] AND F_2 P-0006 x P-1616[b] DATA

	Pod Number	Average Pod Size	Seed Number	Seed Maturity	Shell Thickness
Pod Number		.109	.948**	.335**	.118
Average Pod Size	-.039		.105	.207**	.401**
Seed Number	.946**	-.073		.396**	.152*
Seed Maturity	.327**	-.003	.358**		.398**
Shell Thickness	.150*	.288**	.143*	.070	

[a] P-0006 x P-0963 upper right-hand corner

[b] P-0006 x P-1616 lower left-hand corner

*,** Significantly different from zero at the .05 and .01 levels of probability, respectively (188 d.f. for F_2^a and 223 d.f. for F_2^b).

TABLE XV

PHENOTYPIC CORRELATION COEFFICIENTS ESTIMATED FROM F_2 P-0006 x P-1617[a] AND F_2 P-0006 x P-1618[b] DATA

	Pod Number	Average Pod Size	Seed Number	Seed Maturity	Shell Thickness
Pod Number		-.144*	.953**	.027	.001
Average Pod Size	.007		-.179**	-.025	.581**
Seed Number	.941**	-.046		.029	-.018
Seed Maturity	.216**	.130	.262**		-.047
Shell Thickness	.109	.271**	.104	.079	

[a] P-0006 x P-1617 upper right-hand corner

[b] P-0006 x P-1618 lower left-hand corner

*,** Significantly different from zero at the .05 and .01 levels of probability, respectively (186 d.f. for F_2[a] and 180 d.f. for F_2[b]).

TABLE XVI

PHENOTYPIC CORRELATION COEFFICIENTS ESTIMATED FROM F_2 P-0074 x P-0963[a] AND F_2 P-0074 x P-1616[b] DATA

	Pod Number	Average Pod Size	Seed Number	Seed Maturity	Shell Thickness
Pod Number		-.120	.964**	.279**	.067
Average Pod Size	-.217**		-.135	.069	.456**
Seed Number	.931**	-.272**		.293**	.038
Seed Maturity	.150*	.152*	.148*		-.013
Shell Thickness	-.062	.481**	-.098	.185**	

[a] P-0074 x P-0963 upper right-hand corner

[b] P-0074 x P-1616 lower left-hand corner

*,** Significantly different from zero at the .05 and .01 levels of probability, respectively (167 d.f. for F_2^a and 174 d.f. for F_2^b).

TABLE XVII

PHENOTYPIC CORRELATION COEFFICIENTS ESTIMATED FROM F_2 P-0112 x P-0963[a] AND F_2 P-0112 x P-1616[b] DATA

	Pod Number	Average Pod Size	Seed Number	Seed Maturity	Shell Thickness
Pod Number		-.076	.912**	.178*	-.056
Average Pod Size	-.269**		-.061	-.057	.361**
Seed Number	.969**	-.292**		.209**	-.009
Seed Maturity	.006	.075	.046		.006
Shell Thickness	-.087	.521**	0.128	-.131	

[a] P-0112 x P-0963 upper right-hand corner

[b] P-0112 x P-1616 lower left-hand corner

*,** Significantly different from zero at the .05 and .01 levels of probability, respectively (142 d.f. for F_2^a and 90 d.f. for F_2^b).

TABLE XVIII

PHENOTYPIC CORRELATION COEFFICIENTS ESTIMATED FROM F_2 P-0074 x P-1617[a] AND F_2 P-0112 x P-1617[b] DATA

	Pod Number	Average Pod Size	Seed Number	Seed Maturity	Shell Thickness
Pod Number		-.158*	.889**	.360**	-.018
Average Pod Size	-.096		-.096	.056	-.056
Seed Number	.941**	-.151		.443**	-.011
Seed Maturity	.038	.217*	-.028		-.110
Shell Thickness	.190*	.120	.219*	.146	

[a] P-0074 x P-1617 upper right-hand corner

[b] P-0112 x P-1617 lower left-hand corner

*,** Significantly different from zero at the .05 and .01 levels of probability, respectively (144 d.f. for F_2^a and 101 d.f. for F_2^b).

TABLE XIX

SUMMARY OF PHENOTYPIC CORRELATIONS AMONG DIFFERENT TRAITS OF F_2 POPULATIONS

	F_2 Population											
Characters	0006 0963	0006 1616	0006 1617	0006 1618	0074 0963	0074 1616	0074 1617	0112 0963	0112 1616	0112 1617	0002 1616	0002 1618
Pod Number vs. Average Pod Size	+	-	-*	+	-	-**	-*	-	-**	-	-	-*
Pod Number vs. Seed Number	+**	+**	+**	+**	+**	+**	+**	+**	+**	+**	+**	+**
Pod Number vs. Seed Maturity	+**	+**	+	+**	+**	+*	+**	+*	+	+	+**	-
Pod Number vs. Shell Thickness	+	+*	+	+	+	-	-	-	-	+*	-	-
Average Pod Size vs. Seed Number	+	-	-**	-	-	-**	-	-	-**	-	-	-*
Average Pod Size vs. Seed Maturity	+**	-	-	+	+	+*	+	-	+	+*	-	-
Average Pod Size vs. Shell Thickness	+**	+**	+**	+**	+**	+**	-	+**	+**	+	+	+**
Seed Number vs. Seed Maturity	+**	+**	+	+**	+**	+*	+**	+**	+	-	+**	-
Seed Number vs. Shell Thickness	+*	+*	-	+	+	-	-	-	-	+*	-	-
Seed Maturity vs. Shell Thickness	+**	+	-	+	-	+**	-	+	-	+	+	-

[+] Positive correlation.

[-] Negative correlation.

[*, **] Significantly different from zero at the .05 and .01 levels of probability, respectively.

Singh (5), Bernard (8), Jaswal and Gupta (25), Lin (27), Maralihalli (30), and Stokes and Hull (41).

CHAPTER V

SUMMARY AND CONCLUSIONS

The objective of this study was to evaluate the genetic potential for pod size, shell thickness and seed maturity of eight peanut cultivars, for their possible use in future peanut research. Inheritance studies were carried out for pod size, pod number, seed number, seed maturity, and shell thickness.

Data, computed from parents and F_2 populations, indicated that the pod size trait is controlled by quantitatively acting genes. Low to medium heritability estimates and low genetic advance revealed less chances of achieving significant changes through selection in early generations.

Continuous variation in segregating populations for number of pods suggested quantitative inheritance of the character. Presence of transgressive segregates in the populations indicated possible genetic potential for further improvement of peanut lines, since number of pods is a major component of yield. Estimates for heritability and genetic advance were high, suggesting the possibility of significant achievements in fewer generations through selection.

Frequency distributions for seed maturity were skewed toward early and late, equally. However, fairly simple inheritance was indicated by 10 of the 12 crosses estimating 4 genes or less, controlling the seed maturity. Low to high heritability and genetic advance estimates were obtained for seed maturity.

Studies on number of seeds indicated a desirable number of transgressive segregates appearing in F_2 populations. Since heritability and genetic advance estimates were high, selection of segregates exceeding the parental value will be of special importance in a breeding program focusing on improvements in yield of peanut cultivars.

Inheritance studies on shell thickness revealed that the trait is controlled by multiple genes. Low to high heritability estimates and low to moderate estimates for genetic advance were obtained for this character.

Correlation studies were carried out among five agronomically important traits. Pod number and seed number were positively correlated with seed maturity but negatively correlated with average pod size. Pod number and seed number were not significantly correlated with shell thickness. Significant positive correlation was observed between average pod size and shell thickness. Seed maturity was not significantly correlated with shell thickness.

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