

GENETIC ANALYSIS OF MORPHOLOGICAL
CHARACTERISTICS OF FIELD BEAN
(PHASEOLUS VULGARIS L.) AS EXPRESSED IN A
DIALLEL CROSS

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ABSTRACT

GENETIC ANALYSIS OF MORPHOLOGICAL CHARACTERISTICS OF FIELD BEAN (PHASEOLUS VULGARIS L.) AS EXPRESSED IN A DIALLEL CROSS

By

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The increased yield in rice and wheat has been achieved in conjunction with, and to a large extent as a consequence of, changes in plant type. Both morphological and certain physiological characteristics of these plant types are strongly associated with grain yields. With proper management during the growing season these new plant types respond positively toward high yields.

In field bean, however, ideal plant types for different ecological zones are only beginning to be identified. Perhaps as the traits contributing to high yield in field beans are more clearly identified and better understood genetically, it will be possible in beans, as in rice and wheat, to set about in a methodological fashion the creation of new higher yielding types.

The focus of this thesis is upon the genetic analysis of morphological characteristics believed to be associated with improved yield potential.

Inheritance of morphological characteristics of field beans (Phaseolus vulgaris L.) was studied in 5x5 and 8x8 diallels in 1973 and 1974.

Length of pod in the 8x8, F_1 and 5x5, F_2 , number of seeds per pod (5x5, F_2) and 100-seed weight were found to be inherited additively. Additivity was not detected for days to first flowering, duration of flowering, days to maturity, total plant weight, number of main stem branches, number of main stem nodes, total number of nodes, length of internode (8x8, F_1 and 5x5, F_2) number of racemes (8x8, F_1 and 5x5, F_2), number of seeds per pod (5x5 and 8x8, F_1), number of pods per plant, pod dry weight per plant, number of seeds per plant and seed dry weight per plant.

Heterosis was generally high in the F_1 generation for most traits. The level of heterosis decreased in many traits in the F_2 generations due to the increase of homozygosity.

The heritability estimate of 100-seed weight was the highest (82%) in the 5x5, F_1 data. Length of pod in the 8x8, F_1 had a heritability estimate of approximately 100% and 100-seed weight was 90% in the same set of data. However, in the 5x5, F_2 data, number of seeds per pod and number of seeds per plant were both 90% whereas 100-seed weight was 81%. The rest of the traits studied had much lower heritability estimates (less than 30%).

The variety Swedish Brown (SB) had the highest harvest index in both the 5x5, F_1 and 8x8, F_1 data. The strain 0674 had the lowest H.I. in the 5x5, F_1 and strain 0685 had the lowest in the 8x8, F_1 . In the F_2 , the highest H.I. values were very close; Black Turtle Soup (BTS), and Seafarer (SEA) were the highest with the value of .61 whereas SB and strain 72-7427 were the next highest with the value of .60. The cross 72-7427 x Jules gave the highest H.I. value of .71 in the 8x8, F_1 ; the cross SB x 72-7427 gave the highest H.I. of .61 in the F_2 set of data. Harvest index was not found to be directly related to yield nor of high heritability but it can be useful as one important measure of efficiency of the plant.

Black Turtle Soup was found to be a promising variety in yielding ability. It has highest mean values of number of pods per plant, pods weight per plant, number of seeds per pod and number of seeds per plant. Being a black-seeded variety seemed to associate with high yield. However, if highly mechanized planting is concerned, Tui may be a good substitution. This is because of the erect plant type of Tui which can be grown at a higher number of plants per unit area. Besides Tui is only slightly inferior to BTS in seed yield. With higher number of plants per unit area Tui may be equal to or better than BTS in yield.

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The evaluation of SEA and strain 0674 may not be completely accurate in some characteristics because of their sensitivity to ozone injury. Each variety seemed to have the highest mean value of a particular trait. It, therefore, depends on the breeder to exploit these parental lines and incorporate those traits which have additive effect into a new variety.

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To my parents,
To M. R. Kukrit Pramoj

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INTRODUCTION

In the past decade dramatic increases have been achieved in yields of rice and wheat through joint genetic and physiological responses to reduced plant stature and applied nitrogen. However, the yields of dry bean (Phaseolus vulgaris L.) have remained on a nearly stationary level. The yields increment in rice and wheat have been attributed to changes in plant type or plant architecture and related management technology. The main morphological changes in these plant types are short but strong culms, high number of effective tillers, short erect leaves, nonphotosensitivity and responsiveness to nitrogen.

In dry bean, the ideal plant types for various ecological zones and uses have not yet been generally identified. Perhaps if the traits contributing to high yield were clearly identified and better understood genetically, the bean breeder could work with them to create more successful new varieties.

The purpose of this thesis was to obtain genetic information on the architectural characteristics in beans regarded as important to yield. Two major points need to

be clarified at this stage: One, the architectural components contributory to high yields were to be identified in studies conducted concurrently by other workers associated with but not directly involved in this thesis; and two, some aspects of the genetics of the selected traits were to be deferred to later stages of a comprehensive study.

In the initial stage covered by this thesis, it was planned to obtain information relating primarily to the heritability levels, the extent of heterosis, and the general patterns of gene action involved in each of several morphological and yield characteristics. For this purpose two diallel crosses were produced, a 5 x 5 Diallel in 1973 and an 8 x 8 Diallel in 1974.

Advanced generations of the diallel may be exploited in several ways to obtain additional genetic information supplementary to that manifest in the initial diallel cross.

REVIEW OF LITERATURE

Diallel cross analysis has been developed by Jinks (1954) and Hayman (1954) as a technique for studying quantitative inheritance. Since then it has been used extensively in plant breeding to investigate the genetic control of several traits.

Coyne and Mattson (1964) studied the inheritance of time of flowering in 3 P. vulgaris varieties. They found a different type of inheritance when different varieties of early and late flowering types were crossed and planted at different localities. They proposed that the trait was controlled by three interacting genes. The late flowering plant must be homozygous dominant at the 2 loci AA and BB regardless of the condition of the locus C, or heterozygous at these 2 loci in the presence of CC or Cc or homozygous dominant at one and heterozygous at the other of these loci in the presence of CC or Cc.

Dickson (1967) found that earliness of flowering time of P. vulgaris was conditioned by both recessive and dominant genes. If two varieties, one of which carries the recessive and the other dominant genes, are crossed they exhibited extreme earliness.

There are differences in the date of appearance of first flower between the determinate and indeterminate types of P. vulgaris. It was observed in this study that the determinate bean types tended to flower earlier than the vine or indeterminate type. This phenomenon was also reported by Bliss (1971). The determinate plant type flowered earlier than the indeterminate type in segregating generations.

In peas (Pisum sativum L.), Rowlands (1964) reported that a simple polygenic system was primarily responsible for the control of flowering, with a major gene (Sn) or effective factor which delays flowering and this effect is increased during short days. He also suggested that the development of earlier and late flowering varieties will most probably depend on the discovery of parents where a different relationship exists between node of flowering and time of flowering. Rowlands concluded from the position of the array points on the Wr/Vr graph that lateness is completely dominant to earliness.

In a diallel cross of 7 pea cultivars, Snoad and Arthur (1973) found that time of flowering was due entirely to a simple, additive genetic system and that dominance was not important.

Snoad and Arthur (1973) also studied the length of internode in pea. They found that long internodes

are dominant to short ones. Rowlands (1964) on the other hand, found a more complex system of genic control for this trait. But when two of the arrays were omitted (parents 8 and 10) from the F_2 , and the data were recalculated, a regression line of slope 0.726 ± 0.129 which was not significantly different from 1 was obtained. He found also that the intercept on the W_r axis was significantly different from zero. Thus, a system involving partial dominance was indicated for length of internode.

Length of pod has been studied in several legume crops. In *P. vulgaris*, Dickson (1967) reported no dominance effect regarding this trait. None of the 7 varieties he studied contained all the dominant or recessive genes. Transgressive segregation for pod length was found among the F_2 populations. In cowpea (*Vigna sinensis*), Leleji (1975) found that the genes expressing short pods were partially dominant over those for long pods. This seems to agree with Roy and Richharia (1948) who found the gene action of genes affecting pod length in the F_1 to be incomplete dominance. Transgressive segregation in the F_2 for pod length was also found in cowpea by Arejeetey and Laing (1973). They also found partial dominance of genes for long pod in the F_2 . This result was different from Brittingham's (1950) who reported that there was a decided tendency for the F_1 and F_2

values to be closer to the values of the short podded parent and observed no transgressive segregation in the F_2 .

Jones and Isbell (1956) found that 10 out of 22 F_1 s had pods significantly longer than those of the longer parent in crosses of the southern pea (V. sinensis L.). Five were not significantly different from the longer-podded parent, and 7 were intermediate. This is also not in agreement with Brittingham who found that the F_1 from crosses was usually intermediate between the parents in pod length. Broad-sense heritability estimates for pod length were found to range from 46 to 67% (Leleji, 1975). On the other hand Arjeetey and Laing (1973) found that the narrow-sense heritability estimate for pod length in cowpea was 60.3%.

Coyne (1968) found complete dominance for high number of pods per plant. In cowpea, Arjeetey and Laing (1973) found that the gene action for number of pods per plant in both F_1 and F_2 was additive. In peas (Pisum sativum) Krarup and Davis (1920) reported that number of pods per plant was controlled by additive genic system on the average.

Number of seeds per pod was one of the economic traits that Dickson (1967) studied in P. vulgaris. He observed among the 7 varieties he used in his diallel cross that if all the varieties were present, the

regression line was not significant. However, if 2 of the 7 varieties were excluded the regression line had a slope of $b = 1.13 \pm .20$. He concluded that an additive genic system for number of seeds per pod was indicated for the remaining 5 varieties. In V. sinensis, however, Arjeetey and Laing (1973) found partial dominance for number of seeds per pod and transgressive segregation in the F_2 . Coyne (1968) reported heterosis for number of seeds per pod in P. vulgaris. Leleji (1975) found in cowpea that fewer number of seeds is partially dominant over large number of seeds. Transgressive segregation for fewer number of seeds per pod was also observed.

Jones and Isbell (1956) found in their southern pea (V. sinensis) cross that 12 out of 14 F_1 s of the cross did not differ significantly from the parents, only 2 of the 14 crosses had a number of seeds per pod significantly greater than either parents.

Dickson (1967) found that gene interaction was involved for number of seeds per plant. However, if 2 of the 7 varieties were excluded from the diallel, the regression line was found to approach 1 and partial dominance was indicated.

Seed size or seed weight in legume crops has been studied extensively. Brittingham (1950) crossed two widely separated varieties of southern pea belonging to different sub-species of Vigna sinensis (V. sinensis,

subsp. sesquipedalis, Asparagus Bean) x (V. sinensis, subsp. cylindrica, Catjang). He reported that the mean value of the F_1 generation greatly exceeded the mean of the large seeded parent. Heterosis in seed size was, thus, indicated. Transgressive segregation was found for large seeds and a large number of F_2 segregates had means exceeding the F_1 mean. He found, however, that the extremely small-seeded parent was not recovered in the F_2 .

Leleji (1975) crossed 7 cowpea varieties and found that genes for small seeds were partially dominant over genes for large seeds. Transgressive segregation was found for small seeds. Heritability estimates (broad-sense) ranged from 49% to 80% for seed size.

A certain degree of genic additivity seemed to be indicated for seed size in southern pea (Vigna sinensis). Jones and Isbell (1956) reported that 18 of the crosses had the mean values between parents which differ significantly from each other in pea size. Eleven of the F_1 's were intermediate, 6 were larger than the larger parent and one was smaller than the smaller parent.

Number of main stem branches on bush lines of P. vulgaris was studied by Davis and Frazier (1966). They observed that in one cross the number of branches of the F_1 and F_2 tended to exceed the more heavily branched parent. They found no heterosis for number

of central stem internodes. The expression of central stem internode was found to be conditioned by genes with a net effect of partial dominance.

Krarrup and Davis (1970) reported that number of pods per plant (X), number of seeds per pod (Y), 100-seed weight (Z) and seed yield (W) were controlled by an additive genetic system on the average in peas. The departure from additivity was indicated by deviation of the F_1 from the mid-parent, especially for X, W and seeds per plant. They stated that this deviation was more likely due to epistasis or linkage than to dominance. The value for correlation coefficients decreased in the order: X vs W, Y vs W and Z vs W. Thus the order of importance of yield components upon yield was: first X, then Y and finally Z.

In P. vulgaris, however, Coyne (1968) observed additive gene system for mean seed weight and complete dominance for high number of pods per plant in the F_1 generation in one of his crosses. He also found low heritability estimates for total seed yield and for each of the three yield components.

The report of additive genetic variance for a number of traits by some authors while the others could not detect additive gene system could be due to different varieties used by different authors as pointed out by Coyne (1968).

MATERIALS AND METHODS

Five bean genotypes of different growth characteristics were used as parental lines in 1973, namely:

<u>Lines</u>	<u>Type of Growth</u>	<u>Seed Size and Color</u>
1. Black Turtle Soup (BTS)	Indeterminate	Small, Black
2. Swedish Brown (SB)	Determinate	Medium large, Yellow
3. Strain 0674	Determinate	Small, White
4. Seafarer (SEA)	Determinate	Small, White
5. Strain 72-7427	Determinate	Large, Red

They were planted in the greenhouse in the winter of 1973, and crosses were made between all five varieties in all combinations. Attempts were made to obtain as many crosses of each combination as possible. The F_1 and parental lines were sown in the Crop Science Research Field in East Lansing in the spring. The field plan was a simple lattice design with 4 replications. Five F_1 seeds from each cross and five seeds of each parental line were sown in individual plots at spacing of 10" between seeds and 28" between rows.

The following records were obtained on a per plant basis:

- (1) Flowering date: number of days from emergence to appearance of first flower.
- (2) Duration of flowering: number of days from first bloom to last bloom.
- (3) Maturity date: number of days from emergence to the day when all pods had turned brown and became brittle.
- (4) Plant dry weight: the dry weight at harvest of the whole plant including pods.
- (5) Number of branches: only those attached to the main stem were counted.
- (6) Number of nodes on main stem.
- (7) Pod dry weight: weight in grams of all the harvested pods.
- (8) Number of pods: all the pods harvested after weighing were counted.
- (9) Number of seeds per plant: after shelling the pods all the seeds were counted.
- (10) Seed dry weight: all the seeds after counting were weighed.
- (11) Number of seeds per pod: calculated by:

$$\frac{\text{Number of seeds/plant}}{\text{Number of pods}}$$

(12) 100-seed weight: calculated by:

$$\frac{\text{Seed dry wt.} \times 100}{\text{Number of seeds/plant}}$$

(13) Harvest Index: calculated by:

$$\frac{\text{Seed dry wt.}}{\text{Plant dry wt.}}$$

In the winter of 1974, 8 parental lines were crossed in all combinations in the greenhouse. The first 5 lines were the same as those used in 1973. The following 3 lines were added:

<u>Lines</u>	<u>Type of Growth</u>	<u>Seed Size and Color</u>
6. Tui	Indeterminate	Small, Black
7. Strain 0685	Determinate	Small, White
8. Jules	Indeterminate	Intermediate, White

The field planting of 1974 included the following seed material:

- (a) Eight parental lines
- (b) F_1 seeds resulting from the 8 x 8 diallel crosses
- (c) F_2 seeds from the 1973, 5 x 5 diallel crosses

A split plot design was used with 4 replicates. Each replicate contained 64 plots and each plot was divided into 10 subplots. The 10 subplots were composed of the 2 parents of a cross, the F_1 and reciprocal, and 6 subplots of the F_2 generation of the cross. Each subplot consisted of 5 plants. In cases where there was no F_2 generation, resulting from the 3 additional

parental lines, 6 subplots of Montcalm red kidney beans were grown as substitution to make up 10 subplots per plot. There were 560 subplots with 2800 plants in each replicate. The spacing was 10" by 28", the same as that of 1973.

Data were also recorded in 1974 on a per plant basis. Due to the high plant populations in 1974 and the fact that some of the traits recorded in 1973 did not give satisfactory results they were not recorded in the second year field trial. The traits omitted were: duration of flowering, root weight, stem weight, number of branches. The rest of the traits were the same as in 1973. However, 2 more traits were added in 1974, namely: number of racemes and length of internode.

It should be noted that the field conditions in 1974 were quite different to those of 1973. Normal climatic conditions were observed in 1973. However, in 1974, there occurred a drought spell at the post emergence stage. The plants were adversely affected and there was a delay of first flowering, and of maturity. Sprinkler irrigation was installed later in the season and the plants were irrigated when it was necessary. During the latter part of the pod filling stage, due to irrigation followed by a heavy rainfall a part of the field was flooded, resulting in the loss of a number of plants in the first replicate. At the end of September

1974 several bean plants were damaged by early frost and never reached full maturity. In such cases, only fully matured pods were weighed and the number of seeds for only the matured pods were recorded.

The data were later used to estimate the total pod dry weight, seed dry weight, plant dry weight and number of seeds per pod for each plant damaged by frost.

Missing Data

In the 5 x 5, 1973 trial, the following entries were missing due to insufficient F_1 seed and the loss of the remaining F_1 plants in the plot later in the season:

Replicate 1 cross: 72-7427 x BTS

Replicate 2 cross: SEA x SB

cross: SEA x 0674

Replicate 3 cross: 0674 x SEA

Replicate 4 cross: 0674 x SEA

The mean values from other replicates belonging to the same crosses were used to calculate the missing data according to Snedecor and Cochran's (1967) procedure:

$$x = \frac{aT + bB - S}{(a-1)(b-1)}$$

where:

a = number of treatments

b = number of blocks

T = sum of items with same treatment as missing
item

B = sum of items in same block as missing item

S = sum of all observed items

Diallel Analysis

a) assumptions implicit in the statistical
analysis of the diallel cross:

Jinks and Hayman (1953), Jinks (1954), and Hayman
(1954a), (1954b) who developed the diallel cross theory,
made the following assumptions:

1. The parents used in the cross must be homozygous.
2. The parents must be diploid.
3. There are no reciprocal differences.
4. There is no gene interaction or epistasis.
5. There are no multiple alleles.
6. The genes should be distributed equally.
7. There is no genotype-environment interaction
within locations and years.

The materials used in this study conformed to the
first two assumptions since the bean varieties used were
diploid inbred lines. The reciprocal differences were
tested before proceeding to further analysis. Assumptions
number 4 to 7 will be discussed accordingly in the results
and discussion.

b) analysis and definition of notations.

The computer program of Lee and Kaltsikes (1972), University of Manitoba, Canada, modified for running on the MSU CDC 6500, was used for analyzing the data. This program was developed for the Jinks-Hayman method of diallel analysis. The output provides all statistics for both the diallel regression analysis as well as the diallel variance components estimates and their standard errors.

The mean values from each replicate from each set of data were used for the first computer analysis. Each replicate is treated as a complete experiment for the diallel regression analysis. The means of the variance and covariance statistics over replicates are then used to obtain variance component estimates and standard errors. The sum over replicates was used to do the preliminary analysis of variance in order to obtain families (or genotypes), replicates, and error (environmental) effects. It is a 2-way classification analysis of variance, namely, replicate x family effect.

To obtain the necessary statistics for plotting the limiting parabola, the means over 4 replicates were used.

Reciprocal differences were tested before the Jinks (1954) and Hayman (1954) approach could be used by the above mentioned procedure. The test was performed

according to Snedecor and Cochran's 1967 method. If no reciprocal differences were found, the means over reciprocals were averaged and the V_r and W_r were calculated from the half diallel. V_r is the variance of the r th array and W_r is the covariance of the r th array with the nonrecurring parents.

The statistical notations and components used in the Lee and Kaltsikes (1972) computer program were derived from Hayman (1954). To avoid the complication of Hayman's (1954) notations, the notations of Mather and Jinks are used and described here.

<u>Statistics</u>		<u>Model</u>
V_p	=	$D + E$
\bar{V}_r	=	$1/4D + 1/4H_1 - 1/4 F + \frac{n+1}{2N} E$
\bar{W}_r	=	$1/2D - 1/4F + 1/N E$
$V\bar{r}$	=	$1/4D + 1/4H_1 - 1/4H_2 - 1/4F + \frac{n+1}{2N} E$

The components H_1 , H_2 and F can be defined as follows:

$$H_1 = 4 \bar{V}_r + V_p - r \bar{W}_r - \frac{(3n - 2)}{n} E$$

$$H_2 = r \bar{V}_r - 4 V\bar{r} + 2 \frac{(n^2 - 1)}{n^2} E$$

$$F = 2 V_p - 4 \bar{W}_r - \frac{2(n-2)}{n} E$$

The necessary statistics for plotting the limiting parabola were derived from:

$$W_r^2 = V_r \cdot V_p$$

$$W_r = V_r \cdot V_p$$

The array points displayed on the plane of the W_r/V_r graph are confined within the parabola and the lines of unit slope.

The heterosis interpretations of the results of this study was undertaken with the aid of the tables of the means. Gene action and dominance were interpreted strictly from the W_r/V_r graphs of each trait by following Mather and Jinks (1971).

According to Mather and Jinks (1971) the W_r/V_r graph provides information on three points.

1. It supplies a test of adequacy of the model; in the absence of nonallelic interaction and with independent distribution of the genes among the parents W_r is related to V_r by a straight regression line of unit slope ($b = 1$).

The residual (error) E in this case is derived from the 2-way interaction of replicates \times families (genotypes).

where as:

D = component of variation due to the additive effects of the genes.

H_1 = component of variation due to the dominance effects of the genes.

$$H_2 = H_1 (1 - (u-v)^2)$$

where:

u = proportion of positively acting genes in the parents.

v = proportion of negatively acting genes in the parents and where $u + v = 1$.

$F = 8 [uv (u-v) dh]$. Its sign has an effect on interpretation. If no genes exhibit dominance effects, or if the dominant and recessive alleles of each gene are distributed equally among the parents, $F = 0$. If there is an excess of dominant alleles (or of dominant genic effects) F will be positive. An excess of recessive alleles (or effects) will cause F to be negative. Thus, the sign of F is an indication of the relative frequencies of dominant and recessive alleles in the parents (Crumpacker, Allard, 1962).

n = number of parents in the diallel.

V_o = variance of the parents.

\bar{V}_r = mean variance of the arrays.

\bar{V}_r = variance of one array (r th array).

\bar{W}_r = mean covariance between the parents and the arrays.

E = pooled error variance.

2. If the model is adequate, a measure of the average level of dominance is provided by the departure from the origin of the point where the regression line intercepts the W_r axis. The distance of this point from the origin is $1/4 (D = H_1)$: $D > H_1$ when the intercept is positive and it is then that the dominance is partial or incomplete. When $D = H_1$, the line passes through the origin, and dominance is complete. If $D < H_1$ then the intercept is negative and over dominance is indicated.

3. The position of the array point nearest the origin indicates that a parent contains a preponderance of dominant genes and when furthest from the origin indicates that the parent contains fewer dominant genes or mostly recessive genes. If there is no dominance, $H_1 = 0$ and all the array points cluster at a single point where:

$$V_r = 1/4D = 1/4V_p$$

and

$$W_r = 1/2D = 1/2V_p$$

Test of the Significance of the Regression
Line and the Intercept

a) To test whether the regression line is significantly different from either unity or zero, the following t-test was used:

$$t = \frac{b - b_0}{s_b}$$

where:

b = regression coefficient

s_b = standard deviation of the regression
coefficient

b_0 = 1 or 0 respectively

b) To test whether the intercept is significantly above or below the origin.

$$t = \hat{y}/s\hat{y}$$

where:

$$y = b_0 + b_1 X_1$$

$b_0 = a$ = intercept

b_1 = regression coefficient

$$s\hat{y} = s^2 \left(\frac{1}{n} + \frac{(X - \bar{X})^2}{\sum x^2} \right) = s^2 \left(\frac{1}{n} + \frac{\bar{X}^2}{\sum x^2} \right)$$

Heritability Estimate

The heritability estimate in this program followed that used by Crumpacker and Allard (1962), i.e.

$$h^2 = \frac{1/4D}{1/4D + 1/4H_1 - 1/4F + E}$$

RESULTS AND INTERPRETATION

The summary of mean squares and the significance of variance ratios from the analysis of variance of the 5 x 5, parental and F_1 hybrids in 1973 are shown in Table 2. Significant differences occurred for the 14 traits studied among the 15 populations or genotypes compared (5 parents and progenies from 10 crosses). However, number of main stem nodes per plant did not show significant differences among the genotypes. It was assumed that the prerequisites for further analysis were fulfilled.

The results for each trait will be presented and discussed proceeding from the 5 x 5 diallel F_1 in 1973 to the 8 x 8 diallel F_1 and 5 x 5, F_2 in the 1974 trial. In the 1974 trial, there were 14 parental means in each replicate. Since there were only 6 F_2 means from each cross, six parental means were taken randomly out of the 14 means and averaged for the purpose of comparison. On the other hand, since there were only 2 F_1 means from each cross, 2 of the parental means were then taken randomly from among the 14 means and averaged to compare with the F_1 means. It can therefore be noticed from

Tables 3 and 5 that the same parents do not have the same mean values even though they were planted in the same year. For example, the mean value of days to flowering of BTS in Table 5 is 44.9 whereas the mean value in Table 3 is 45.2 and so on. Therefore, the F_2 families will be compared to their parental means in the same table and the F_1 hybrids of the 8 x 8 will be compared to their parental means as presented in Table 3.

Days to First Flower

The number of days from emergence to first day the plant flowered was recorded on a single plant basis.

5 x 5, F_1

The ranking of the mean values of the 5 parents in the order of first to last flowering was: strain 72-7427 = 25.3, SB = 28.7, SEA = 30.5, strain 0674 = 35.1 and BTS = 36.9 (Table 1). Strain 72.7427 is a red kidney line with large leaves and determinate plant type. SB has approximately the same plant type as strain 72-7427 and also has several morphological characters in common. SEA and strain 0674 represent the navy bean determinate type with small leaves. They also possess several additional characters in common. BTS is the only indeterminate type, with small leaves and purple flower, in this parental group. As shown in Table 1, BTS flowered latest among the 5 parents. It has been generally observed in beans

Table 1. Mean values for parents and F_1 hybrids of the 5 x 5 diallel crosses in 1973.

	Days to		Duration of	Days to		# Main Stem	# main stem	# Pods/Plant
	1st Flower	Flowering		Maturity	Plant Dry			
BTS SE 0674 SEA 72-7427	36.9	20.4	89.4	100.9	7.9	7.3	61.1	
	28.7	22.8	89.5	68.9	7.5	4.2	31.8	
	35.1	28.0	92.6	51.0	10.1	5.0	54.5	
	30.5	22.7	74.8	55.9	9.8	5.4	58.2	
	25.3	24.7	85.0	78.3	9.3	4.1	23.6	
BTS SB	34.8	22.0	90.9	80.6	7.8	6.4	40.9	
	33.3	29.4	105.3	202.6	7.4	6.7	129.2	
	39.5	22.9	101.0	155.8	9.2	7.7	96.1	
	35.5	23.8	92.5	104.5	9.8	8.3	44.9	
	34.9	20.0	91.5	119.7	7.1	6.5	67.0	
0674	37.2	30.7	100.5	135.0	12.5	5.9	66.5	
	28.5	28.0	90.7	124.0	10.6	5.1	64.2	
	27.6	27.1	90.0	100.3	10.5	4.1	31.1	
	48.3	20.7	101.1	195.4	8.3	8.4	121.5	
	37.6	31.0	94.5	131.8	12.1	6.6	66.6	
SEA 72-7427	39.4	19.1	82.5	45.2	9.1	4.6	49.1	
	37.8	23.5	89.6	113.2	10.9	5.2	56.8	
	46.9	20.8	94.6	146.8	9.5	7.6	70.8	
	31.1	24.4	84.6	120.4	9.6	4.9	62.3	
	31.7	19.2	86.0	66.0	8.9	6.8	54.8	
72-7427x	29.9	25.5	81.5	130.8	10.1	4.6	55.4	
	26.4	18.3	78.8	60.5	7.3	4.5	13.6	
	27.0	22.4	87.4	91.4	7.9	4.4	29.9	
	34.7	25.3	87.5	99.8	11.6	5.1	45.1	
	28.2	27.2	84.3	103.3	10.1	4.8	48.3	

Table 1. (cont.)

		Pod Dry Wt./ Plant (gm)	# Seeds/Pod "Y"	100-Seed Wt. (gm) "Z"	# Seeds/Plant	Seed Dry Wt./ Plant (gm)	Harvest Index
BTS		80.6	5.4	17.3	338.9	58.7	.58
SB		54.9	3.6	39.5	109.7	42.9	.63
0674		35.3	3.8	12.6	201.7	25.2	.50
SEA		44.7	4.1	13.9	235.9	33.2	.60
72-7427		64.8	3.6	55.2	85.6	46.2	.59
BTS	x SB	68.2	3.9	26.3	209.3	53.8	.64
	x 0674	153.4	5.6	16.3	720.9	111.8	.56
	x SEA	122.1	5.4	18.9	527.2	93.6	.60
	x 72-7427	86.8	5.3	30.9	237.4	66.5	.64
SB	x BTS	99.8	4.6	23.8	329.1	78.1	.65
	x 0674	88.4	4.3	22.8	293.1	69.4	.50
	x SEA	95.2	4.7	26.3	290.2	76.7	.61
	x 72-7427	80.1	3.9	49.0	130.3	62.9	.63
0674	x BTS	141.5	5.0	16.2	622.4	105.0	.50
	x SB	91.5	4.4	25.1	300.9	74.9	.59
	x SEA	34.7	4.8	13.0	202.9	27.6	.62
	x 72-7427	83.7	4.7	23.2	266.1	60.5	.54
SEA	x BTS	113.9	4.6	20.8	408.6	85.9	.58
	x SB	93.4	4.4	26.9	277.2	75.2	.63
	x 0674	53.6	4.7	15.9	253.3	40.7	.57
	x 72-7427	103.8	4.9	29.9	266.9	80.3	.61
72-7427	x BTS	47.7	4.0	57.3	62.3	33.8	.57
	x SB	74.3	4.3	47.2	127.9	58.5	.64
	x 0674	71.9	4.9	24.5	217.7	52.6	.53
	x SEA	82.5	4.8	55.2	231.1	63.2	.61

Table 2. Analysis of variance of the 5 x 5, parental and F₁ hybrids, 1973, summary of mean squares and significance of variance ratios.

	d.f.	Days to 1st flower		Duration of Flowering		Days to Maturity		Plant Dry Wt.	
		M.S.	VR	M.S.	VR	M.S.	VR	M.S.	VR
Replications	3	6.584	.752	13.804	1.404	24.915	.605	5158.613	1.302
Families (Genotypes)	24	158.660	18.113**	53.968	5.488**	207.776	5.047**	9467.477	2.390**
Rep x Fam (Error)	72	8.759		9.834		41.170		3961.489	
		# of Main Stem Branches		# of Main Stem Nodes		Pod Dry Wt./Plant		# of Seeds/Plant	
		M.S.	VR	M.S.	VR	M.S.	VR	M.S.	VR
Replications	3	1.540	.441	24.731	1.261	298.876	.178	3868.821	.164
Families (Genotypes)	24	9.357	2.676**	30.027	1.532	3616.823	2.155**	97341.751	4.128**
Rep x Fam (Error)	72	3.496		19.605		1677.996		23580.394	
		# of Pods/Plant (X)		# of Seeds/Pod (Y)		100-Seed Wt. (Z)		Seed Dry Wt./Plant (W)	
		M.S.	VR	M.S.	VR	M.S.	VR	M.S.	VR
Replications	3	150.031	.182	.252	.929	.603	.070	148.982	.158
Families (Genotypes)	24	2866.614	3.482**	1.199	4.415**	661.169	76.961**	2079.229	2.209**
Rep x Fam (Error)	72	823.295		.272		8.591		941.045	
Harvest Index									
		Harvest Index							
		M.S.	VR						
Replications	3	.006	2.023						
Families (Genotypes)	24	.008	2.853**						
Rep x Fam (Error)	72	.003							

that the indeterminate type tends to flower later and over a somewhat longer period than the determinate plant type. (Early and late flowering genotypes do, however, occur in both types.) Bliss (1971) reported that the determinate plant type in segregating generations of crosses of 7 cultivars flowered earlier than the indeterminate type.

From the mean values of the F_1 hybrids in Table 1, it appears that 8 out of the 10 hybrids had mean values greater than that of the mid-parent value; four hybrids had mean values greater than that of the late-flowering parent. Two hybrids had mean values smaller than the mid-parent value.

The W_r/V_r graph (Figure 1) shows that the regression of W_r on V_r is significantly different from zero but not significantly different from unity ($b = .62 \pm .19$). The regression line intersects the W_r axis above the origin ($a = 3.12 \pm 4.15$) but not significantly different from zero, indicating partial to complete dominance. The $\sqrt{H_1/D}$ value of 1.76 indicates over dominance. On balance the evidence suggests partial to complete dominance. Strain 0674 appears to contain a preponderance of dominant genes for later flowering. It is believed that ozone injury caused the delay in growth and development of strain 0674. The later development when climatic conditions were favorable resulted in long duration of

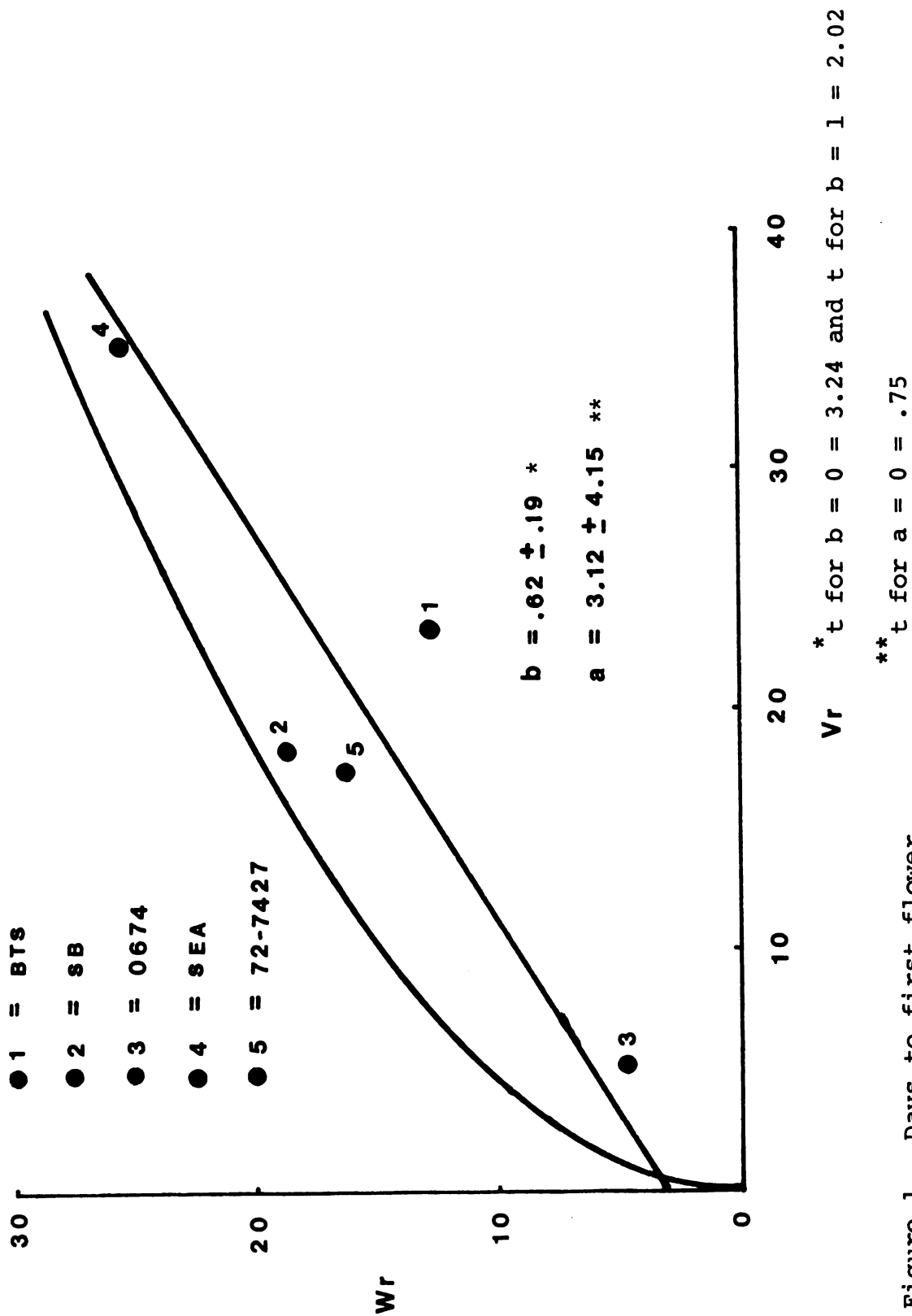


Figure 1. Days to first flower.

flowering of this genotype. Parent 4 (SEA) contains a preponderance of recessive genes for earlier flowering. Parents 2 (SB) and 5 (72-7427), which are very similar in several phenotypic characters, seem to have similarly behaving genotypes with respect to this trait. Parent 1 (BTS), which is distinctively different from the other 4 parents, appears to be an outlier in this case. Since BTS, SB and strain 72-7427 are located in the middle of the regression field it is indicative that they contain an intermediate balance of recessive and dominant genes for appearance of first flower. The heritability was 29% for this trait, as estimated in this F_1 diallel set.

8 x 8, F_1

The mean number of days to first flower of the 8 parents, from early to late, ranked in the following order: strain 72-7427 = 28.0, SB = 33.8, SEA = 34.8, strain 0674 = 35.4, Jules = 36.1, BTS = 45.2, strain 0685 = 48.6 and Tui = 50.5 (Table 3). The analysis of variance showed that there were no significant differences among replicates, but highly significant differences among the genotypes existed (Table 4). All of the original 5 varieties used in the 1974 trial flowered later than in 1973. Different environmental conditions in the two years presumably caused these differences. It was observed that there was a drought period in 1974 at

Table 3. Mean values for parents and F₁ hybrids of the 8 x 8 diallel crosses in 1974.

	Days to 1st Flower	Days to Maturity	Plant Dry wt. (gm)	Tot. number of nodes	Length of Internode(mm)	# Racemes/ Plant	# Pods/ Plant "X" of Pod	Average Length of Pod (mm)
BTS	45.2	98.5	95.7	57.5	89.0	26.8	53.6	93.9
SB	33.8	94.8	89.5	30.9	151.2	18.6	35.1	108.4
0674	35.4	84.7	61.8	41.8	135.4	20.9	49.8	80.4
SEA	34.8	82.1	64.6	39.9	114.2	20.8	51.6	82.8
BTS	39.8	92.4	92.3	49.9	104.4	23.0	46.1	100.7
SB	51.9	107.4	150.0	124.8	116.3	41.9	84.6	93.7
0674	47.4	99.9	123.3	95.1	108.2	37.7	75.2	88.6
SEA	39.6	96.0	137.4	53.6	156.9	24.1	54.0	133.1
72-7427	55.2	107.0	241.6	196.5	137.0	54.9	102.8	101.7
0685	47.2	101.3	122.2	76.6	94.8	33.3	65.2	97.9
TUI	42.1	96.8	132.9	83.3	111.7	31.2	59.8	103.3
JULES								
BTS	89.2	105.2	105.2	60.9	112.4	25.5	49.9	104.9
SB	39.9	98.5	108.5	55.8	201.9	24.5	50.9	95.7
0674	33.4	92.3	139.5	56.0	177.9	29.5	64.6	102.2
SEA	28.9	87.4	80.5	26.5	155.7	14.4	26.5	125.3
72-7427	48.6	110.0	160.1	78.2	229.8	34.8	58.5	101.4
0685	48.0	105.9	132.5	83.8	125.3	33.1	53.7	106.5
TUI	34.4	85.0	107.7	60.5	108.7	24.4	45.3	110.3
JULES								
BTS	43.2	108.0	165.6	135.6	117.7	43.1	92.7	93.2
SB	41.8	98.8	101.8	47.1	200.3	24.4	49.9	96.4
0674	33.2	79.5	62.9	34.2	109.5	19.8	50.6	83.2
SEA	38.2	93.2	98.7	50.3	193.8	21.6	43.1	111.21
72-7427	42.7	97.7	147.1	66.6	186.9	36.3	73.4	99.6
0685	44.3	100.6	141.5	91.7	106.7	35.3	78.5	91.4
TUI	39.9	93.2	116.3	87.3	119.6	32.9	63.7	95.3
JULES								
BTS	48.8	100.2	152.8	105.4	112.3	39.3	83.9	92.2
SB	34.9	91.7	125.8	46.3	177.7	27.2	58.6	100.5
0674	33.9	81.3	73.6	46.2	115.9	23.2	59.8	83.6
SEA	33.3	88.1	105.5	37.3	160.1	19.4	43.1	112.8
72-7427	36.4	85.8	87.9	51.6	144.8	23.5	55.8	91.2
0685	45.6	96.9	143.4	82.3	101.1	39.1	71.2	95.9
TUI	35.8	87.7	132.2	76.9	106.6	39.9	78.8	91.5
JULES								

Table 3. (cont.)

		Pod Dry Wt./ Plant (gm)	# Seeds/Pod "y"	100-seed wt. "z" (gm)	# seeds/ plant	Seed Dry Wt./ Plant (gm)	Harvest Index
BTS	x	71.9	5.8	18.4	318.9	56.7	.62
SB	x	65.4	3.3	42.7	122.8	51.9	.66
0674	x	41.6	4.1	14.7	209.1	31.6	.53
SEA	x	53.1	4.2	18.4	223.4	40.4	.54
BTS	x	72.9	4.7	25.9	255.1	59.9	.65
SB	x	104.3	6.6	14.1	531.3	76.0	.52
0674	x	105.4	5.3	18.2	370.2	73.4	.59
SEA	x	103.0	5.3	44.4	183.6	81.1	.59
72-7427	x	155.1	5.7	18.9	662.2	109.8	.46
0685	x	90.8	6.2	17.3	443.9	71.4	.59
TUI	x	104.1	4.8	29.7	287.9	85.6	.65
JULES	x						
SB	x	84.8	4.9	27.6	264.2	69.1	.59
0674	x	70.9	4.4	24.6	227.4	56.5	.53
SEA	x	105.4	4.3	29.9	292.9	84.6	.61
72-7427	x	63.8	3.7	48.6	103.5	48.9	.60
0685	x	92.2	4.3	27.8	265.5	70.9	.45
TUI	x	96.8	4.7	30.2	239.6	75.6	.54
JULES	x	88.5	3.9	41.9	194.2	75.4	.70
0674	x	120.5	6.1	15.2	576.6	88.0	.53
SB	x	68.6	4.4	24.2	234.9	54.8	.50
SEA	x	47.6	4.9	14.9	182.9	34.9	.56
72-7427	x	66.6	4.4	25.8	223.9	51.3	.52
0685	x	93.9	4.8	17.2	369.6	66.9	.46
TUI	x	105.4	5.4	19.1	424.7	80.9	.59
JULES	x	92.2	4.6	25.8	289.4	74.6	.64
SEA	x	106.9	5.4	17.7	460.2	83.6	.61
SB	x	95.4	4.3	29.3	261.3	76.9	.57
0674	x	56.7	4.5	15.7	261.2	42.4	.63
72-7427	x	80.6	4.1	32.1	186.5	60.8	.56
0685	x	66.1	4.2	21.3	246.2	50.8	.58
TUI	x	111.5	5.6	21.5	382.5	87.5	.61
JULES	x	102.8	3.6	28.7	311.2	83.3	.64

Table 3. (cont.)

	Days to 1st Flower	Days to Maturity	Plant Dry wt. (gm)	Tot. number of nodes	Length of Internode (mm)	# Racemes/ Plant	# Pods/ Plant "X"	Average Length of Pod (mm.)
72-7427	28.0	90.2	77.9	24.4	147.6	11.5	21.3	151.2
0685	48.6	104.4	118.1	74.6	195.6	30.6	60.3	103.4
TUI	50.5	103.9	99.6	56.3	90.1	24.8	50.6	105.5
JULES	36.1	87.0	101.8	72.2	97.4	22.8	39.9	106.0
72-7427 x BTS	38.7	95.1	135.1	52.5	157.9	23.3	52.9	131.8
x SB	28.4	86.9	81.9	26.0	152.6	15.0	26.9	125.8
x 0674	36.9	91.4	105.4	54.2	183.8	22.3	46.9	141.4
x SEA	34.5	87.6	119.7	47.9	165.5	19.8	47.1	113.4
x 0685	43.8	99.5	137.6	55.8	205.8	24.8	44.2	122.0
x TUI	48.0	103.6	117.6	72.5	100.5	31.5	47.5	114.5
x JULES	40.8	98.4	135.6	88.3	140.5	29.5	45.3	118.9
0685	57.5	111.1	222.6	161.4	154.4	49.6	92.4	103.1
x SB	50.5	113.9	155.2	63.5	248.4	29.6	62.3	104.6
x 0674	42.3	98.4	132.3	61.1	187.7	32.0	67.7	100.9
x SEA	42.8	101.6	108.4	61.8	192.7	25.4	51.8	100.8
x 72-7427	46.7	102.2	154.1	61.3	226.4	28.7	51.9	121.1
x TUI	51.5	106.1	179.1	107.5	123.4	40.8	75.2	109.0
x JULES	44.3	100.8	179.9	117.3	142.7	40.3	70.9	102.7
TUI	53.9	107.0	99.6	91.9	94.2	33.2	63.8	104.0
x SB	47.5	106.2	135.4	77.5	117.6	33.0	55.7	106.2
x 0674	46.5	101.5	133.5	86.7	106.9	35.3	69.6	94.4
x SEA	47.1	99.1	133.9	90.0	103.9	38.8	71.6	94.8
x 72-7427	47.9	103.6	117.6	72.5	100.5	31.4	47.8	114.5
x 0685	51.3	106.3	141.7	96.6	109.6	34.6	60.6	106.3
x JULES	41.9	96.7	85.9	45.5	79.2	22.5	40.0	102.8
JULES	41.9	99.1	138.8	85.3	108.8	34.4	64.4	104.6
x SB	39.7	97.7	164.8	98.6	135.7	38.9	61.1	109.7
x 0674	36.7	91.7	106.6	86.9	113.0	32.9	62.7	94.7
x SEA	35.2	88.9	131.9	81.7	113.0	33.6	66.2	98.5
x 72-7427	39.6	98.3	124.4	83.1	130.8	29.4	40.2	123.9
x 0685	43.9	100.7	186.4	127.1	143.8	42.3	73.2	102.4
x TUI	38.8	94.9	111.1	67.5	87.8	24.3	43.2	110.6

Table 3. (cont.)

		Pod Dry Wt./ Plant(gm)	# Seeds/ "Y"	Seeds/Pod "Y"	100-seed wt. "Z" (gm)	# seeds/ plant	Seed Dry Wt./ Plant(gm)	Harvest Index
72-7427		65.4	3.8		54.9	82.2	45.9	.60
0685		80.1	4.6		22.3	285.7	58.8	.44
TUI		73.9	5.9		17.9	313.6	57.6	.54
JULES		79.7	4.6		36.0	180.9	67.2	.62
72-7427	x BTS	105.9	4.6		43.7	181.3	80.2	.61
	x SB	62.5	3.4		49.5	121.2	69.7	.52
	x 0674	72.1	4.8		26.3	205.8	55.4	.57
	x SEA	88.2	4.3		34.0	203.0	68.2	.59
	x 0685	91.0	4.8		30.7	214.7	67.6	.48
	x TUI	88.6	5.5		28.5	251.9	68.5	.58
	x JULES	100.9	4.7		39.1	206.6	81.2	.71
0685	x BTS	141.0	6.1		17.3	588.2	98.8	.55
	x SB	109.4	4.9		27.1	318.6	84.6	.47
	x 0674	84.4	4.8		17.7	379.4	62.4	.55
	x SEA	78.0	4.8		23.3	246.9	57.5	.52
	x 72-7427	112.3	4.6		32.0	257.7	80.4	.46
	x TUI	127.4	5.9		22.6	435.0	98.3	.56
	x JULES	127.2	5.2		30.6	361.2	109.1	.61
TUI	x BTS	96.7	6.7		16.9	442.9	71.3	.56
	x SB	98.2	5.1		27.1	308.9	77.2	.52
	x 0674	95.6	5.8		18.0	397.3	67.1	.59
	x SEA	99.9	5.6		19.4	406.8	79.1	.58
	x 72-7427	88.6	5.4		28.5	254.3	69.4	.54
	x 0685	90.8	5.7		21.9	362.6	78.0	.55
	x JULES	67.2	5.2		25.3	218.7	54.1	.63
JULES	x BTS	109.8	4.9		28.1	317.1	88.1	.69
	x SB	134.5	4.8		37.8	290.4	112.4	.64
	x 0674	84.8	4.3		25.6	287.8	67.9	.65
	x SEA	104.9	4.2		30.9	304.0	86.3	.61
	x 72-7427	95.6	4.8		40.0	202.0	76.5	.62
	x 0685	134.7	5.2		30.0	399.4	113.2	.64
	x TUI	97.3	5.7		27.7	264.8	71.7	.69

Table 4. Analysis of variance of the 8 x 8, parental and F₁ hybrids in 1974, summary of mean squares and significance of variance ratios.

d.f.	Days to Flowering	Days to Maturity	Plant Dry Wt./Plant		Total # of Nodes				
	M.S.	VR	M.S.	VR	M.S.	VR			
Replications	3	10.751	2.158	31.600	2.381	6814.509	7.787**	826.518	3.872*
Families (Genotypes)	63	182.573	36.641**	231.081	17.408**	4946.349	5.652**	4120.067	19.362*
Rep x Fam (Error)	189	4.983		13.274		875.103		213.455	
Total	255								
		Length of Internodes	# of Racemes/Plant		Pod Dry Wt./Plant		# of Seeds/Plant		
		M.S.	VR	M.S.	VR	M.S.	VR	M.S.	VR
Replications		4975.175	19.668**	143.580	4.101**	2237.097	4.610**	18130.236	3.744*
Families (Genotypes)		6494.198	25.673**	278.861	7.964**	2085.347	4.298**	52770.025	10.898**
Rep x Fam (Error)		252.960		35.015		485.231		4841.997	
		# of Pods/Plant (X)	# of Seeds/Pod (Y)		100-Seed Wt. (Z)		Seed Dry Wt./Plant (W)		
		M.S.	VR	M.S.	VR	M.S.	VR	M.S.	VR
Replications		990.358	7.937**	1.557	12.023**	4.982	1.196	1232.358	5.017**
Families (Genotypes)		1031.110	8.264**	2.091	16.146**	356.353	87.146**	1299.823	5.291**
Rep x Fam (Error)		124.770		.130		4.089		245.655	
		Average Length of Pod	Harvest Index						
		M.S.	VR	M.S.	VR				
Replications		55.497	5.543**	.004	3.317*				
Families (Genotypes)		659.931	65.909**	.015	12.759**				
Rep x Fam (Error)		10.013		.001					

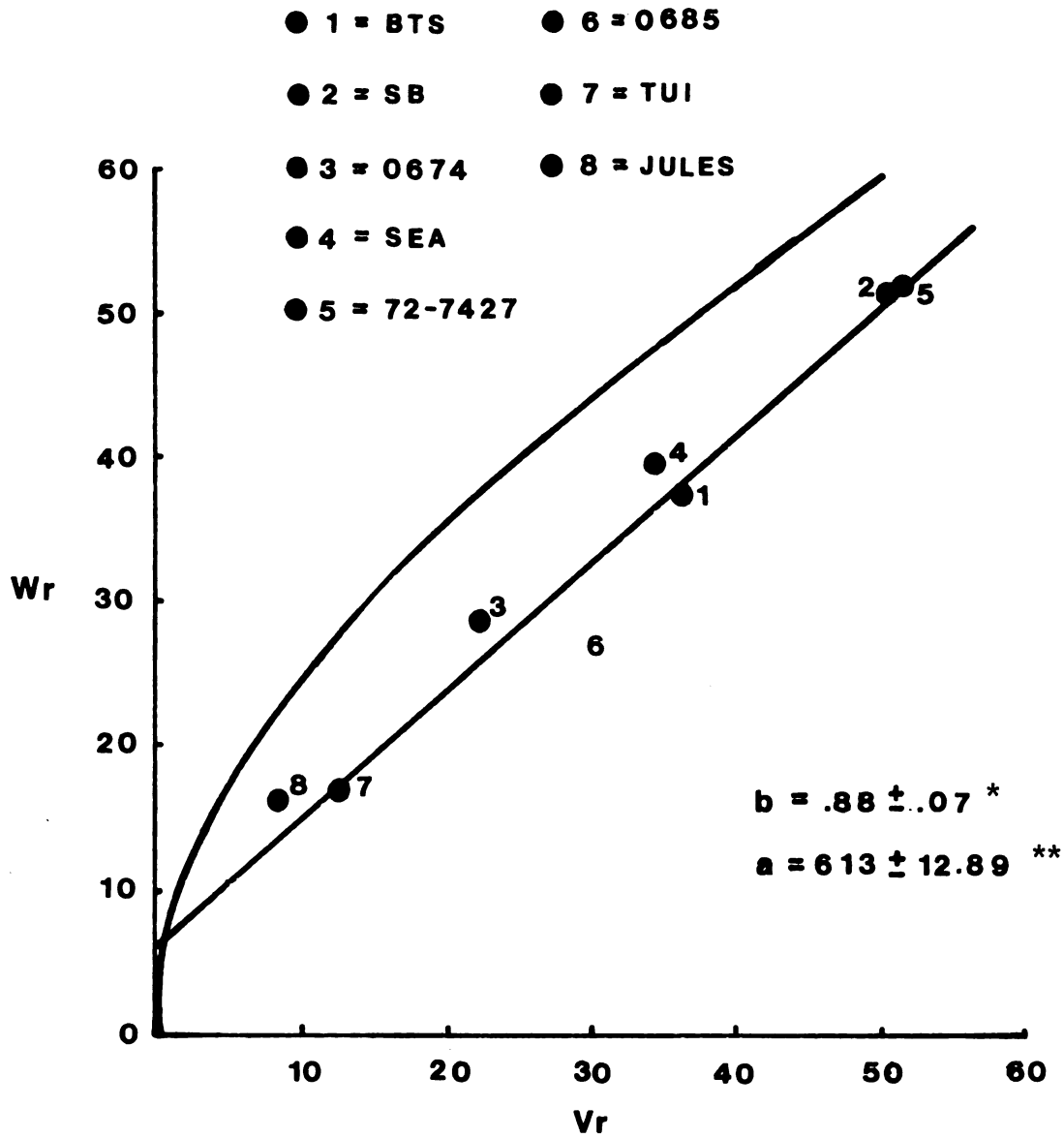
* 5% Sig. Differences

** 1% Sig. Differences

the early post-emergence stage. This is thought to have caused the delay in growth and development of the plant, resulting in delayed flower appearance.

Twenty-two out of the 28 F_1 hybrids had mean values greater than that of the mid-parent value, and 8 hybrids had mean values greater than that of the late flowering parent. Six hybrids had mean values smaller than that of the early flowering parent. The hybrid that flowered the latest was the one derived from the cross BTS x 0685 (55.2) and its reciprocal, 0685 x BTS (57.5). The first hybrid to flower was the one derived from the cross SB x 72-7427 (28.9) and its reciprocal, 72-7427 x SB (28.4) (Table 3).

Figure 2 shows the W_r/V_r graph of the 8 x 8, F_1 . The regression line is significantly different from zero but not significantly different from 1 ($b = .88 \quad .07$). The line intersects above the point of origin ($a = 6.13$) indicating apparent partial to complete dominance as the $\sqrt{H_1/D}$ value is 1.11. All the array points seem to fit the regression line very well, with parents 7 and 8 carrying a preponderance of the dominant genes since they are located near the point of origin and parents 2 and 5 containing a preponderance of recessive genes since they show both high variance and high covariance. The positions of the points representing BTS, 0674 and 0685 indicate that they contain neither an excess of



* t for b = 0 = 13.54 and t for b = 1 = 1.78

** t for a = 0 = .48

Figure 2. Days to first flower (8 x 8, F_1).

dominant genes nor an excess of recessive genes. Since the F value was -20.38 it is indicative of an excess of recessive alleles among the parents as a set. The heritability estimate was 32% ($h^2 = .32$).

5 x 5, F_2

Table 5 shows the mean values for the parents and the F_2 families in the 1974 trial. Eight out of 10 F_2 families gave mean values exceeding that of the mid-parent values and 4 out of the 8 F_2 gave mean values exceeding those of the late flowering parents. Two F_2 families had mean values smaller than that of the mid-parent values. The array means (Table 4) show that there are additive effects from the F_1 to the F_2 generations in all the families except those derived from the parent 0674.

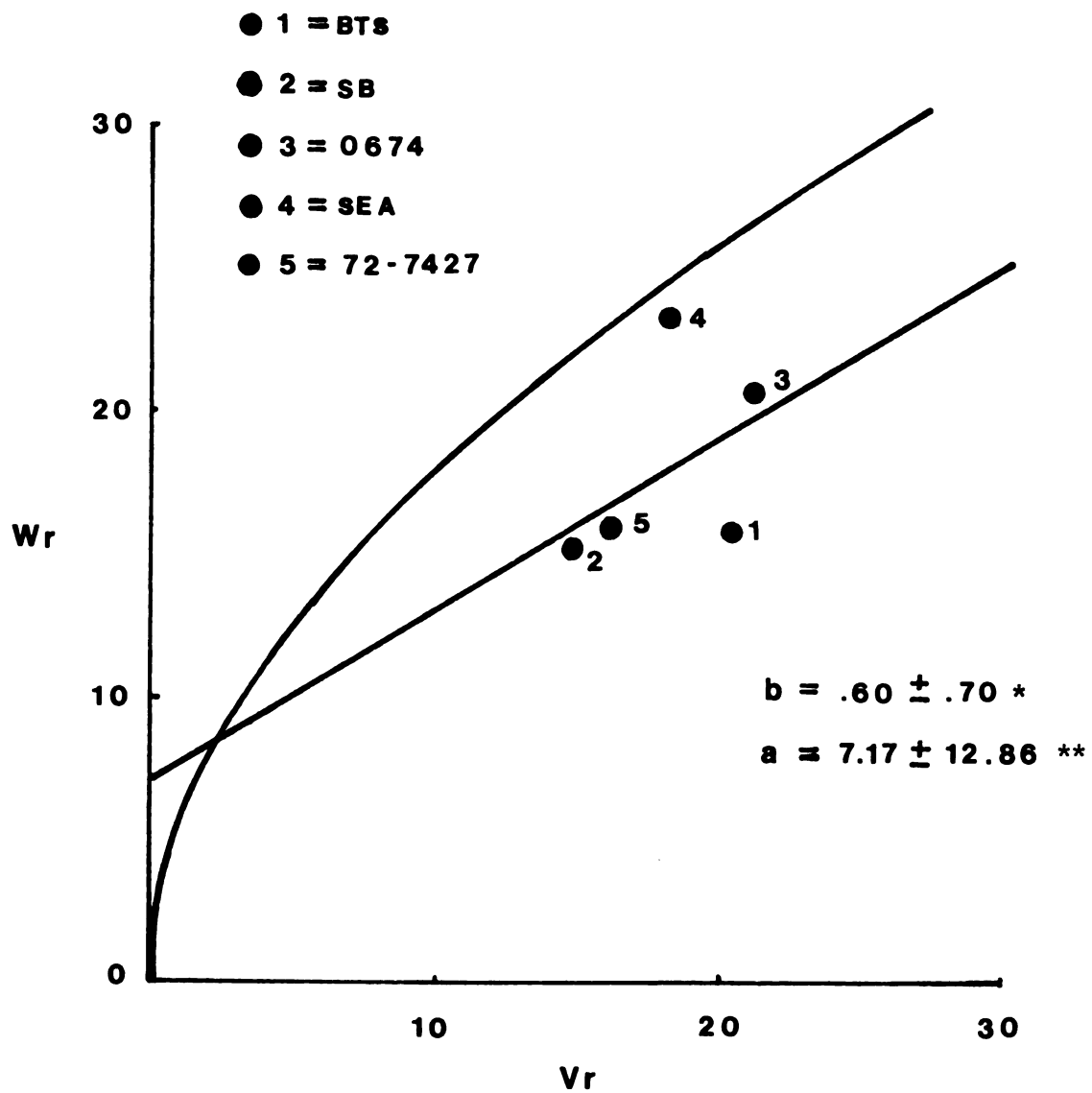
Figure 3 shows the W_r/V_r graph of the 5 x 5, F_2 . The regression of the W_r on V_r is neither significantly different from 1 nor zero ($b = 0.6 \pm .70$). The line intersects the W_r axis above the origin ($a = 7.17 \pm 12.86$) and significantly different from 0, indicating the genes controlling days to first flower are in the partially dominant range, on the average. The evidence on the graph indicates genic interaction. In Figure 1, the position of parent 3 (0674) was near the point of origin indicating that it contained the dominant genes,

Table 5. Mean values for parents and F₂ generations in 1974.

	Days to 1st Flower	Days to Maturity	Plant Dry wt. (gm)	Total number of nodes	Length of Internode (mm)	# Racemes/ Plant	# Pods/Plant
BTS	44.9	98.5	95.7	56.5	88.6	25.5	53.5
SB	34.2	94.8	89.5	33.5	150.1	18.5	35.9
0674	35.4	84.7	61.8	40.0	129.4	20.1	47.2
SEA	34.4	82.1	64.6	41.6	113.4	20.9	52.5
72-7427	28.9	90.2	77.9	26.7	155.7	10.8	21.3
BTS	38.7	95.2	111.8	56.7	113.2	28.2	57.3
x SB	46.9	97.5	77.5	68.7	105.4	24.8	50.9
x 0674	44.6	94.9	100.7	72.2	106.4	30.8	60.9
x SEA	36.9	90.7	82.6	43.9	106.0	20.3	38.9
x 72-7427							
SB	37.3	91.5	101.5	50.9	111.2	24.1	47.8
x BTS	38.9	96.3	97.8	47.3	163.8	25.2	55.3
x 0674	35.7	91.3	83.8	40.6	143.9	21.5	46.9
x SEA	30.3	89.2	72.2	24.9	146.9	14.1	25.9
x 72-7427							
0674	46.9	99.3	115.8	74.0	124.0	33.2	69.9
x BTS	41.6	98.8	103.8	46.8	175.5	25.1	54.9
x SB	37.7	86.6	70.0	42.1	133.3	22.3	51.3
x SEA	38.1	93.9	88.7	44.4	166.9	21.3	42.5
x 72-7427							
SEA	44.6	94.9	99.1	74.7	107.7	30.7	63.9
x BTS	35.4	93.3	108.6	48.5	163.9	26.5	54.5
x SB	34.7	78.5	58.2	34.7	122.4	20.1	46.8
x 0674	34.2	88.6	82.7	33.9	139.8	17.5	34.4
x 72-7427							
72-7427	36.7	90.8	82.7	44.0	106.7	20.3	38.8
x BTS	29.8	89.5	88.6	26.7	141.3	14.9	29.1
x SB	38.1	94.6	94.3	45.7	179.3	19.9	40.8
x 0674	34.8	90.7	80.3	38.4	169.3	20.6	40.9
x SEA							

Table 5. (cont.)

	Length of Pod (mm.)	Pod Dry Wt./ Plant(gm)	# Seeds/ Pod	100-Seed Wt. (gm)	# Seeds/ Plant	Seed Dry Wt./ Plant(gm)	Harvest Index
BTS	95.7	71.1	5.8	15.9	303.9	55.8	.61
SB	109.3	66.4	3.3	42.7	123.7	52.6	.60
O674	80.4	38.7	4.1	14.7	200.6	29.1	.52
SEA	81.2	52.9	4.2	18.4	218.5	40.1	.61
74-7427	139.0	62.8	3.8	54.9	85.3	46.8	.60
BTS	98.9	84.3	4.4	27.7	241.9	66.8	.60
x SB	87.3	52.6	4.9	16.2	244.0	39.7	.52
x O674	87.0	75.3	4.9	19.3	303.5	58.7	.59
x SEA	109.0	62.5	4.9	26.0	182.3	47.4	.58
x 72-7427							
SB	103.9	77.1	4.6	27.9	216.2	60.3	.60
x BTS	91.3	65.9	3.9	25.2	206.5	50.8	.54
x O674	91.0	61.9	3.9	26.0	188.3	48.6	.59
x SEA	126.9	55.9	3.6	47.1	92.2	43.4	.61
x 72-7427							
O674	89.2	82.7	4.9	17.6	360.7	63.7	.55
x BTS	91.9	71.6	3.9	25.3	225.4	56.6	.55
x SB	85.2	51.5	4.5	16.7	236.2	39.3	.56
x SEA	111.4	64.7	4.2	26.0	175.9	45.9	.52
x 74-7427							
SEA	88.2	71.2	5.0	16.7	334.6	65.0	.55
x BTS	94.2	79.4	3.9	27.4	226.3	62.1	.58
x SB	82.4	41.9	4.4	14.6	212.8	31.1	.53
x O674	110.3	62.1	4.2	30.1	156.8	47.2	.57
x 72-7427							
74-7427	107.8	62.5	5.0	25.7	185.7	47.7	.59
x BTS	128.4	67.9	3.7	46.9	110.7	52.2	.59
x SB	113.9	65.1	4.3	26.4	181.1	48.1	.52
x O674	103.8	58.6	3.8	27.9	160.9	44.8	.56
x SEA							



* t for $b = 0 = .86$ and t for $b = 1 = .58$

** t for $a = 0 = .56$

Figure 3. Days to first flower (5×5 , F_2).

however, in Figure 3, this point shifted to the far right. The data here appears to be inconsistent with previous interpretation, due primarily to strain 0674 having switched its position drastically from near the origin in the F_1 to the far right in the F_2 . Parent 4 (SEA) shows its consistency regarding this trait in that it continues to behave as though it contained a preponderance of recessive genes controlling days to first flower. BTS, SB and strain 72-7427 also were positioned consistently on the graph in both generations. Even though the heritability estimate was 15% for the F_2 , the h^2 values in the 5 x 5, F_1 was 29% and 32% for the 8 x 8, F_1 ; the evidence from the "D" values in the three sets of data suggests that days to first flower is moderately heritable and can be transferred to the progenies. "F" has a negative value of -27.32 indicating that most of the parents contain recessive alleles. The estimates of additive variance (D) in both generations were low (D = 15.22 in 5 x 5, F_1 , D = 21.70 in 5 x 5, F_2). However, the array means (Table 6) show that there are additive effects in all the families except those derived from strain 0674. Therefore, on the basis of the array means, it is not at all impossible to select parents for making crosses to obtain progenies with either late or early flowering habit.

Table 6. Analysis of variance of the 5 x 5, parental and F_2 generations in 1974, summary of mean squares and significance of variance ratios.

d.f.	Days to Flowering		Days to Maturity		Plant Dry Wt.		Total # of Nodes		
	M.S.	VR	M.S.	VR	M.S.	VR	M.S.	VR	
Replications	3	5.719	.463	32.308	4.741**	4094.120	23.219**	425.649	8.030**
Families (Genotypes)	24	85.497	6.920**	107.358	15.755**	954.748	5.415**	807.377	15.232**
Rep x Fam (Error)	72	12.355		6.814		176.328		53.006	
		Length of Internodes		# of Racemes/Plant		Pod Dry Wt./Plant		# of Seeds/Plant	
	M.S.	VR	M.S.	VR	M.S.	VR	M.S.	VR	
Replications	3	5215.474	25.941**	66.459	7.578**	1895.429	19.143**	18032.774	15.756**
Families (Genotypes)	24	2574.406	12.805**	111.836	12.752**	520.913	5.261**	19167.155	16.747**
Rep x Fam (Error)	72	201.053		8.770		99.013		1144.491	
		# of Pods/Plant (X)*		# of Seeds/Pod (Y)		100-Seed Wt. (Z)		Seed Dry Wt./Plant (W)	
	M.S.	VR	M.S.	VR	M.S.	VR	M.S.	VR	
Replications	3	575.356	14.004**	1.032	21.284**	1.457	.623	1110.732	18.687**
Families (Genotypes)	24	569.249	13.856**	1.349	27.829**	464.962	198.982**	356.064	5.991**
Rep x Fam (Error)	72	41.084		.048		2.337		59.437	
		Length of Pod		Harvest Index					
	M.S.	VR	M.S.	VR					
Replications	3	236.385	5.988	5.719	.463				
Families (Genotypes)	24	1015.565	25.616**	85.497	6.920**				
Rep x Fam (Error)	72	39.646		12.355					

** 1% Sig. Difference

Duration of Flowering

5 x 5, F₁

The analysis of variance showed that there were no significant differences among replications but there were significant differences among the genotypes in duration of flowering (Table 1). Strain 0674 was the variety with the longest mean duration of flowering of 28 days. Strain 72-7427 had the second longest mean value of the trait of 24.7 days. SB and SEA had about the same mean value of the trait of 22.8 and 22.7 respectively. BTS was the variety with the shortest mean duration of flowering of 20.4 days. Six out of the 10 F₁ hybrids gave a mean duration of flowering longer than that of the parents. Those were the crosses involving BTS x 0674, BTS x SEA, SB x 0674, SB x SEA, SB x 72-7427 and SEA x 72-7427. It is noticed from the six crosses mentioned that the varieties BTS and SB produced an F₁ with heterotic effect only when used as pistillate parents whereas strain 72-7427 and strain 0674 gave hybrids with heterosis when used as the pollinate parent. SEA, however, was not consistent regarding this trait.

Figure 4 shows the W_r and V_r graph for the 5 x 5, F₁. The regression line is not significant ($b = .17 \pm .37$). The simple additive effect model cannot be applied to this set of data. The computed "D" value was 10.40 and the average degree of dominance was 1.58; since the

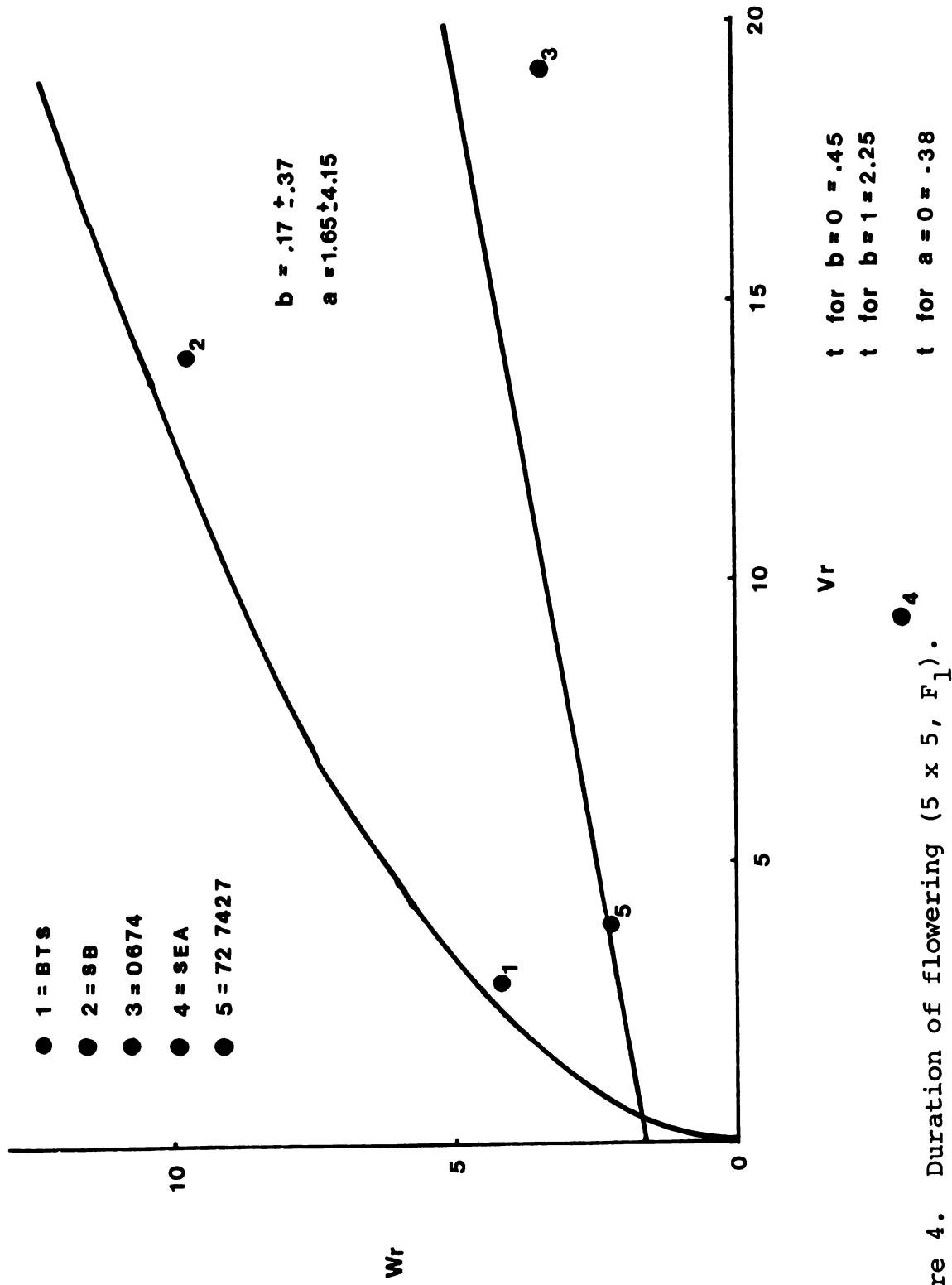


Figure 4. Duration of flowering (5×5 , F_1).

array points are so widely scattered in Figure 4, it is concluded that the data may not be reliable. The heritability estimate was 15%.

As to the positions of the array points, parents 1 and 5 appear to show a certain level of dominant genes, parent 2 appears to contain the recessive genes. Parents 3 and 4 seem to be the outliers, particularly parent 4 (0674). It was discussed earlier that strain 0674 was very much affected by ozone injury. Strain 0674 resumed its growth and development later in the season when climatic conditions were favorable again. It continued to produce flowers. However, the season was not long enough for its second phase of development; most of the flowers developed into small pods which were not fully filled.

This trait was not measured in 1974.

Days to Maturity

5 x 5, F₁

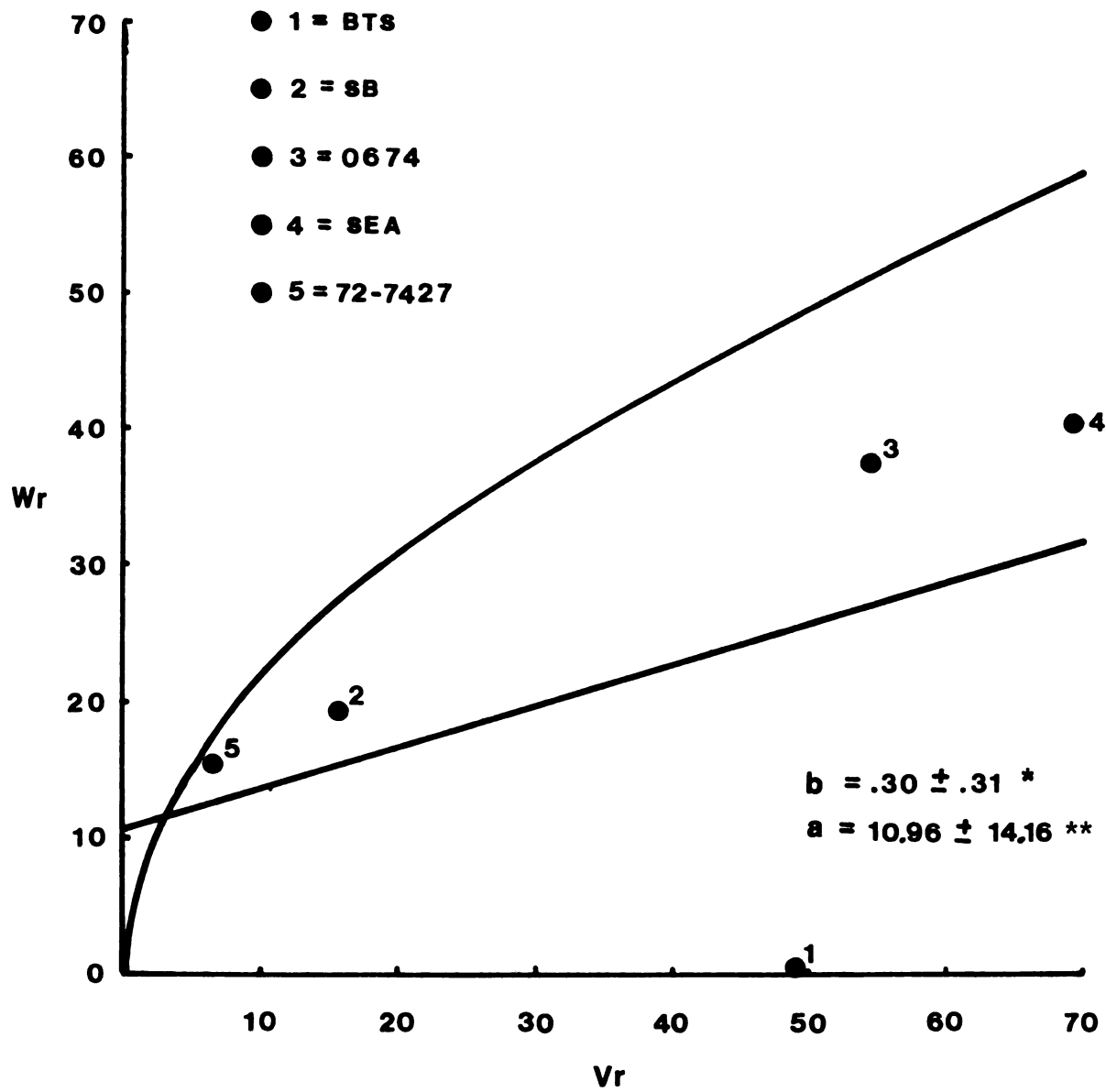
The analysis of variances of days to maturity showed that there were no significant differences among replicates but highly significant differences among the genotypes (Table 2). Inspecting the mean over replicates in Table 1, it appears that SEA was the earliest and strain 0674 was the latest maturing variety with mean values of 74.8 and 92.6 days respectively. Strain 72-7427 and varieties BTS and SB had mean numbers of days to maturity of 85, 89.4 and 89.5 respectively.

It was surprising to see that SEA and strain 0674 which have several morphological characters in common did not behave similarly regarding this trait. However, the differences between the two means was only about 8 days. It was observed that both 0674 and SEA were affected by ozone injury during the pod-filling stage. The leaves were senesced prematurely and abscised. Therefore, normal photosynthetic activities were disrupted and the pods were not fully filled. Strain 0674 appeared to be more affected by ozone injury. After this period, due to favorable climatic conditions, strain 0674 resumed its growth and development but not SEA. The flowers that strain 0674 produced at this later stage delayed its duration of flowering and maturity.

The other pair of parents which have several characters in common, i.e. SB and strain 72-7427, gave a difference in mean values of only 4.5 days. BTS which was expected to be the latest maturing variety did not prove to be so. However, the array mean of the hybrids derived from BTS does show the highest value (Table 1) which implies that any hybrid arising from this common parent will be the latest in maturity as compared to the hybrids from other crosses. A test of the F_1 and its reciprocal indicated there was no significant difference. Nine out of 10 F_1 hybrids had mean values exceeding that of the mid-parent values. In fact, 7 out of the 9 hybrids

had mean values greater than that of the later maturing parent. The only hybrid that had the mean value smaller than that of the mid-parent value was derived from 0674 x SEA (Table 1).

Figure 5 shows the W_r/V_r graph of the 5×5 , F_1 . The regression is not significant ($b = .30 \pm .31$) and it intersects the W_r axis above the point of origin ($a = 10.96 \pm 14.16$) but not significantly different from 0. This indicates genic interaction. The positions of the points representing strain 72-7427 and SB are within the parabola and close to the point of origin indicating that strain 72-7427 and SB contain a preponderance of dominant genes. On the other hand, the positions of strain 0674, SEA are on the top right of the graph showing that strain 0674 and SEA contain a preponderance of recessive genes for this trait. It is interesting to notice that SB and strain 72-7427 which have several morphological characters in common position close to each other whereas strain 0674 and SEA with similar plant type also position not very far from each other. Perhaps each pair of the parents mentioned have similar genotypes regarding this particular trait. The hybrids derived from SB and strain 72-7427 or strain 0674 and SEA do contain similar effects regarding dominant and recessive genes. The position of BTS is just above the V_r axis and almost 50 units from the W_r axis. It follows that



* t for $b = 0 = .98$, t for $b = 1 = 2.26$

** t for $a = 0 = .77$

Figure 5. Days to maturity ($5 \times 5, F_1$).

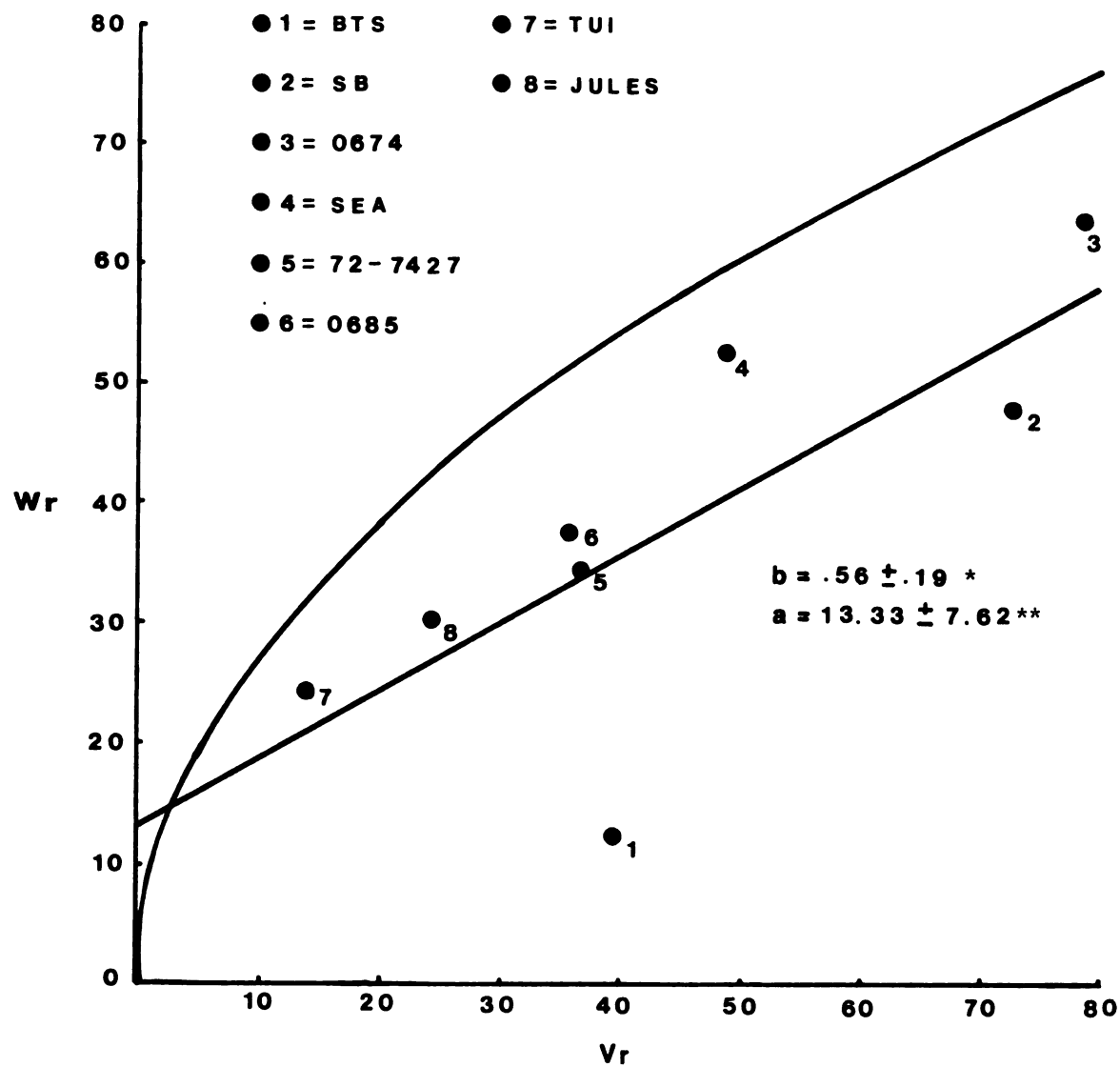
BTS has produced arrays with a very large variance but small covariance. BTS has a very distinctive phenotype as compared to the others. Genotypically it should also be very different, hence the genotype x environment interaction could affect the covariances. As Mather and Jinks (1971) pointed out respecting variation of highly inbred domestic plants like the small-seeded cereals, the interactions are large, and the covariances could be materially affected. It is this array point (1), that causes the slope to be closer to zero and nonsignificant. Were BTS to be excluded from consideration the interpretation would be more straightforward.

8 x 8, F₁

All the original five varieties have the mean number of days to maturity in 1974 larger than their behavior in 1973 except the strain 0674, the differences ranging from 5.2 days to 9.2 days. As stated above for the dates to first flower, this was undoubtedly due to different environmental conditions between the two years. The variety BTS was the latest maturing variety, as expected, with a mean value of 98.5 days. Also as expected, SEA was the earliest variety to mature with a mean value of 82.1 days, and these values agree well with the 1973 ranking as regards earliness. The other three varieties did not have the same ranking as in 1973.

This could be due to the more stable genotype of SEA regarding this particular trait. Change of environment did not have much affect on SEA as compared to the other 4 varieties. Out of 28 F_1 hybrids examined, 10 had mean values exceeding their late maturing parent. Fifteen out of 28 hybrids had mean values in between the two parents and 3 had mean values less than the early maturing parent (Table 3).

Figure 6 shows the W_r/V_r graph for the 8 x 8, F_1 . The regression line is significantly different from zero but not significantly different from unity ($b = .56 \pm .19$). The line intersects the W_r axis above the point of origin ($a = 13.33 \pm 7.62$) but not significantly different from zero indicating complete dominance. Examining the position of the array points one can see that most of them fit the regression line quite well except point 1 representing BTS. In comparing the position of BTS on both the 5 x 5 and 8 x 8, F_1 graphs it seems clear that BTS has a gene system which is both unique and consistent regarding this trait. SB seems to shift its position. The shifting of position of SB from the dominant side in Figure 5 to the recessive side in Figure 6 was undoubtedly caused by the additional 3 parental lines. This suggests that multiple alleles control this trait. The 3 new parental lines contain a stronger level of dominant genes than SB. This new interaction forced SB to shift toward the recessive side.



* t for $b = 0 = 2.95$ and t for $b = 1 = 2.29$

** t for $a = 0 = 1.75$

Figure 6. Days to maturity (8×8 , F_1).

5 x 5, F₂

Table 5 shows the mean values for the parents and the F₂ populations planted in 1974. The three parents which have the mean number of days from emergence to harvesting of 90 days and above were strain 72-7427, SB and BTS. The differences ranged from 90.2 days for strain 72-7427 to 98.5 days for BTS. Strain 0674 and SEA had mean values of 84.7 and 82.1, respectively.

The F₂, Wr/Vr graph (Figure 7) shows that the regression line is significantly different from $b = 0$ but not from $b = 1$ ($b = 1.16 \pm .16$). The line intersects the Wr axis below the point of origin ($a = -9.51 \pm 2.16$) but not significantly different from zero. Therefore a gene system with dominance but without the complication of genic interaction is indicated in the F₂ generation. From the position of the array points, it appears that BTS, SB and 72-7427 contain a preponderance of dominant genes. It can be hypothesized that late maturing is controlled largely by dominant genes and early maturing is controlled largely by recessive genes. It can be observed that without the presence of the 3 new parental lines, SB has retained its position on the dominant side. The additive genetic variance (D) has the value of 42.38. The heritability estimate is 14% for days to maturity which is relatively low. The "F" value of 43.42 indicates an excess of dominant genes among this set of

●1 = BTS

●7 = TUI

●2 = SB

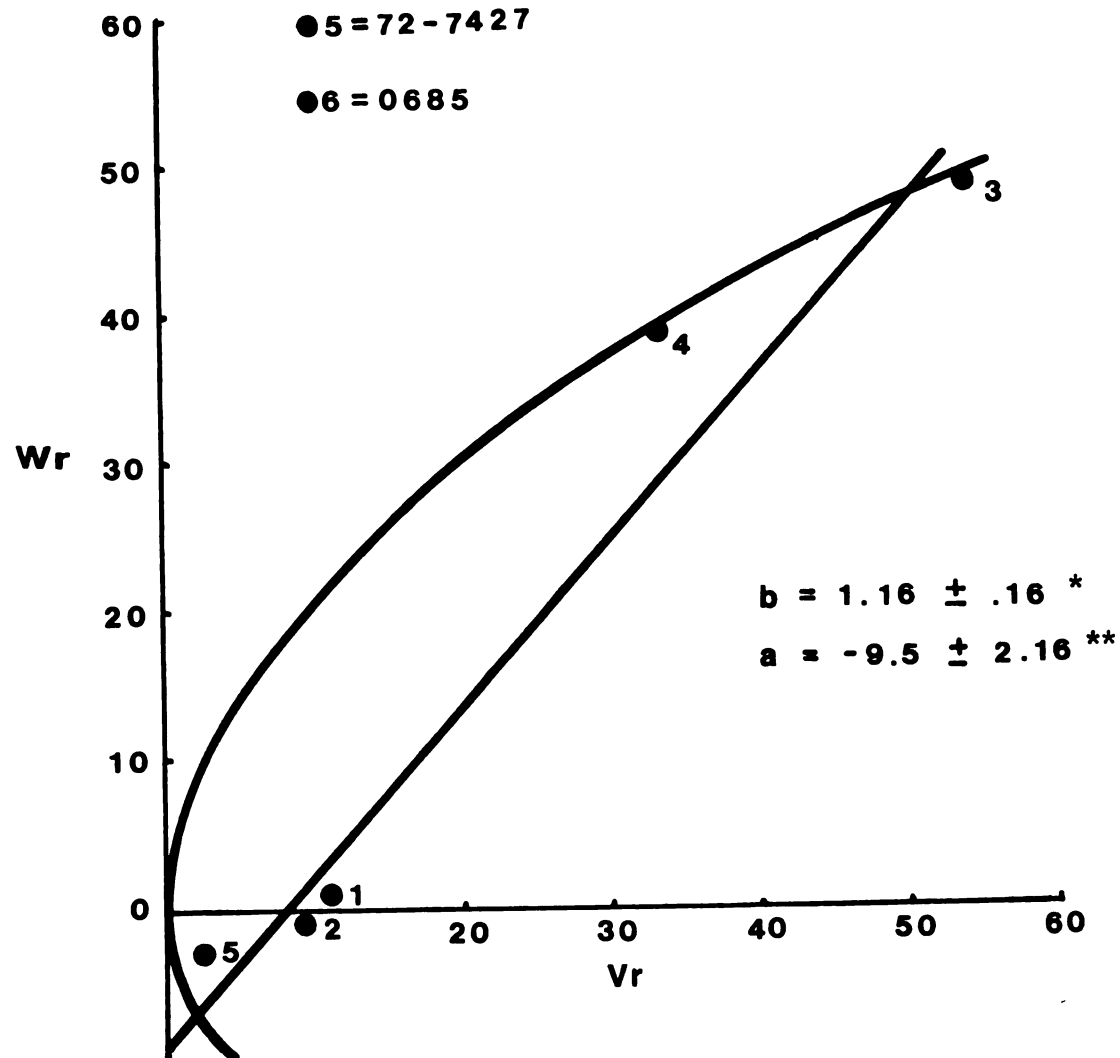
●8 = JULES

●3 = 0674

●4 = SEA

●5 = 72-7427

●6 = 0685



* t for $b = 0 = 7.28$, t for $b = 1 = -1.0$

** t for $a = 0 = 2.03$

Figure 7. Days to maturity (5×5 , F_2).

parents for this trait. The F_2 populations derived from BTS, SB and 72-7427 seemed to be reasonably uniform in maturity. However, those derived from SEA and 0674 showed several days difference in maturity, particularly those resulting from 0674 and SEA and its reciprocal. Ozone injury is thought to be the cause, since both 0674 and SEA were very sensitive to this environmental factor.

Plant Dry Weight

5 x 5, F_1

The analysis of variance shows that there were no significant differences among the replicates but there were highly significant differences among the genotypes. Different plant types certainly contributed to the difference in this trait. There was no significant difference between the F_1 and its reciprocal. Among the 5 parental varieties, BTS had the highest mean plant weight of 100.9 gm and 0674 had the smallest mean plant weight of 51.0 gm (Table 1). SB, SEA and 72-7427 had mean values of 68.9, 55.9 and 78.3 gm, respectively. Eight out of 10 hybrids had mean values exceeding that of the highest parent in the cross. Two hybrids had mean values lower than that of the mid-parent values. BTS x 0674 and its reciprocal produced hybrids with highest mean plant weights of 202.6 gm and 195.4 gm, respectively. The hybrid with the lowest mean value derived from the cross 0674 x SEA (45.2).

It can be seen in Table 7 that BTS has the highest array mean in both F_1 and F_2 . All the array means decreased in the F_2 generations. The heritability estimate was $-.16$ which has to be considered as zero. The large negative estimate for "D" of -3385.36 , indicates that there was a very high error variance. Therefore, further interpretation will not be reliable. It is assumed that this set of data does not fit the model. However, the W_r/V_r graph presented in Figure 8 indicates that the regression line is neither significantly different from $b = 0$ nor $b = 1$ ($b = .34 \pm .26$). The line intersects below the point of origin but not significantly different from 0 ($a = -452.10 \pm 561.83$). The intermediate slope value is indicative of genic interaction being involved in the expression of total plant weight. Genic interaction, as deduced from the W_r/V_r graph, merely obscures the manifestation of genic additivity or dominance. It does not, in itself, exclude them. More explanation will be given in the section of "Discussion."

The position of the array points indicates that strain 72-7427 and variety SB contain a preponderance of recessive genes. Variety SEA seems to contain a balanced proportion of dominant and recessive genes. BTS, which is the only indeterminate type among the 5 parental lines, behaves as an outlier. It has the highest mean plant weight, as stated earlier. It is not surprising

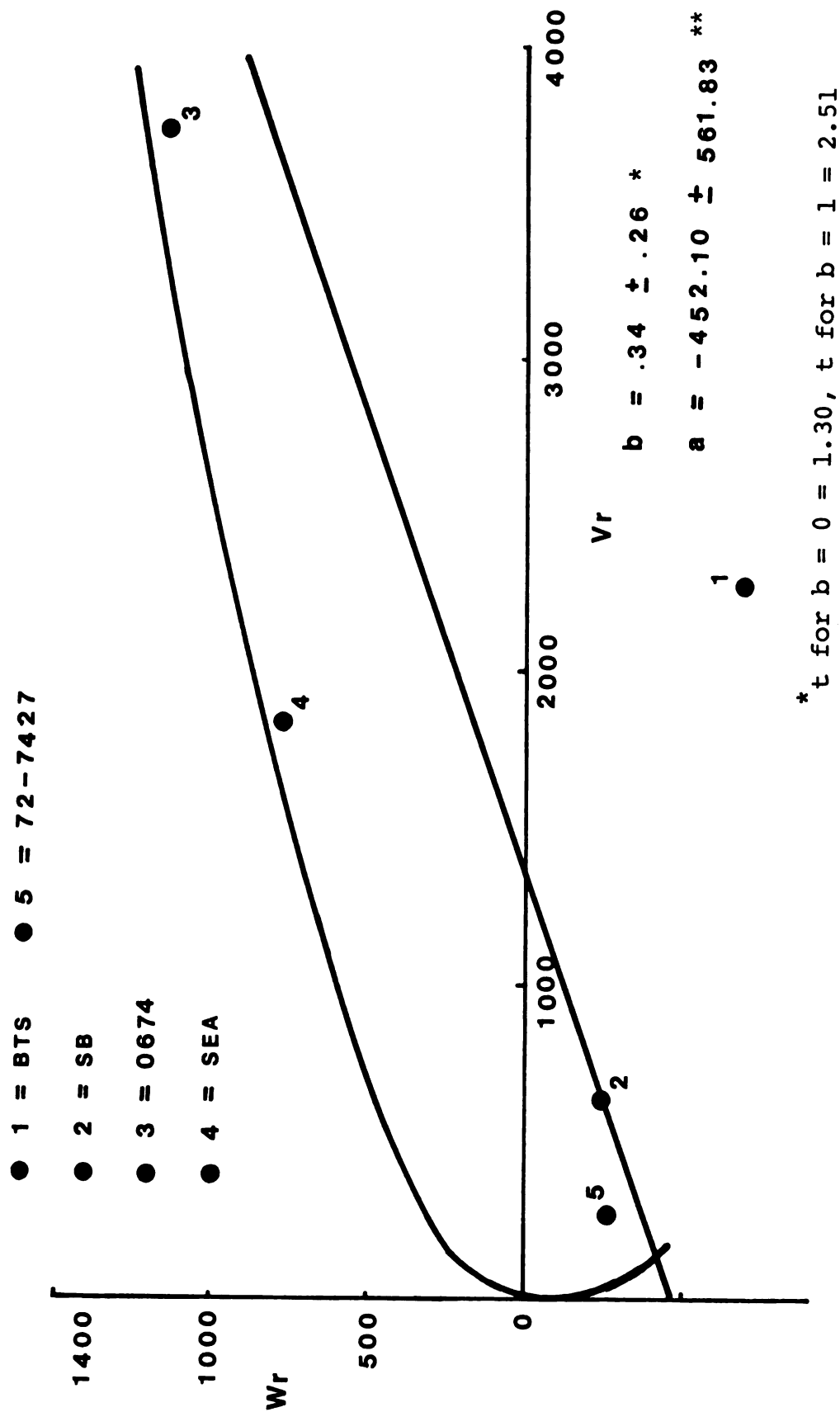


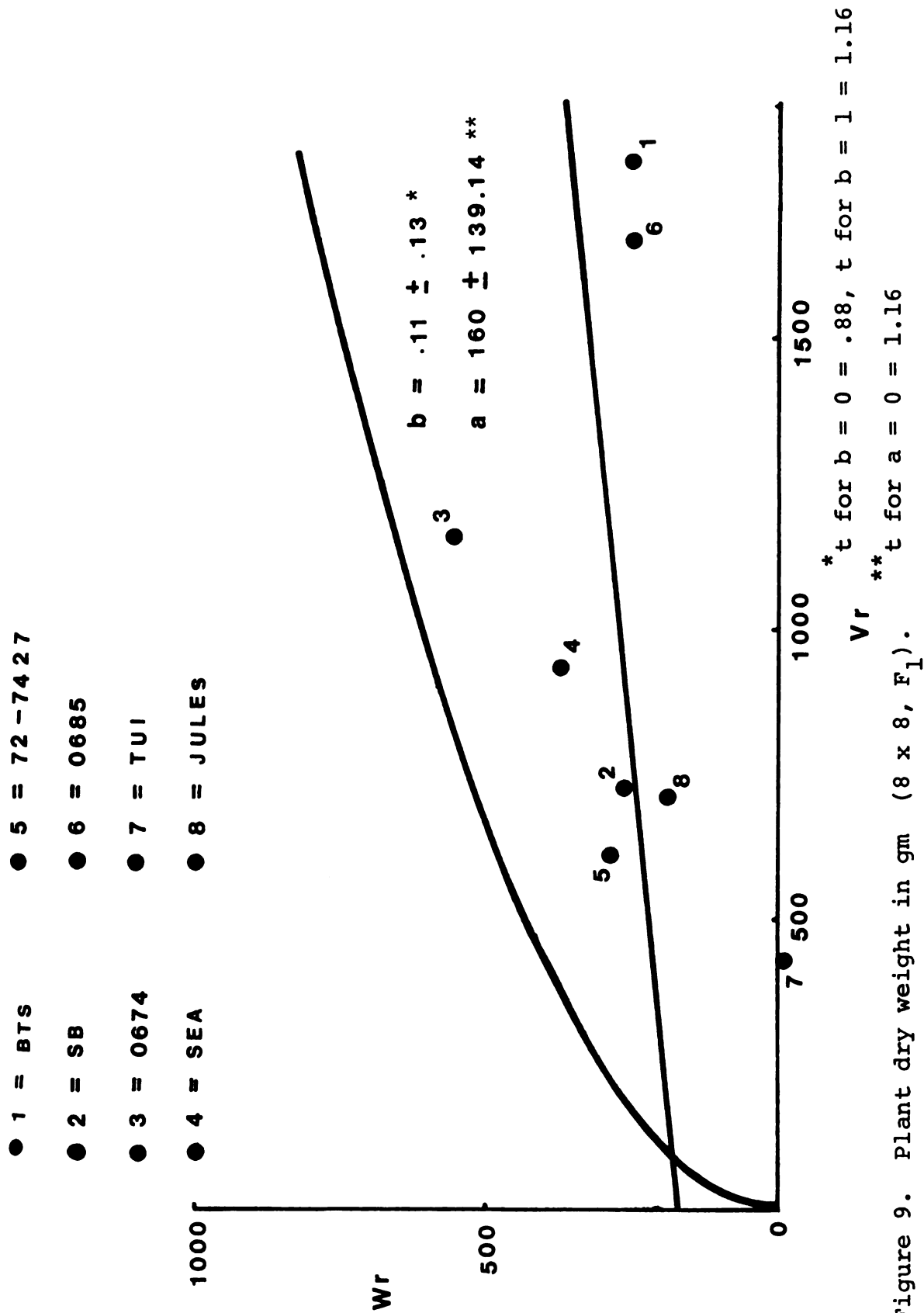
Figure 8. Plant dry weight in gm (5 x 5, F_1).

that its position on the graph will be far away from the others. The contrasting phenotypes and interacting loci would cause this difference.

8 x 8, F_1

The rankings of plant dry weight in grams of the parental varieties in the 1974 trial from the highest to lowest mean values were as follows: strain 0685 = 118.1, Jules = 101.8, Tui = 99.6, BTS = 95.7, SB = 89.5, 72-7427 = 77.9, SEA = 64.6 and strain 0674 = 61.8 (Table 3). Twenty-three out of the 28 F_1 hybrids had mean plant dry weights higher than that of either parent. The means of 4 hybrids were in between the two parents and the mean of one hybrid (Tui x Jules) was lower than that of the lower parent in the cross (Table 3). The cross involving BTS x 0685 and its reciprocal gave hybrids with the highest mean plant dry weight of 241.6 and 222.6 gm, respectively (Table 5). The hybrids with the lowest mean plant dry weight derived from the cross 0674 x SEA and its reciprocal (62.9 and 73.6 gm respectively).

The W_r/V_r graph (Figure 9) shows that the regression line is significantly different from $b = 1$ and it is not significantly different from $b = 0$ ($b = .11 \pm .13$). The simple additive gene system cannot apply to this case. The estimate of "D" also has a negative value of -325.94 as with the 1973 data. This is probably due to the high

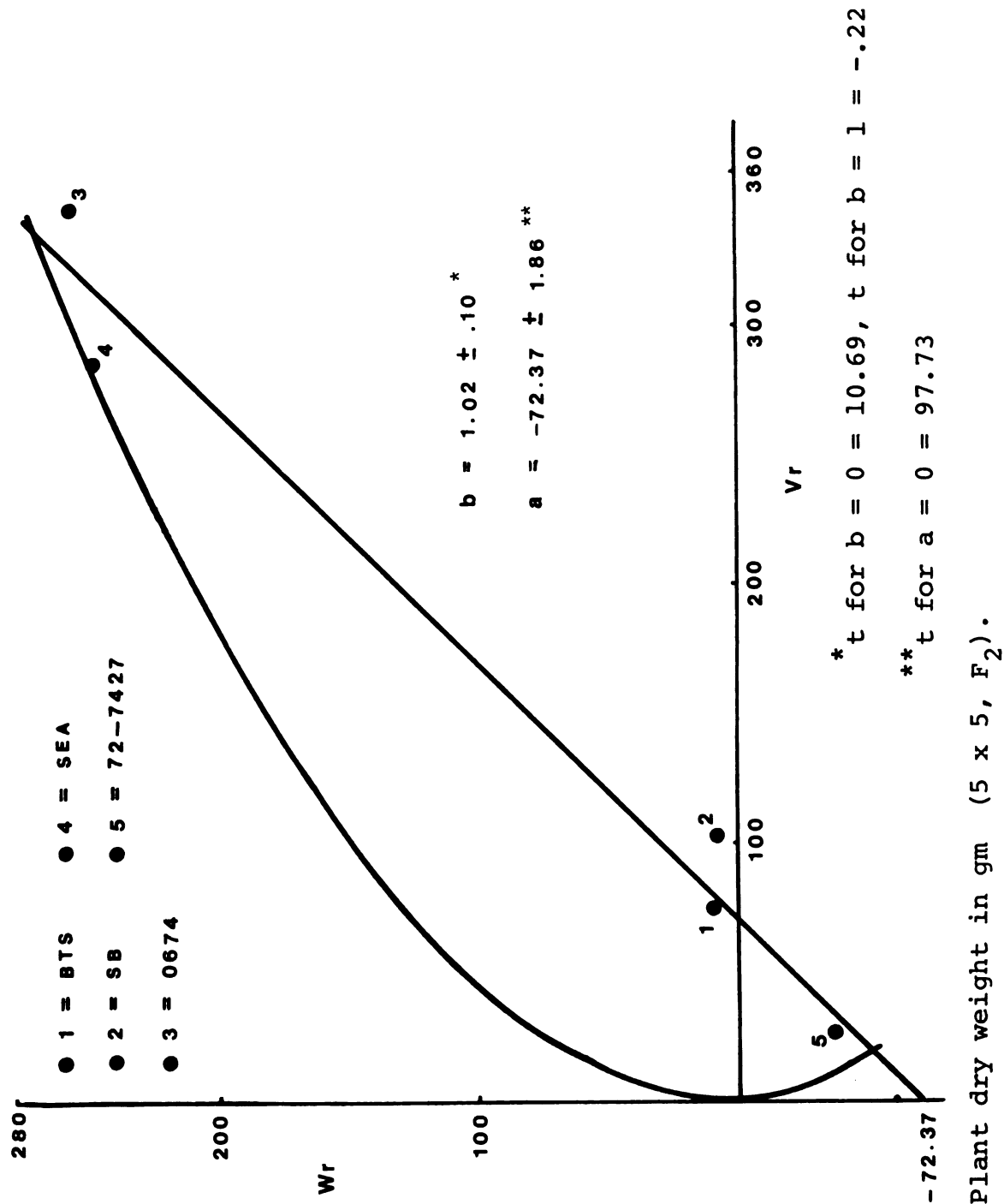


error variance associated with this trait ($E = 875.10$). Therefore the assumption of no gene interaction is not valid in this case. It is observed that the arrays which show interaction are BTS and strain 0685. If these two array points are omitted the remaining arrays may suggest a different slope, i.e. a slope of $b = .7$ is possible and a different interpretation of the mode of gene action is expected. (Strictly speaking, if one or another parental array is to be excluded from the W_r/V_r graph, a new regression line should be calculated omitting all data involving the excluded parents. In the present instances, an approximate line has been fitted by eye to the original array points, without recalculating the array variances and covariances.)

5 x 5, F_2

Table 5 shows that 6 out of 10 F_2 populations (excluding their reciprocals) had mean plant weights greater than that of their heavier parent, 3 populations had their means in between that of the two parents and 1 family gave a mean value smaller than that of the lighter parent. These mean values were all smaller than those of the F_1 generations due to a lower level of heterozygotes (Table 4).

The W_r/V_r graph in Figure 10 shows that the regression line is significantly different from $b = 0$



but not significantly different from $b = 1$ ($b = 1.02 \pm .10$). The line intersects the W_r axis significantly below the point of origin ($a = -72.3 \pm .86$) indicating over-dominance. This agrees with the interpretation from the $\sqrt{H_1/D}$ value of 4.05. The fact that BTS, SB and strain 72-7427 are located near the point of origin indicates that these parents contain mostly dominant genes controlling this trait and strain 72-7427 has most of the dominant genes among the 3 parents (Figure 10). Strain 0674 and SEA contain mostly recessive genes as indicated by their positions on the top right of the graph. There is not much difference, however, between the array means of these 2 groups of parents. It may be assumed that plant dry weight is influenced both by dominant and recessive genes. The heritability estimate is essentially zero ($h^2 = .04$). However, the mean values in the 8×8 , F_1 indicated that the heaviest hybrids derived from the most vigorous plants and the lightest hybrids from smallest parents (Table 3); it is, therefore, believed that this trait is heritable and can be transferred to selected families in the next generation.

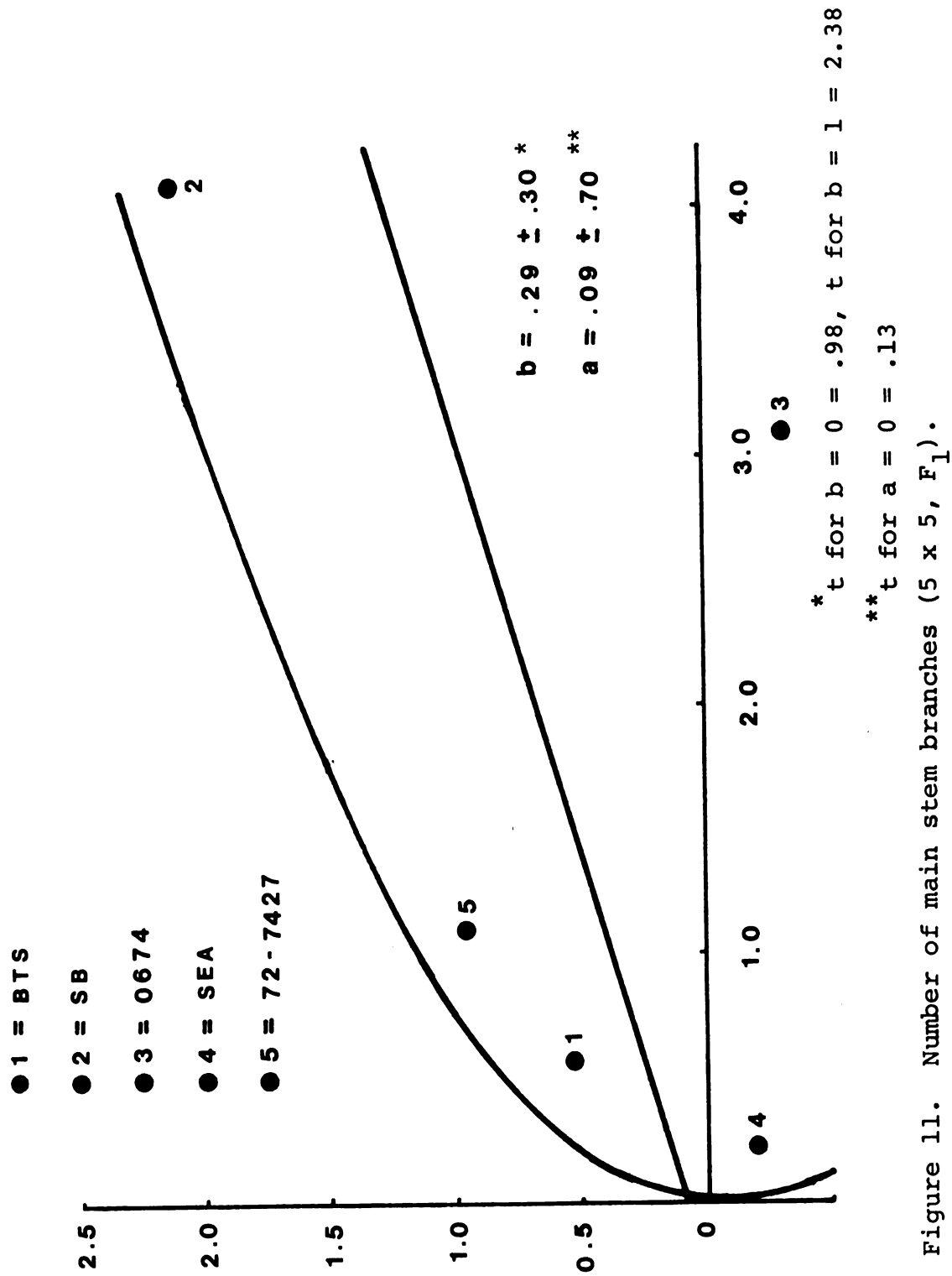
Number of Main Stem Branches

5 x 5, F_1

The number of branches on the main stem were counted at maturity and recorded on the individual plant basis. Table 1 indicates that strain 0674 bore the

highest number of main stem branches with a mean value of 10.08, SEA, 72-7427, BTS and SB had mean values of 9.8, 9.3, 7.9 and 7.5, respectively. Six out of 10 F_1 hybrids gave mean values greater than the mean value of the high parent. Two hybrids had mean values greater than that of the mid-parent value and 2 hybrids had mean values smaller than that of the low parent. It is interesting to observe that when both strain 0674 and SEA were crossed with other varieties all the hybrids showed heterosis except when these two parents were crossed to each other. It appears that strain 0674 and SEA are similar genetically.

The regression of W_r on V_r in Figure 11 shows that it was not significant from zero ($b = .29 \pm .30$). Genic interaction is indicated. The assumption of no gene interaction is not valid. However, examining the array points indicates that SEA contains the highest number of dominant genes. BTS and strain 72-7427 appear to contain a certain portion of dominant genes. SB contains the most recessive genes regarding this trait. Parent 3 (0674) is the outlier in this case and causes the slope of the regression to deviate from unity. As it was mentioned earlier, strain 0674 resumed its growth after being affected by ozone injury. This genotype and environmental interaction in the later stage of development probably increased error variation, causing the

Figure 11. Number of main stem branches (5×5 , F_1).

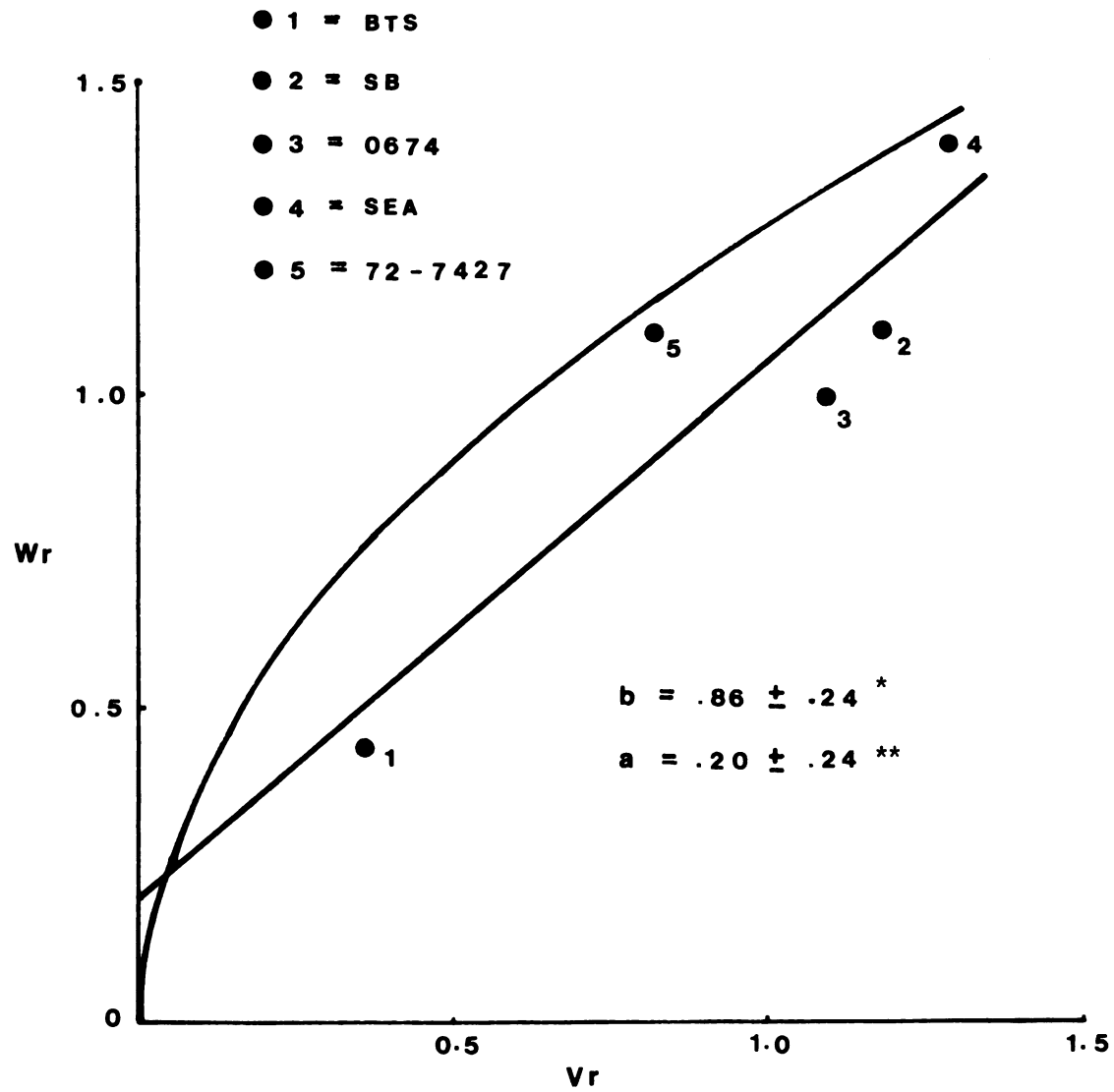
negative value of "D." This is the trait that would be most strongly affected by density differences due to differential loss of plants in plots.

Number of Main Stem Nodes

5 x 5, F₁

The analysis of variance shows that there were no significant differences either among the replicates or the genotypes (Table 2). BTS had the highest mean number of main stem nodes with the value of 7.3, strain 0674, SEA, SB and strain 72-7427 had mean values of 5.4, 5.0, 4.2 and 4.1, respectively. No significant differences between the F₁ and its reciprocal could be detected. Four hybrids had mean values greater than the mid-parent value and 3 had mean values exceeding that of the parent with the higher number of main stem nodes. Three hybrids had mean values smaller than the mid-parent values.

Figure 12 shows the Wr/Vr graph of the number of main stem nodes, 5 x 5, F₁. The regression line was not significantly different from unity but significantly different from zero ($b = .86 \pm .24$). The position of the array points representing SB, strain 0674, SEA and strain 72-7427 shows that they all possess recessive genes controlling this trait, with SEA being the extreme in this respect. BTS appears to contain more of the dominant genes. The evidence from the Wr/Vr graph seems to



* t for $b = 0 = 3.62$, t for $b = 1 = .61$

** t for $a = 0 = .82$

Figure 12. Number of main stem nodes (5×5 , F_1).

indicate that the indeterminate type (BTS) contained the dominant genes and the determinate types (SB, strain 0674, SEA and strain 72-7427) contained most of the recessive genes controlling number of main stem nodes. Nevertheless, the estimate of h^2 and D had values of -.23 and -17.24 respectively indicated that there was a large error variance ($E = 19.61$) in this set of data. Therefore, no interpretation can be made with confidence with regard to dominance and additive effects of the genes controlling this trait.

Because of insignificant differences among the genotypes regarding this trait it was decided to determine the total number of nodes of the whole plant in the 5×5 , F_2 and 8×8 , F_1 populations.

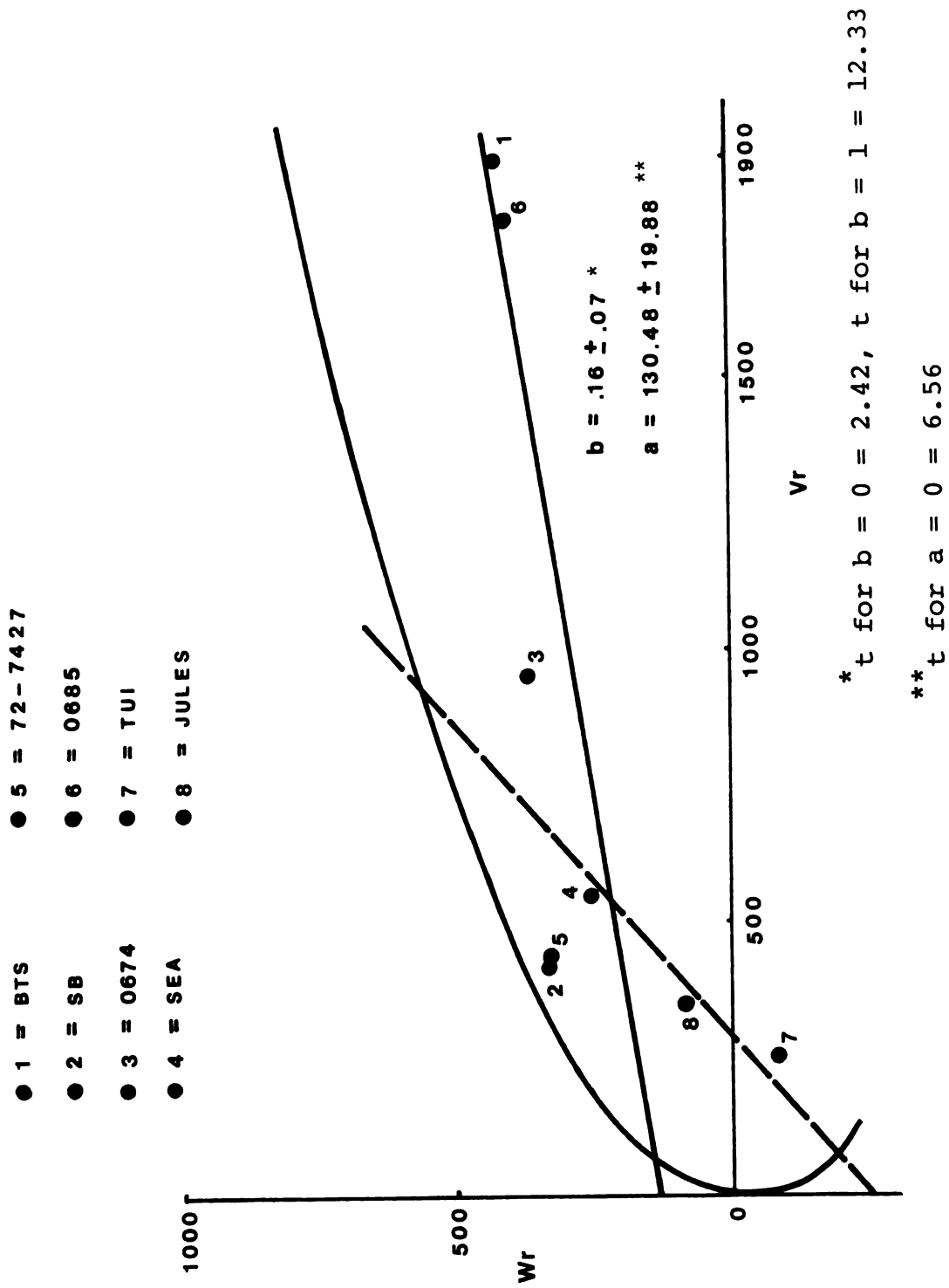
Total Number of Nodes

8×8 , F_1

Total number of nodes consisted of all the nodes counted on every stem. This should give a better picture of the phenotype of the parents and that of the segregating populations. Analyses of variance show there were no significant differences among replicates but highly significant differences among genotypes (Table 4). The branchy vigorous determinate type of strain 0685 gave the highest mean value of number of nodes (74.6) and the determinate, strain 72-7427 gave the lowest mean value

of 24.4. Jules, BTS, Tui, strain 0674, SEA and SB gave mean values of 72.2, 57.5, 56.4, 41.8, 39.9 and 30.9 nodes, respectively. Heterosis was strongly expressed in total number of nodes. Eighteen had mean values exceeding the mean values of the parent with large mean number of nodes and 6 had mean values greater than the mid-parent values. However, 4 hybrids had the mean values smaller than the parent with smaller mean (Table 3). The hybrid derived from BTS x 0685 gave the highest mean value of 196.5 (Table 3).

The regression of W_r on V_r (Figure 13) shows that the line was significantly different from unity but not significantly different from zero ($b = .16 \pm .07$). The regression line intersects the W_r axis above the origin ($a = 130.4 \pm 19.88$) and is significantly different from 0, indicating genic interaction. The position of the array points representing BTS and strain 0685 obviously caused the regression line to deviate significantly from unity. If we omit BTS and strain 0685 and draw a new regression line (dotted line) the remaining parental arrays would fit this line fairly well. It is apparent, then, that Tui contains a certain degree of dominant genes and strain 0674 contains the recessive genes. The other parents, SB, SEA, strain 72-7427 and Jules appear to contain an intermediate proportion of dominant genes.

Figure 13. Total number of nodes (8 x 8, F_1).

It is not clear why parents 1 (BTS) and 6 (0685) were positioned on the far right of the graph. They both had very high variances but low covariances. They looked as if they contain a preponderance of recessive genes which agreed with the estimate of F ($= -720.46$). Genotype-environmental interaction involving these two parents is probably the cause of this deviation. The heritability estimate was practically zero ($h^2 = .03$).

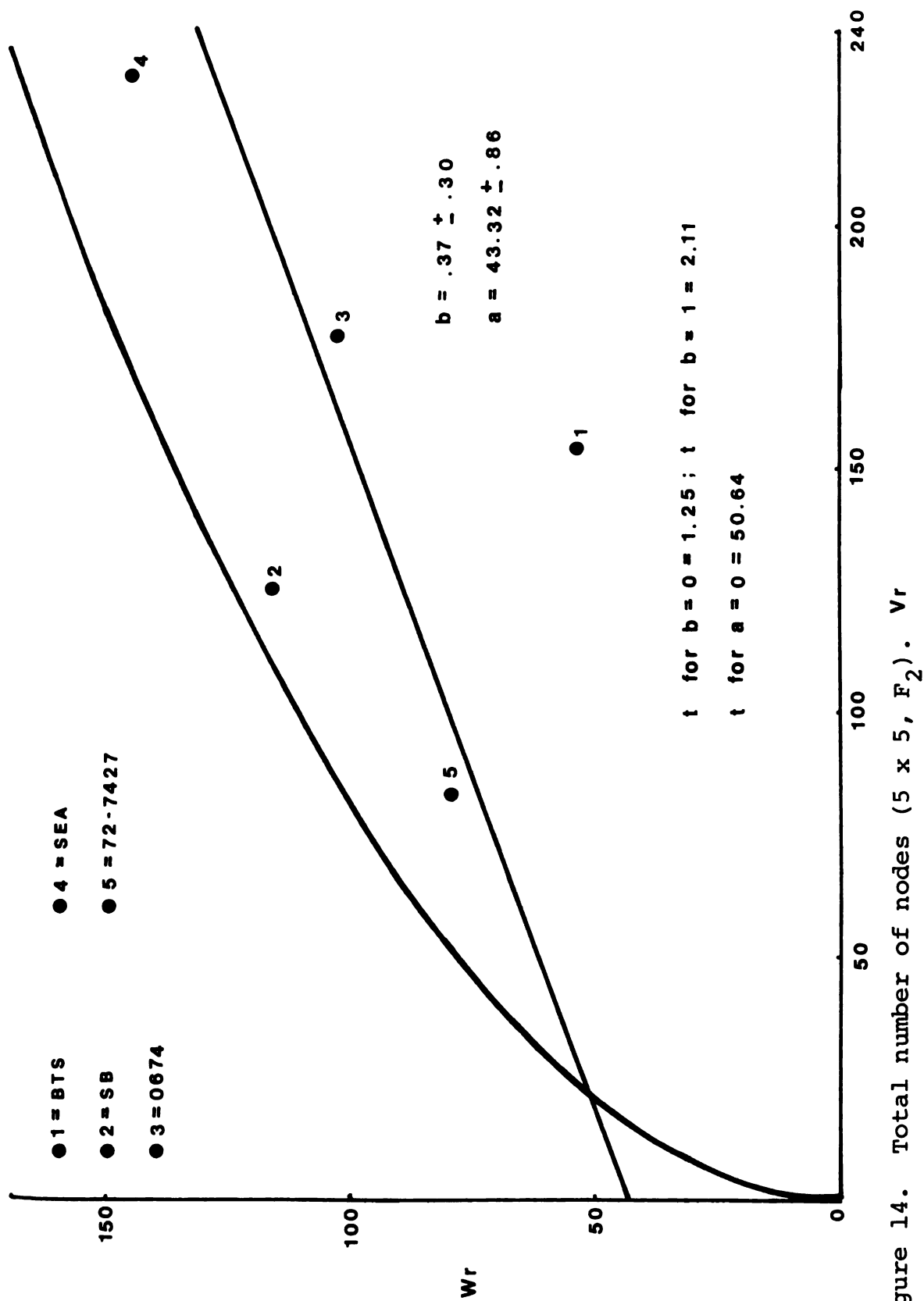
5 x 5, F_2

The total number of nodes of the whole plant was counted among the 5 x 5, F_2 populations instead of counting the number of main stem nodes as in the 5 x 5, F_1 . It was found in the analysis of variances (Table 6) that there were significant differences among replicates and among genotypes.

The mean values of the parents agreed very well in rank with the mean values for number of main-stem nodes in 1973. BTS with a mean of 56.5, strain 72-7427 with a mean of 26.7 were the highest and lowest, respectively (Table 5). SEA, strain 0674 and SB had mean values of 41.6, 40.0 and 33.5 nodes, respectively. Six out of 10 F_2 populations had mean values exceeding that of the high parent. Two F_2 populations had mean values greater than the mid-parent values but smaller than the high parent. Two F_2 populations had mean values lower than that of the mid-parent value.

Figure 14 shows the W_r/V_r graph of the 5×5 , F_2 . The regression of W_r on V_r is not significant ($b = .37 \pm .30$) as was the case for 8×8 , F_1 . Hence, there was no real relationship between W_r and V_r . The line intersects the W_r axis above the origin, ($a = 43.33 \pm .86$) and significantly different from 0, indicating genic interaction. The estimate of F was -417.18 indicating that there was an excess of recessive genes for this trait in this sample of lines. According to the position of the array means, parent 4 (SEA) contained a preponderance of recessive genes. None of the varieties seemed to contain a preponderance of dominant genes. Parent 1 (BTS) which differed phenotypically and genotypically from the others was the outlier causing the regression to deviate from unity.

Number of nodes is a complex trait. It is well understood that this trait effects other sequential traits, i.e. number of leaves, number of racemes, number of pods, etc. It is highly influenced by stand and density. BTS is an indeterminate type of bean. If occasional plants within plots are missing during vegetative development, BTS could extend its growth in other directions, hence, producing longer stems, higher number of nodes, etc. Being of bush type, other parents did not have much extension of growth and development to effect number of nodes. Therefore, those parents SB,

Figure 14. Total number of nodes (5 x 5, F_2). V_r

strain 0674, SEA, strain 72-7427 position well within the parabola except strain 0674 which is slightly below the unit regression line. The heritability estimate in the F_2 population is low ($h^2 = .04$).

Length of Internode

8 x 8, F_1

The length of internode was not measured in the 1973 trial therefore no data for 5 x 5, F_1 were available. In the 1974 trial it was decided to measure the length of internode. This was to provide a morphological picture of the individual line as well as for the segregating generations regarding this trait.

Three of the longest internodes in each plant were measured and averaged to be the length of internode of that plant.

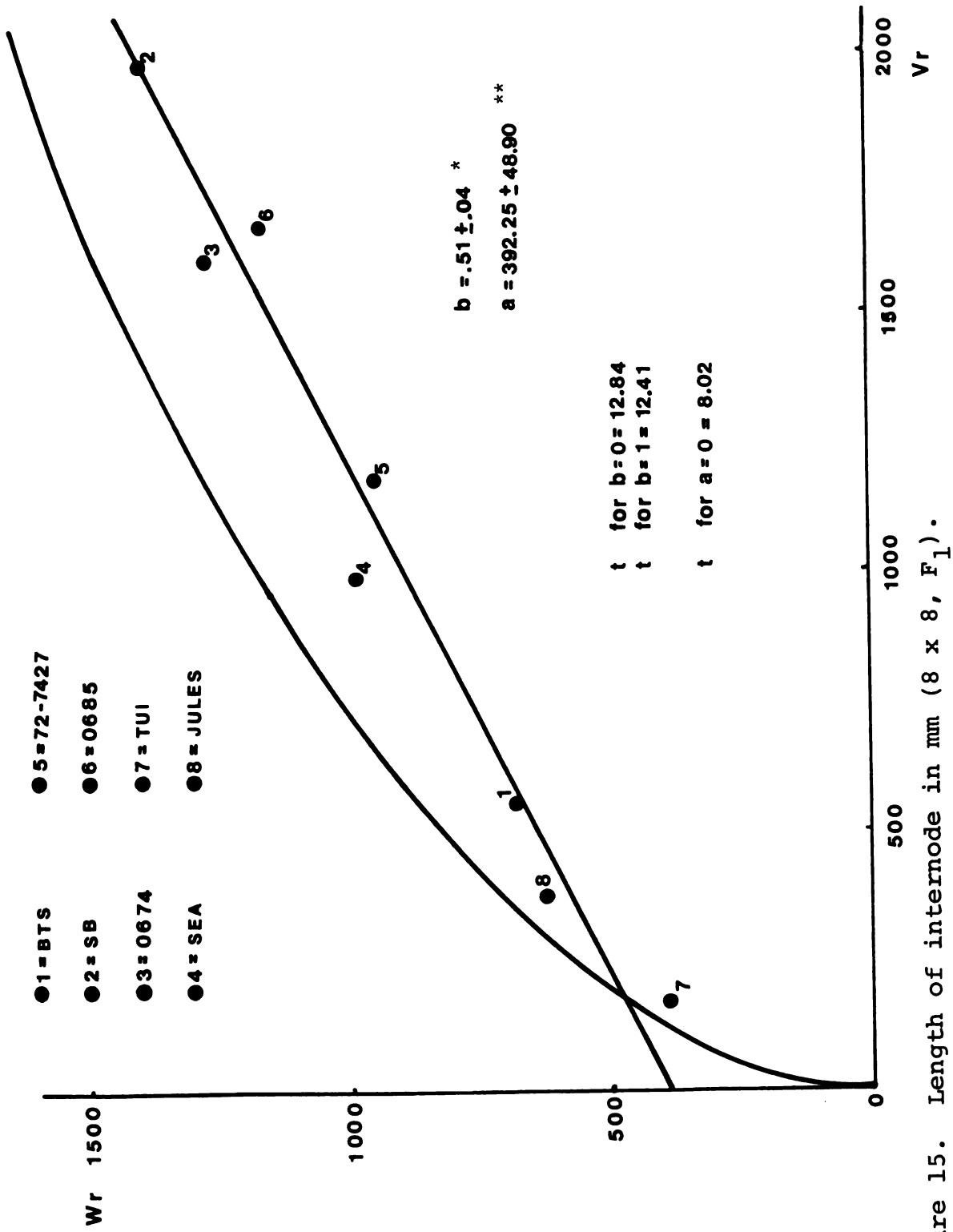
Table 3 shows the mean length of internode of the parental and F_1 hybrids derived from the 8 x 8 crosses. It appears that the determinate type of dry bean has the longest internode (0685 = 195.6 m.m.) and the indeterminate type has the shortest (BTS = 89.0 m.m. Table 3).

Of the 28 F_1 hybrids, 17 had means exceeding mid-parent values and 12 had mean values exceeding that of the long internode parent. Eleven F_1 hybrids had mean values smaller than that of mid-parent values. The hybrid derived from the cross 0685 x SB gave a mean value of

248.4 which was the highest. Tui x Jules gave the hybrid with the lowest mean value of 79.2. Tui x BTS also gave a hybrid with short internode (94.2).

The W_r/V_r graph presented in Figure 15 shows that the regression line is significantly different from $b = 0$ and $b = 1$ ($b = .51 \pm .04$) indicating genic interaction plays a major role in determining length of internode. Balancing the evidence on the graph, particularly the intersection of the regression line on the W_r axis, it is believed that genic interaction is involved and the calculated value of $\sqrt{H_1/D} = 1.2081$ should not be relied upon as indicative of the prevailing mode of gene action.

The positions of the array points show that Tui, Jules and BTS contain a preponderance of dominant genes, strains 0674, 0685 and the variety SB contain a preponderance of recessive genes. SEA and strain 72-7427 appear to contain a balanced proportion of dominant and recessive genes. Since the "F" value is 1386.33, indicating an excess of dominant genes among the parental lines, SEA and strain 72-7427 may contain a higher proportion of dominant than recessive genes. The array means of strain 0685 and SB were the highest (183.9 and 174.8, Table 8) and the positions of the two parents are on the recessive side; it is therefore reasonable to believe that these two parents will produce offspring

Figure 15. Length of internode in mm ($8 \times 8, F_1$).

with long internodes if they are crossed and that long internodes are controlled by recessive genes. BTS, Tui and Jules are all indeterminate type. According to their array positions they all contain dominant genes. Therefore, it is also reasonable to assume that short internodes are controlled by dominant genes.

5 x 5, F₂

Among the 5 original parental lines, strain 72-7427 had the longest mean internode length of 155.7, SB, strain 0674, SEA and BTS had mean values of 150.1, 129.4, 113.4 and 88.6 respectively (Table 5). The ranking of the 5 parental lines here are not in the same order as found in 8 x 8, F₁ (Table 3). They were, in fact, the same group of parents, grown in the same field. The differences in ranking were due to the number of means taken to compare with their corresponding F₁ (Table 3) or F₂ (Table 5). In Table 3, only 2 parental means were averaged whereas in Table 5, because there were 6 F₂ plots, 6 parental means were randomly taken from the overall 14 means to average and compare with the F₂ means. The mean value of strain 72-7427 in Table 5 is larger than its corresponding mean value in Table 3 simply because the 6 parental means which were randomly taken happened to have large values and the 2 means taken to be averaged as the parental mean in Table 3 happened

to have small values. Since the parental means in Table 5 were averaged from a larger number of values, therefore, they are more reliable.

Six out of 10 F_2 families examined had mean values exceeding that of the mid-parent values and 3 out of 6 F_2 had mean values larger than that of the parent with long internode. Four F_2 's had mean values smaller than that of the mid-parent values. Three out of 4 F_2 's mentioned derived from crosses involving BTS as the maternal parent and 1 derived from the cross SB x 72-7427. The F_2 family with the longest internode was the one resulting from the cross 0674 x 72-7427 (166.9, Table 5) and the F_2 family with the shortest internode was the one derived from BTS x 0674 (105.4, Table 5).

The W_r/V_r graph presented in Figure 16 shows that the regression line is significantly different from $b = 0$ but not from $b = 1$ ($b = .68 \pm .24$). The intercept on the W_r axis is above the origin but not significantly different from 0 ($a = 132.25 \pm 121.32$) indicating complete dominance. The $\sqrt{H_1/D}$ value of 1.98 which indicates over dominance does not agree with the interception of the regression line. It is obvious from the graph that the interception is above the origin and the array points fit the line very well. Therefore, the calculated value of $\sqrt{H_1/D}$ is not believed to be reliable and the

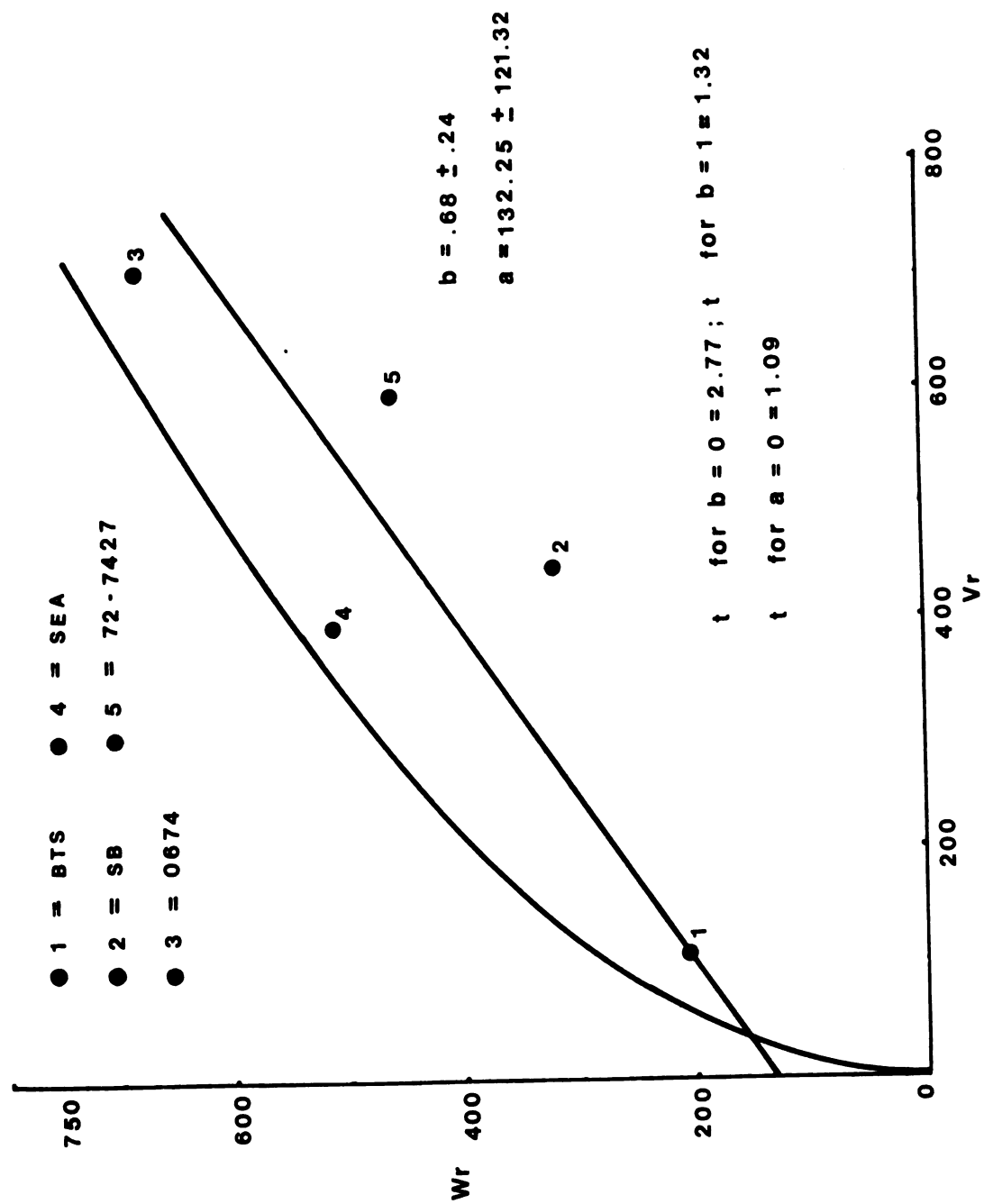


Figure 16. Length of internode in mm ($5 \times 5, F_2$).

interpretation probably should be done strictly from the evidence on the graph, which suggests partial to complete dominance.

The array points indicate that BTS contains a preponderance of dominant genes. Strain 0674 contains a preponderance of recessive genes. Strain 72-7427 contains a higher proportion of dominant and recessive genes. The "F" value of -743.48 indicates that there is an excess of recessive genes among the parental lines. Since the positions of more points are on the recessive side, the "F" value confirms the picture on the graph. BTS (parent 1), which is the only indeterminate type among the 5 parents, possesses dominant genes. Its position in the 8 x 8, F_1 is also on the dominant side together with other two indeterminate lines (Tui and Jules). This consistency shows that short internodes are controlled by dominant genes.

The heritability estimate is 14% which is low. This indicates that length of internode is not highly heritable in the F_2 . It would be difficult to select efficiently in the F_2 . It also suggests that in F_3 or advanced generations selection for this trait should be on a family basis and not on an individual plant basis.

Number of Racemes Per Plant

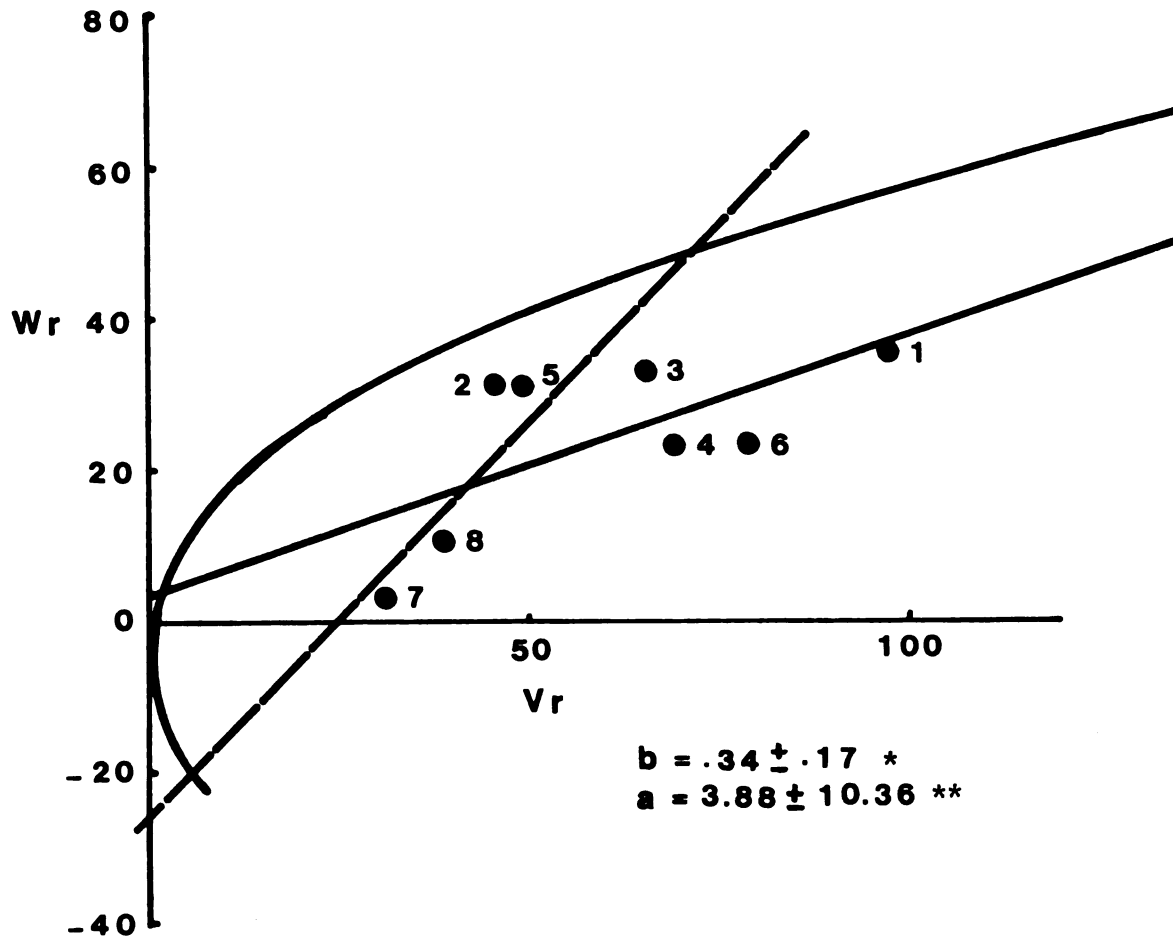
8 x 8, F_1

Number of racemes was not counted in the 1973 trial. In 1974 this trait was included and it was determined from both the F_1 and the F_2 populations.

Among the 8 parental lines, it appears in Table 3 that strain 0685 had the highest mean number of racemes (30.6) and strain 72-7427 had the lowest mean of 11.5. Twenty-four out of the 28 F_1 's had mean values greater than that of mid-parent values and 21 out of that 24 F_1 's had means greater than the mean of the high parent. Four crosses resulted in F_1 's which had mean values lower than that of their mid-parent values. They were: SB x 72-7427 (14.4), 0674 x SEA (19.8), SEA x 0685 (23.5) and Tui x Jules (22.5). The cross involving SB x 72-7427 and its reciprocal gave hybrids with the lowest mean number of racemes of 14.4 and 15.0 respectively. The hybrid derived from the cross BTS x 0685 gave the highest mean value of 54.9. It is also shown in Table 8 that the array means of strain 0685 and BTS were among the highest (34.6 and 34.1).

The situation presented by the W_r/V_r graph (Figure 17) is confusing. The regression is shown to be significantly different from $b = 1$ but not significantly different from $b = 0$. The simple additive gene system cannot be applied to this case. Furthermore, the computed

- | | |
|------------|---------------|
| ● 1 = BTS | ● 5 = 72-7427 |
| ● 2 = SB | ● 6 = 0685 |
| ● 3 = 0674 | ● 7 = TUI |
| ● 4 = SEA | ● 8 = JULES |



* t for $b = 0 = 2.04$ and t for $b = 1 = 4.01$

** t for $a = 0 = 0.37$

Figure 17. Number of racemes per plant (8 x 8, F_1).

"D" has a negative value of -2.86. Gene interaction is believed to be involved. Therefore this set of data does not fit the "no gene interaction" assumption for the diallel model. The positions of the array points look disturbing particularly those representing BTS, strain 0685 and SEA. If a new regression line is drawn (dotted line) as shown by omitting BTS, strain 0685 and SEA, the line would fit other array points and would be significantly different from $b = 0$ but not from $b = 1$. From this new position of the regression line, SB, strain 0674 and strain 72-7427 may be said to contain recessive genes and Tui and Jules contain a moderate level of dominant genes. However, the interpretation from this set cannot be considered reliable since "D" has a negative value.

5 x 5, F_2

Nine out of 10 F_2 populations examined had mean values exceeding that of the mid-parent values (Table 5). The only population that had a mean value lower than that of the mid-parent value was the one derived from SB x 72-7427 (14.1). The cross BTS x SEA appeared to give an F_2 population with the highest mean number of racemes. The F_2 derived from the cross SB x 72-7427 had the lowest mean number of racemes. The array means (Table 8) also show that the lowest values belong to SB and strain 72-7427.

Table 7. The array means of different traits for the F_1 and F_2 (5 x 5) taken from Tables 1 and 3.

	BTS	SB	0674	SEA	72-7427
Days to First Flower					
F_1	36.0	31.4	39.7	34.0	28.3
F_2	42.4	35.3	39.9	36.7	33.7
Days to Maturity					
F_1	95.8	92.4	92.1	84.3	84.6
F_2	95.4	92.6	92.6	87.5	91.2
Plant Dry Wt.					
F_1	128.9	109.6	107.3	103.9	86.7
F_2	93.7	88.9	88.0	82.7	84.7
# Main Stem Branches					
F_1	8.4	9.7	10.1	9.6	9.3
# Main Stem Nodes					
F_1	7.3	5.2	5.9	5.9	4.6
Pods Dry Wt./Plant					
F_1	102.2	83.7	77.3	81.9	68.2
F_2	69.2	65.5	61.8	61.5	63.4
# of Seeds/Plant					
F_1	406.7	230.5	318.8	288.4	144.9
F_2	255.1	165.4	239.8	229.8	144.7
# of Pods/Plant (X)					
F_1	74.4	52.1	69.7	60.3	32.1
F_2	52.3	42.4	53.2	50.8	34.2
# of Seeds/Pod (Y)					
F_1	5.1	4.2	4.5	4.5	4.3
F_2	5.0	3.9	4.3	4.3	4.1
100-Seed Wt. (Z)					
F_1	21.9	32.3	18.0	21.5	47.9
F_2	21.0	33.8	20.0	21.6	36.4
Seed Dry Wt./Plant					
F_1	76.9	66.0	58.6	63.1	50.9
F_2	53.7	51.1	46.9	49.1	47.9
Harvest Index					
F_1	.60	.60	.55	.60	.59
F_2	.58	.59	.54	.57	.57

Table 8. The array means of different traits for the F₁ and F₂ (8 x 8) taken from Tables 1 and 5.

	BTS	SB	0674	SEA	72-7427	0685	TUI	JULES
Days to 1st Flower								
F ₁	46.1	38.0	39.8	37.9	37.4	48.0	48.3	38.9
F ₂	42.4	35.3	39.9	36.7	33.7			
Days to Maturity								
F ₁	99.9	95.4	94.5	89.2	94.1	104.8	103.6	94.7
F ₂	95.4	92.6	92.6	84.5	91.2			
Plant Dry Wt.								
F ₁	136.9	115.4	111.9	110.7	113.9	156.2	122.8	133.2
F ₂	93.7	88.9	88.0	82.7	84.7			
Total # of Nodes								
F ₁	92.2	56.6	69.3	60.7	52.7	88.6	77.1	87.8
F ₂	59.6	39.5	49.5	46.7	36.3			
Length of Internode								
F ₁	114.8	174.8	129.3	129.1	156.8	183.9	100.3	115.5
# Racemes/Plant								
F ₁	34.1	25.6	26.7	29.1	22.2	34.6	31.7	32.3
# Pods/Plant (X)								
F ₁	67.7	48.1	62.7	62.9	41.5	66.6	57.5	56.4
F ₂	52.3	42.4	53.2	50.8	34.2			
Pod Dry Wt./Plant								
F ₁	101.1	83.5	79.5	84.1	84.3	107.5	88.9	105.2
F ₂	69.2	65.5	61.8	61.5	63.4			

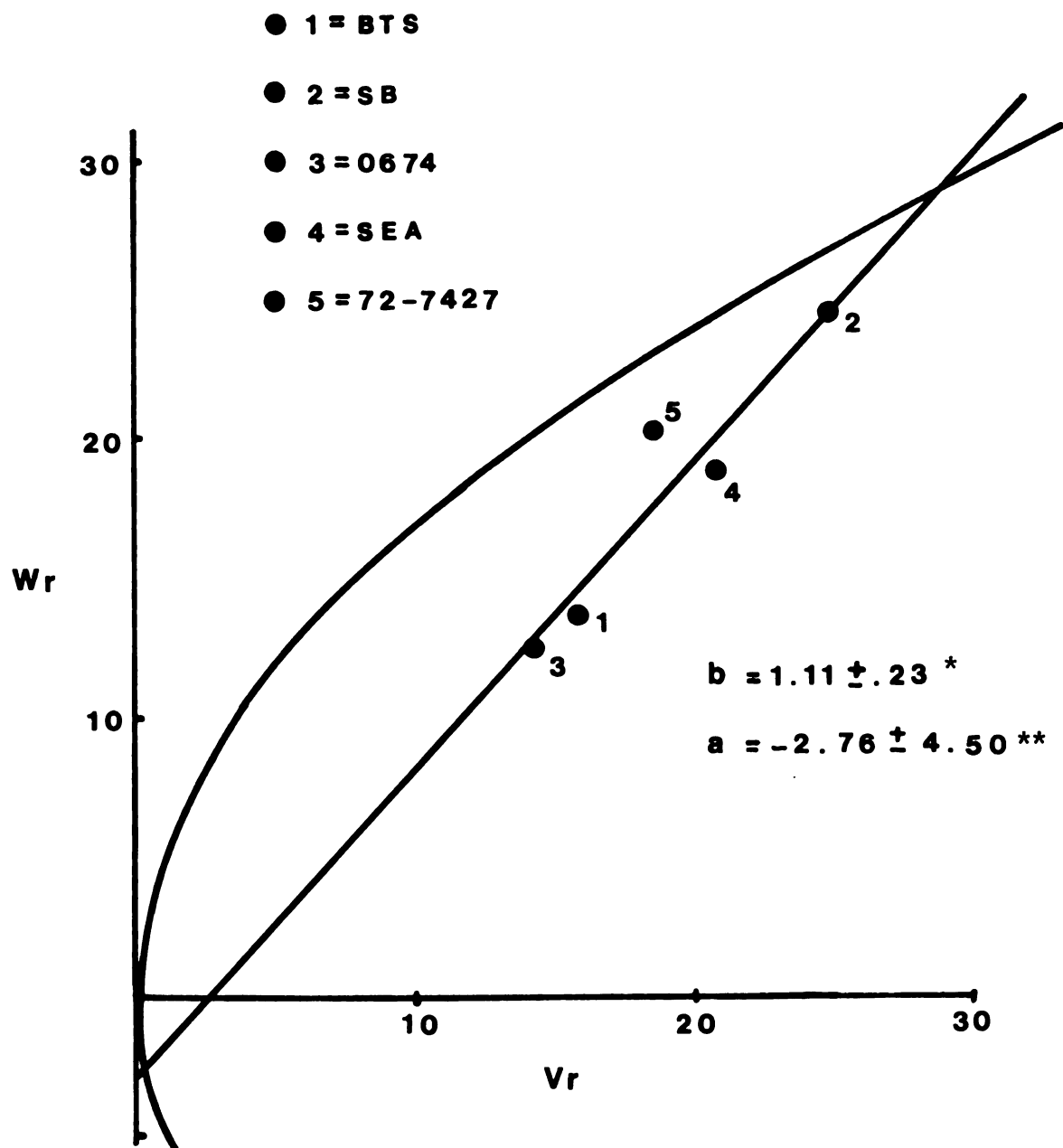
Table 8.. (cont.)

	BTS	SB	0674	SEA	72-7427	0685	TUI	JULES
Length of Pod F ₁	101.6	106.8	83.8	83.5	127.4	105.7	103.6	106.3
# Seeds/Plant F ₁ F ₂	381.6 255.1	212.5 165.4	313.9 239.7	291.6 229.8	183.3 144.7	359.5	338.1	280.8
# Seeds/Pod (Y) F ₁ F ₂	5.6 5.0	4.2 3.9	4.8 4.3	4.5 4.3	4.5 4.1	5.1	5.7	4.8
100-Seed Wt.. (Z) F ₁ F ₂	23.4 21.0	34.2 33.8	19.6 20.0	23.1 21.5	38.3 36.4	24.1	21.9	32.0
Seed Dry Wt./Plant F ₁ F ₂	76.8 53.7	66.6 51.1	60.4 46.9	65.7 49.1	64.6 47.9	81.2	69.1	85.4
Harvest Index F ₁ F ₂	.58 .58	.59 .59	.54 .54	.59 .57	.51 .57	.52	.56	.65

Figure 18 shows that the regression of W_r on V_r is significantly different from $b = 0$ but not from $b = 1$ ($b = 1.11 \pm .23$). The intercept is below the origin but not significantly different from 0 ($a = -2.76 \pm 4.496$) indicating that the dominance is complete. The $\sqrt{H_1/D}$ value, however, was 2.1733 which indicated over dominance. The evidence from the graph and $\sqrt{H_1/D}$ is suggestive of complete to slight over-dominance.

The position of the array points show that SB contains a preponderance of recessive genes. SEA and strain 72-7427 contain a lesser proportion of recessive genes. Strain 0674 and BTS appear to contain a balance proportion of dominant and recessive genes. The position of the points agree well with the "F" value of -39.6466 which indicates that there is an excess of recessive genes among the parental lines.

The heritability estimate is 11% which is not very high for this trait. Since additivity of the gene system was not indicated, selection for this trait may be difficult in the present sample of lines and their intercrosses; the gene action picture, however, does not imply that great difficulty would necessarily be encountered in a larger sample of parental lines.



* t for $b = 0 = 4.73$ and t for $b = 1 = .46$

** t for $a = 0 = .61$

Figure 18. Number of racemes per plant (5 x 5, F_2).

Number of Pods Per Plant5 x 5, F₁

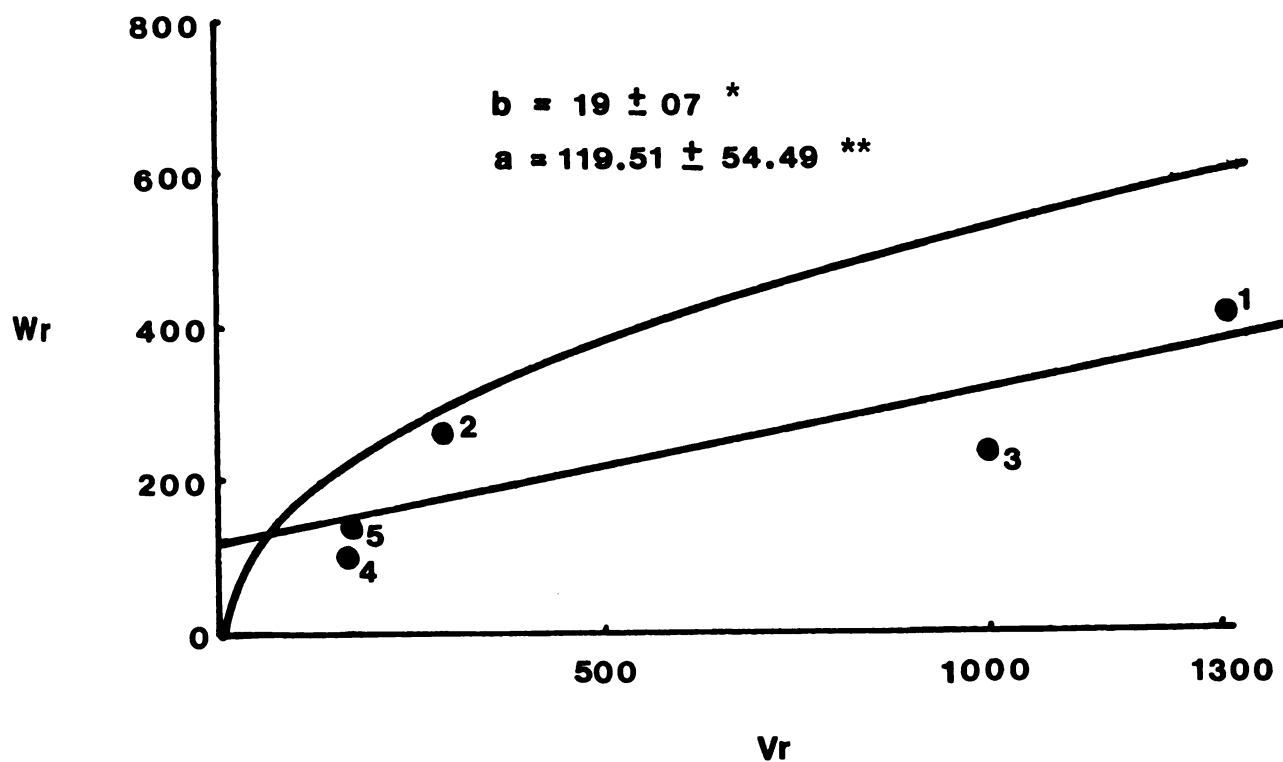
The analysis of variance shows that there were no significant differences among the replicates but there were highly significant differences among the genotypes (Table 2). BTS had the highest mean number of pods of 61.1 and strain 72-7427 had the lowest mean value of 23.6, SEA, strain 0674, and SB had mean values of 58.2, 54.5 and 31.8 respectively (Table 1).

Inspecting the mean values of the F₁ hybrids, it was found that 9 out of 10 hybrids had mean values exceeding the mid-parent values. Six of the 9 hybrids had mean values greater than that of the high parent. There was only one hybrid, i.e. from the cross 0674 x SEA, which gave a mean value lower than the low parent. In fact the reciprocal of the cross BTS x 72-7427 also gave a mean value lower than that of the low parent and, hence, there were only 2 hybrids and their reciprocals out of the 20 crosses (including reciprocals) that had mean values lower than that of the low parents. SEA and strain 0674 are very sensitive to ozone as noted earlier. Their hybrids seemed to suffer as much as the parents. Early abscission of leaves greatly affect the yield components. Number of pods per plant (X) is the first component in the sequence and was the first to be affected. The hybrids from the cross BTS x 0674 and its reciprocal

were superior to the others regarding total number of pods per plant (BTS x 0674 = 129.2 and 0674 x BTS = 121.5, Table 1). Having larger pod size and fewer number of pods per plant, strain 72-7427 appeared to give hybrids with smaller mean number of pods per plant when crossed with other parents. Strain 0674 and SEA which had similar phenotype did not give a heterotic effect when they were crossed.

Figure 19 shows the W_r/V_r graph of the 5 x 5, F_1 . The regression is not significant ($b = .19 \pm .07$) as was the case for number of nodes (8 x 8, F_1 and 5 x 5, F_2) and the point of intercept is not significantly above the origin ($a = 119.51 \pm 54.49$) according to the t-test. This indicates that there were genic interactions among the genes in the parental lines which controlled this trait. However, the locations of the array points representing SEA, strain 72-7427 and SB show that they contain a preponderance of dominant genes. The position of strain 0674 and BTS indicates that they contain a preponderance of recessive genes. The estimate of heritability is $-.10$, which is equivalent to zero. The estimate of "D" is -471.05 . Therefore, the estimation of other components were not at all reliable and no valid interpretation can be applied to this particular set of data. Possibly the 8 x 8, F_1 or 5 x 5, F_2 data can give a better picture of the gene system controlling this complex trait.

- 1 = BTS ● 4 = SEA
 ● 2 = SB ● 5 = 72-7427
 ● 3 = 0674



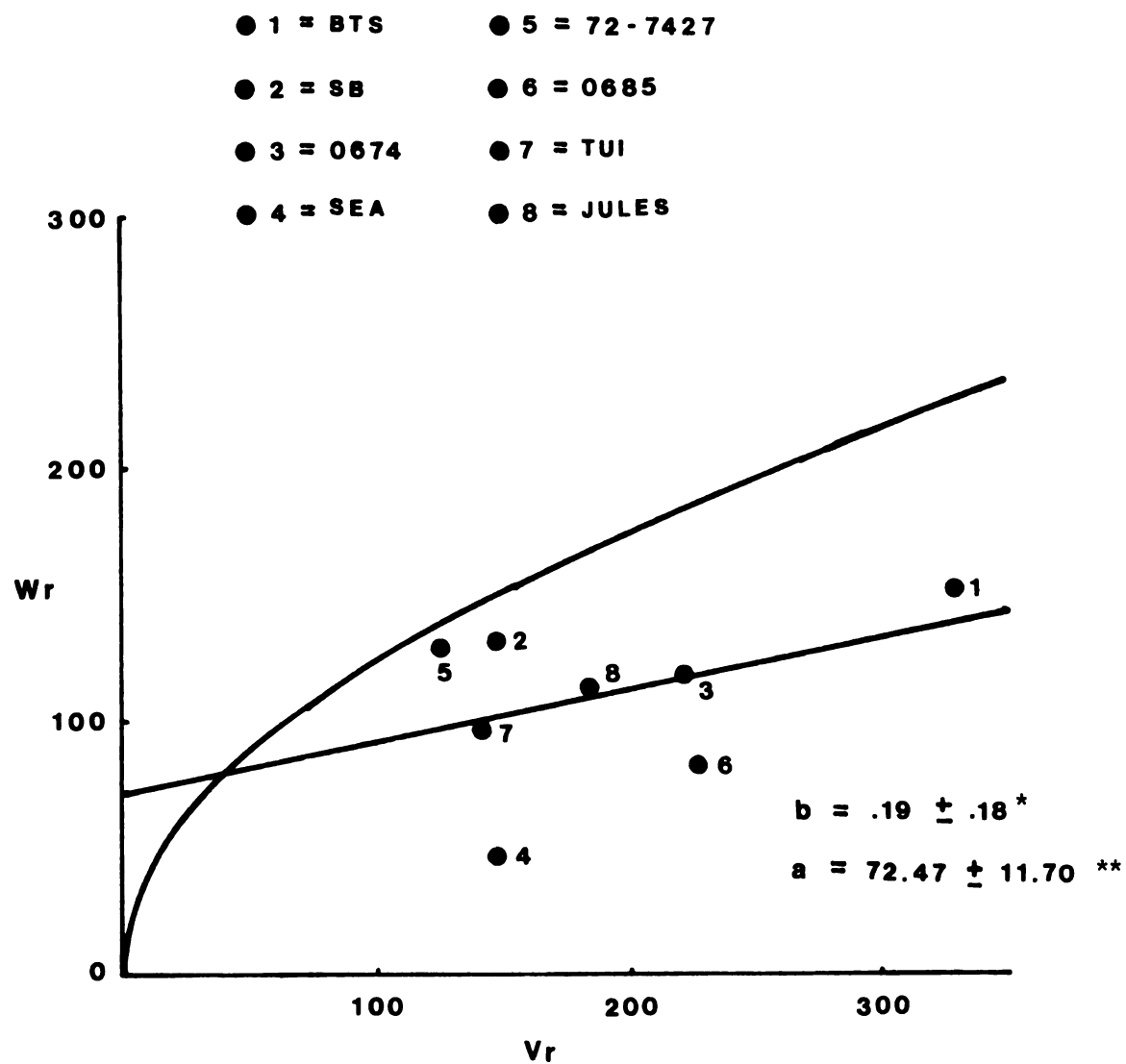
* t for $b = 0 = 2.65$
 t for $b = 1 = 11.23$
 ** t for $a = 0 = 2.19$

Figure 19. Number of pods per plant (5 x 5, F_1).

8 x 8, F₁

The analysis of variance indicates that there were highly significant differences among the genotypes. The mean values of strain 0685, BTS, SEA, Tui, strain 0674, Jules, SB and strain 72-7427 were 60.3, 53.6, 51.6, 50.6, 49.8, 39.9, 35.1 and 21.3 respectively (Table 3). All the 28 F₁ hybrids examined had mean values greater than that of the mid-parent values. The cross BTS x 0685 and its reciprocal gave hybrids with the highest mean values of 102.8 and 92.5 respectively. The array means of BTS and strain 0685 were 67.7 and 66.6 which were the two highest array means (Table 8). From the above results it is reasonable to believe that using strain 0685 and BTS as parents would give progenies with high number of pods per plant.

The regression of W_r on V_r was not significant ($b = .19 \pm .18$) (Figure 20). Genic interaction is indicated as the prevailing mode of gene action, although a certain amount of dominance and recessivity is not precluded. As the estimate of "F" was -202.97, this indicates that there was an excess of recessive genes among parental lines. Judging from the position of the array points none of the parents contain any preponderance of dominant genes. The position of the array point representing BTS indicates that it contains a preponderance of recessive genes. The positions of the rest of the



* t for $b = 0 = 1.06$ and t for $b = 1 = 4.46$

** t for $a = 0 = 6.20$

Figure 20. Number of pods per plant (8 x 8, F_1).

array points seemed to indicate that they contain a balanced proportion of dominant and recessive genes. The evidence from the W_r/V_r graph indicates that genic interaction is involved in controlling this trait in the 8×8 , F_1 generation.

The heritability estimate is only 3%, a value not uncommon for traits as subject to complex genic and environmental influences as is this one.

5 x 5, F_2

The analysis of variance of the F_2 populations shows that there were significant differences among the replicates and among the genotypes as they were in the 8×8 , F_1 . Eight out of 10 F_2 populations had mean values greater than their mid-parent values (Table 5). Two of the crosses that had mean values smaller than that of the mid-parent values involved the crosses between SB x 72-7427 and SEA x 72-7427. If the array means of the 5×5 , F_1 were compared with that of the 5×5 , F_2 it can be seen that all the array means decreased in the F_2 populations except those derived from strain 72-7247 (Table 7). This is consistent with effects influenced by genetic heterozygosity.

The regression of W_r on V_r (Figure 21) shows that it was significantly different from zero but not significantly different from unity ($b = .92 \pm .18$). The

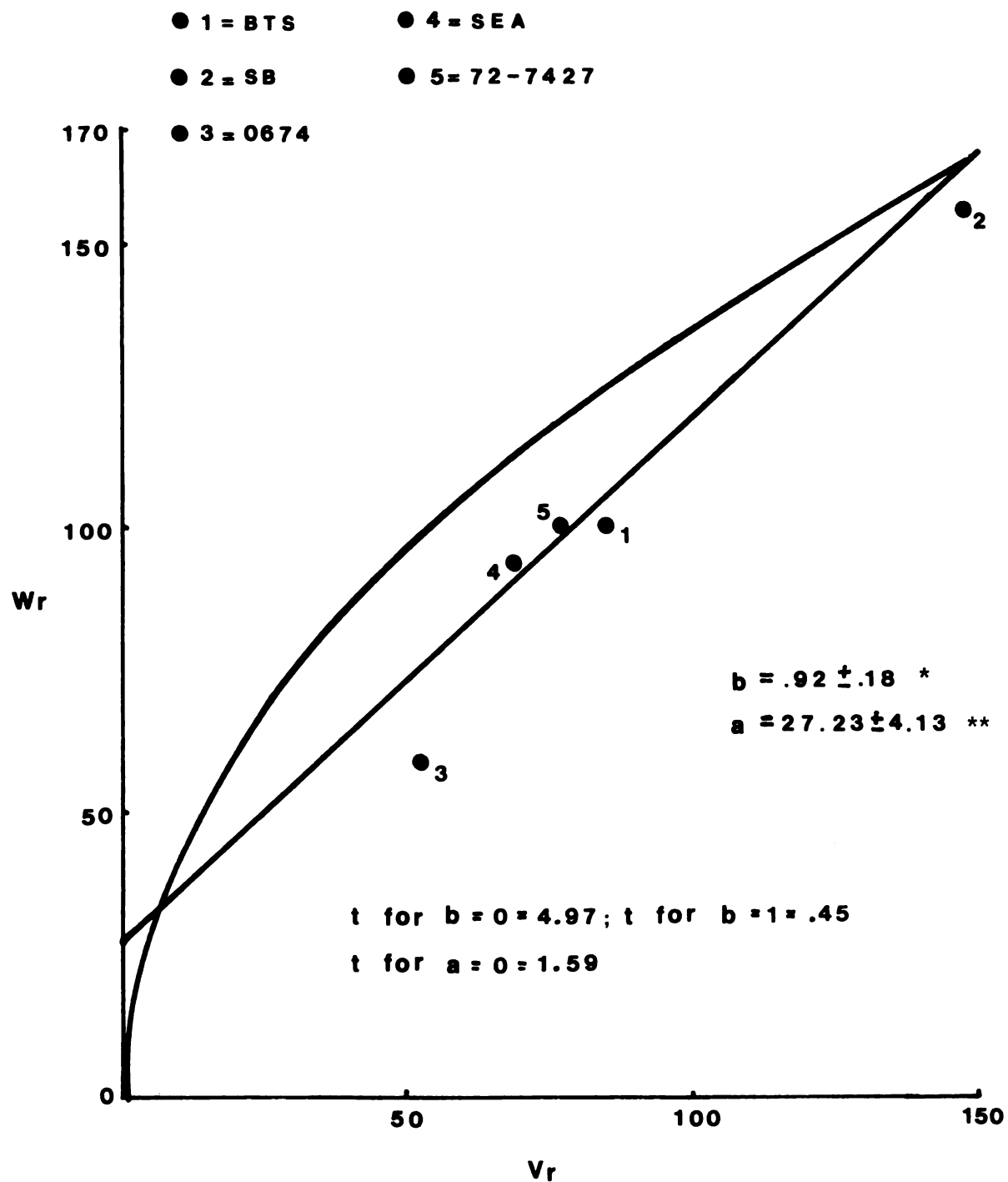


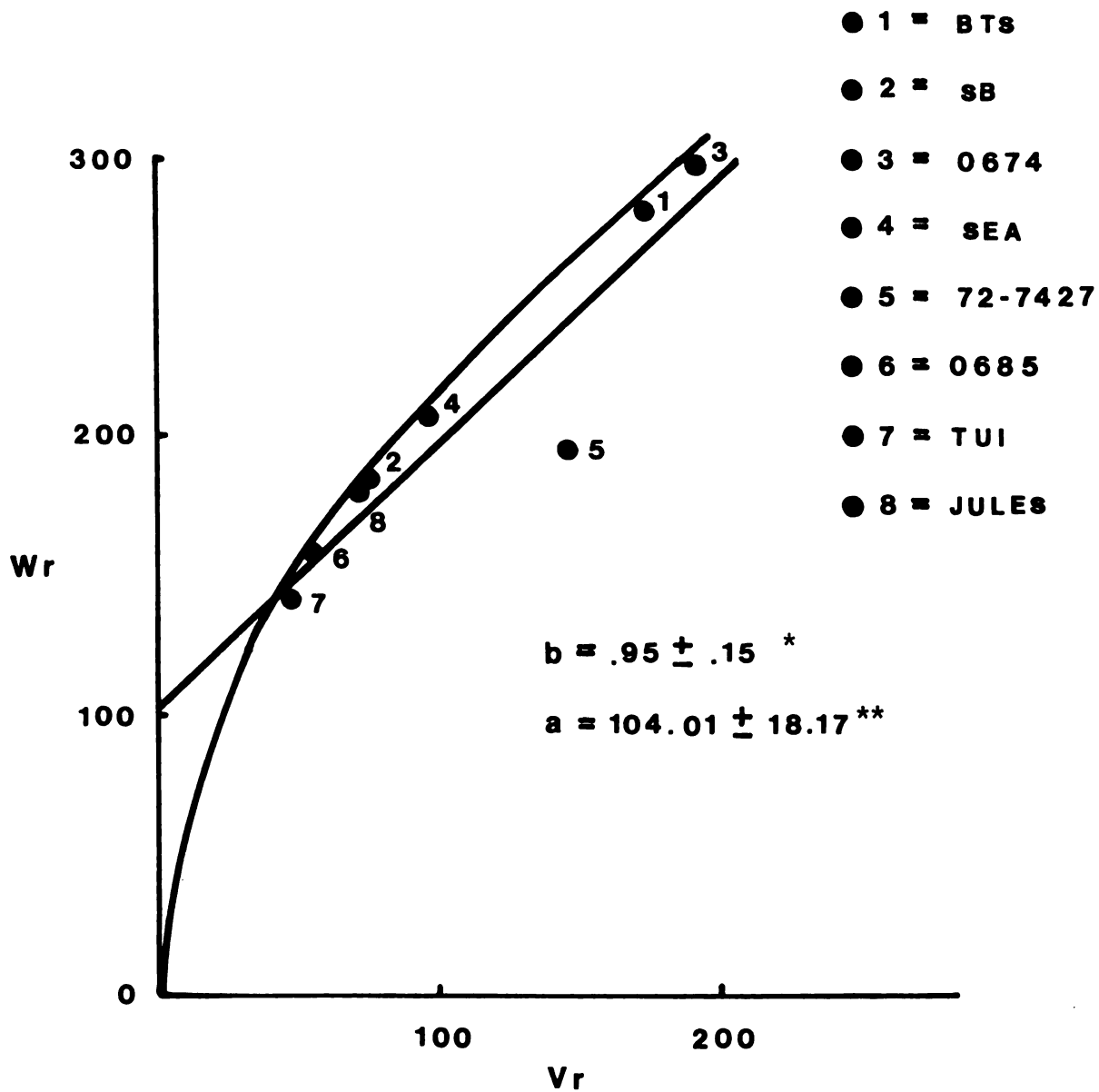
Figure 21. Number of pods per plant (5 x 5, F_2).

regression line intersects the W_r axis above the origin ($a = 27.33 \pm 4.13$) but not significantly different from 0 which indicates complete dominance. SEA, strain 72-7427 and BTS appear to contain a moderate proportion of dominant genes. Strain 0674 seems to contain a certain level of dominant genes higher than SEA, strain 72-7427 and BTS. The shifting position of SB from the dominant side in Figure 19, to the recessive side in Figure 21 can only be attributed to the decrease in heterozygosity in the F_2 . The estimate of heritability was .21 which was acceptable. Number of pods per plant (X) is a complex trait and is one of the primary yield components. It is the first trait in the sequence of yield components and is the function of pods/racemes, racemes/node, nodes/branch, branches/plant. Thus, any environmental factors affecting the above traits affect "X" also. The estimate of "D" was 162.21 indicating that additive effects existed. The "F" estimate was -187.31 indicating that there was an excess of recessive genes among the parents. To get a reasonable prediction as to the degree of dominance and additive affects it is necessary to have the 5 x 5, F_2 data excluding the variances and covariances of the other 3 additional varieties in the 1974 trial.

Length of Pod8 x 8, F₁

Length of pod was not included in the 1973 data. In 1974, it was decided to include this trait in the study. Three longest pods were taken from the 8 x 8, F₁ and 5 x 5, F₂ plant population to determine the average length of pod of each plant. The mean length of pod of the 8 x 8, F₁ is shown in Table 3. Among the 8 parental lines tested, 72-7427 appeared to have the highest mean pod length (151.2 mm. Table 3) and strain 0674 had the shortest pod of 80.4 mm. Fourteen out of the 28 hybrids examined had mean values greater than that of the mid-parent values but there were only 4 means greater than the mean of the long pod parent. Those 4 hybrids derived from the crosses, SB x Jules, 0674 x SEA, SEA x Jules and 0685 x Tui. Fourteen hybrids had means smaller than that of their mid-parent values. BTS x 72-7427 produced the hybrid with the longest pod.

Figure 22 presents the Wr/Vr graph of the 8 x 8, F₁. The regression of Wr on Vr is significantly different from $b = 0$ but not from $b = 1$ ($b = .95 \pm .15$). The intercept on the Wr axis is above the origin and is significantly different from 0 ($a = 104.21 \pm 18.17$). These two points, the unit slope and the intercept, taken together, indicate partial dominance for genes affecting pod length. This evidence is also confirmed



* t for $b = 0 = 6.23$ and t for $b = 1 = .36$

** t for $a = 0 = 5.74$

Figure 22. Length of pod in mm (8×8 , F_1).

by the $\sqrt{H_1/D}$ value of .39. However, the consistency of the regression line here and later in the F_2 , the high h^2 value of about 100% ($h^2 = 1.10$) and high "D" value as mentioned earlier, strongly suggested that the genes controlling this trait are, on the average, largely additive in their action. Furthermore, the closeness of the regression line to the parabola suggests that the dominance effect is minimal.

The position of the points representing parents Tui, strain 0685, Jules and SB indicate that they contain a preponderance of the partially dominant genes. Parents BTS and strain 0674 contain a preponderance of the recessive genes. Parent SEA seems to contain a slightly higher proportion of partially dominant than of recessive genes. Parent strain 72-7427 contains a balance of partially dominant and recessive genes. The position of strain 72-7427 shows that it is the outlier in this case. Strain 72-7427 was the determinate type with the longest pod as compared to the others among the 8 parental lines.

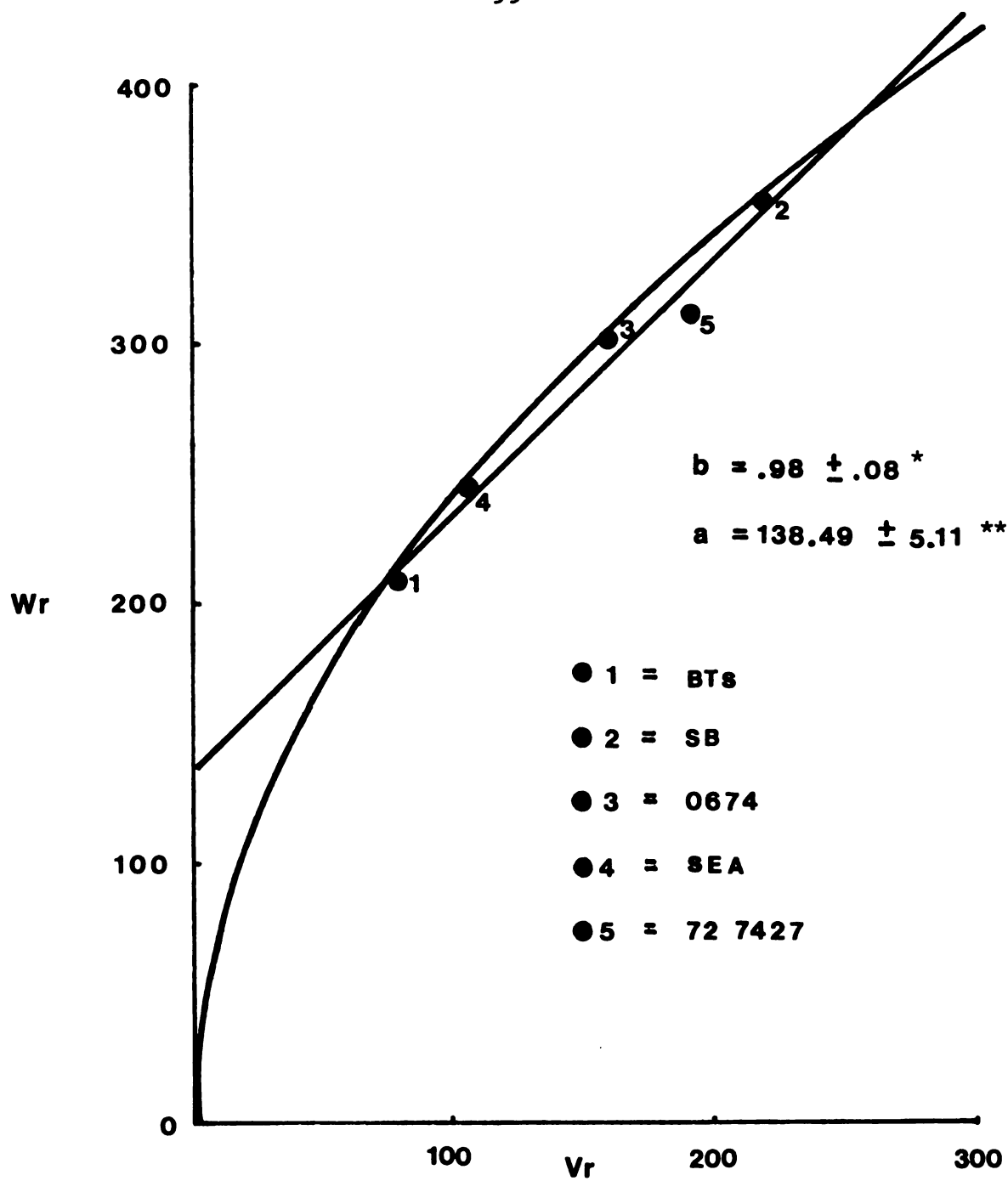
5 x 5, F_2

Table 5 shows the mean values for parents and F_2 populations. Only 4 out of the 10 F_2 populations examined had mean values greater than the mid-parent values, and only one (0674 x SEA) had a mean exceeding the mean of the greater parent (Table 5). Six of the

F_2 populations had means smaller than that of their mid-parent values. The F_2 derived from SB x 72-7427 had the longest pod (126.9) and the shortest pod length was the one derived from 0674 x SEA (85.2).

Figure 23 shows the W_r/V_r graph of 5 x 5, F_2 . The graph has a similar picture to that of the 8 x 8, F_1 . The regression of W_r on V_r is significantly different from $b = 0$ but not from $b = 1$ ($b = .98 \pm .08$) indicating an additive gene system for this trait exists in the F_2 . The "D" value of 6732.63 is in support of this assumption. However, the intercept on the W_r axis is above the origin and is significantly different from 0 ($a = 138.49 \pm 5.11$) indicating partial dominance. The $\sqrt{H_1/D}$ value of .84 also confirms the existence of partial dominance. Nevertheless, the close relationship between the regression line and the parabola suggests that dominance plays a small role in the determination of length of pod (Whitehouse et al., 1958).

The position of the points indicates that BTS contains the highest proportion of dominant genes. SEA contains a lesser level of dominant genes. Strain 0674 contains a balance of dominant and recessive genes. SB contains a preponderance of recessive genes and strain 72-7427 contains a lower level of recessive genes than SB. The "F" value of -5609.24 suggests that there is an excess of recessive genes among the parental lines. The



* t for $b = 0 = 11.71$ and t for $b = 1 = .24$

** t for $a = 0 = 5.29$

Figure 23. Length of pod in mm (5×5 , F_2).

heritability estimate of 31% in the F_2 generation is not high as compared to 100% in the 8 x 8, F_1 . The additional parents in the 8 x 8 add greatly to the additive variance for this trait and in addition the variance estimates are based on a greater number of plots than in the 5 x 5, and are therefore estimated with greater precision.

Balancing the evidences in Figures 22 and 23, it is believed that an additive gene system exists and that dominant plays a small part in controlling pod length.

Pod Dry Weight Per Plant

5 x 5, F_1

The analysis of variance shows that there were no significant differences among the replicates but there were highly significant differences among the genotypes. Among the 5 parental lines, BTS had the highest mean total pod dry weight of 80.6 gm and strain 0674 had the lowest mean value of 35.3 gm. SB, SEA and strain 72-7427 had mean values of 54.9, 44.7 and 64.8 gm respectively (Table 1). BTS, SB and strain 72-7427 were not affected by ozone injury. SEA and strain 0674 were the only 2 parents sensitive to ozone injury. As has already been discussed in the previous sections, strain 0674, in particular, was very much affected by ozone injury. Even though it could recover and resumed its growth later,

the season was not long enough for the plant to produce photosynthate for the pods it produced. Consequently, a large portion of the pods were very light in weight and affected the pod dry weight of the plant.

Examining the mean values of the hybrids (Table 1), it was found that 9 out of 10 crosses gave hybrids with mean values exceeding mid-parent values. Six out of the 9 hybrids had mean values greater than that of the high parent. The hybrid derived from the cross 0674 x SEA gave a mean value of 34.7 gm which was lower than 39.9 gm, the mid-parent value of this cross. It was observed that when strain 0674 was crossed with SEA, the resulting F_1 hybrids did not show any heterotic effect as compared to those hybrids derived from crosses between parents with contrasting phenotypes.

The best parental combination which produced the hybrids with greatest mean pod dry weight was that between BTS x 0674 (BTS x 0674 = 153.42, Table 1).

The regression of W_r on V_r (Figure 24) is neither significantly different from $b = 0$ or $b = 1$, indicating large errors or genic interaction. As the additive genetic variance (D) has a negative value of -1262.99, the calculated values of other genetic components are not reliable. It is assumed that gene interaction plays a role in determining total pod weight. This is not surprising because total pod weight is a complex trait.

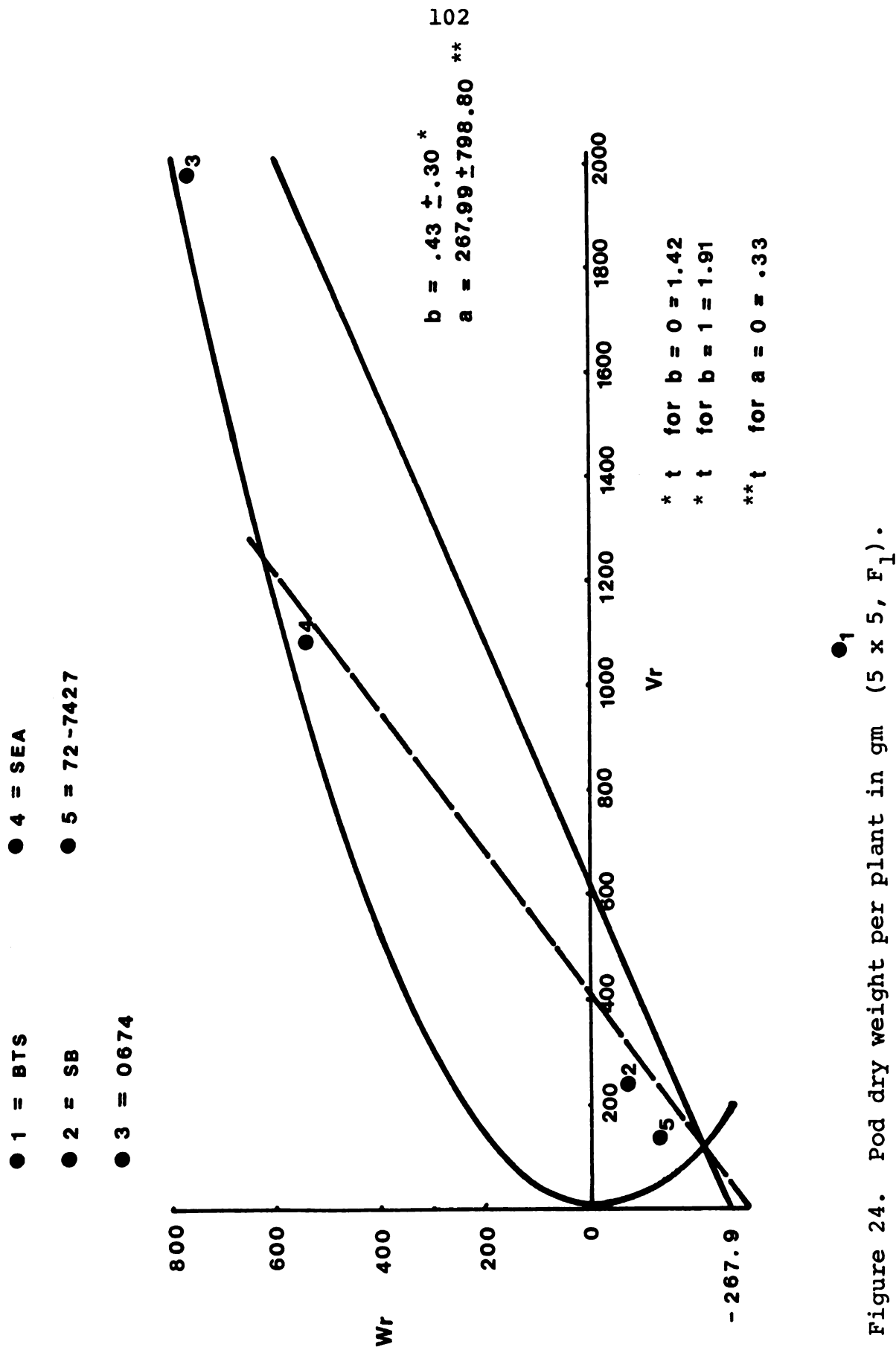


Figure 24. Pod dry weight per plant in gm (5 x 5, F₁).

It can be affected by number of pods per plant (X) and number of seeds per pod (X) and stand density. The interaction between these 2 yield components with the environment and the intra-plant competition among the components can greatly affect total pod weight.

Since gene interaction is believed to play a role in this trait the assumption of "no gene interaction" does not fit this set of data. However, if we omitted BTS which was the only indeterminate type and strain 0674 which was sensitive to ozone injuries a new regression line can be drawn (dotted line). The new regression line may be significant and indicates a real relationship between W_r and V_r . The remaining three parents, namely, strain 72-7427, SB and SEA would fit the line very well. Thus, their position indicates that SB and strain 72-7427 contain a preponderance of dominant genes and SEA contains a preponderance of recessive genes. However, no attempt was conducted to recalculate the W_r and V_r of the three remaining parents.

8 x 8, F_1

The analysis of variance indicated that there were significant variations among genotypes (Table 6). The mean pod weights of the 8 parental lines were:
 strain 0685 = 80.1 gm, Jules = 79.7 gm, Tui = 73.9 gm,
 BTS = 71.9 gm, SB = 65.4 gm, strain 72-7427 = 65.4 gm,
 SEA = 53.1 gm and strain 0674 = 41.6 gm (Table 3).

There were 2 out of the 28 F_1 hybrids examined which had a mean pod weight lower than the mid-parent values. The cross between BTS x 0685 gave a hybrid with the highest mean value of 155.1 (Table 3). Again, the poorest combination appeared to be between 0674 x SEA which gave the mean value of 47.6 gm. The cross between SB x 72-7427, another pair of similar phenotype, also gave hybrids with low mean pod weight (SB x 72-7427 = 63.8 gm, 72-7427 x SB = 62.5 gm). It can be seen from Table 8 that the array means of the F_1 derived from strain 0685, Jules and BTS were 107.5, 105.2, and 101.1 gms, respectively, which were the three highest array means. It is reasonable, therefore, to believe that if they were used as the parents in the crosses they would probably give hybrids with high mean pod weights.

The W_r and V_r graph (Figure 25) shows that the regression is not significant ($b = .43 \pm .20$). Genic interaction is indicated. The array points were very much scattered in the graph. BTS appeared to have a strong influence in causing the deviation of the regression line from a unit slope of 1. If the regression line were redrawn as shown by the dotted line all the array points except 1 and 6 would fit very well. Among the 5 parents tested in 1973, BTS gave the highest mean pod weight (Table 1). In 1974, strain 0685 gave the highest mean pod weight (Table 3). BTS and strain 0685 have

● 1 = BTS

● 5 = 72-7427

● 2 = SB

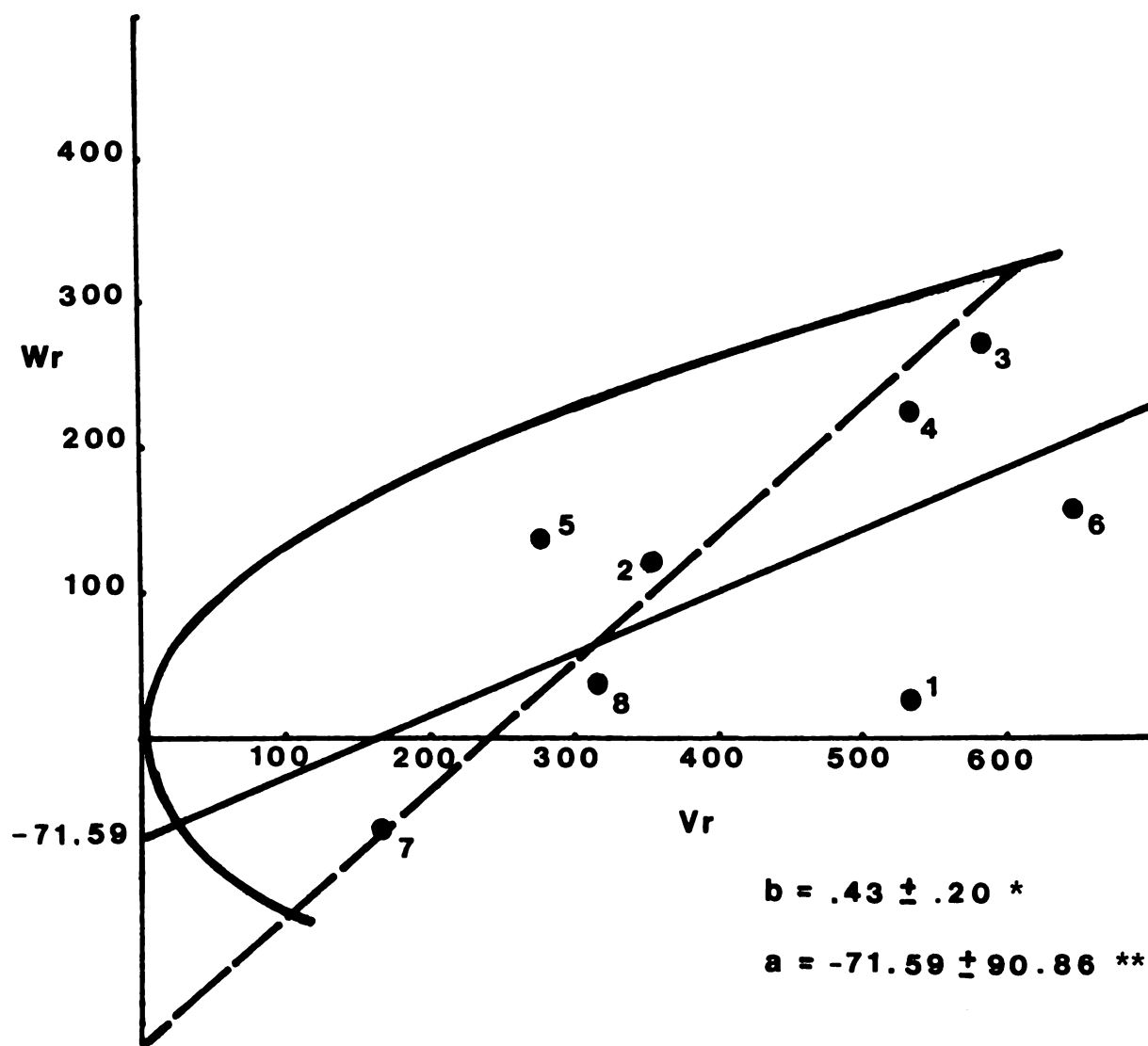
● 6 = 0685

● 3 = 0674

● 7 = TUI

● 4 = SEA

● 8 = JULES



* t for $b = 0 = 2.18$, t for $b = 1 = 2.83$

** t for $a = 0 = .79$

Figure 25. Pod dry weight per plant in gm (8×8 , F_1).

unique gene systems controlling this trait. BTS was the only indeterminate type among the 5 parents in 1973 and its phenotype was different from the other two indeterminate lines in 1974. Strain 0685 also had a very strange character and growth habit. When it was grown under greenhouse conditions in the winter for cross pollination, it became a vine type. This same line when grown under field conditions was a bush type with vigorous vegetative growth. It also had a very different plant type when compared with other bush lines grown in 1974. These two distinctive genotypes behaved differently from the others and might have sufficient influence on the regression line to cause it to deviate from a slope of 1.

The computed negative value of "D" (-282.39) upset the whole picture of the graph. Gene interactions are, therefore, assumed to exist and the assumption of "no gene interaction" is again not valid in this case.

5 x 5, F₂

Significant differences were found among replicates and among genotypes as they were with total number of pods (Table 6). BTS gave the highest mean pod dry weight of 71.1 gm. SB, strain 72-7427, SEA and 0674 gave mean values of 66.4, 62.8, 52.9 and 38.7 gm, respectively. Seven out of 10 F₂ populations still had mean values greater than the mid-parent value. Three

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F_2 populations had mean values lower than the mid-parent values. The F_2 population derived from the cross BTS x SB had the highest mean pod dry weight (84.3 gm, Table 5). The F_2 population derived from the cross 0674 x BTS which gave the highest mean value in the F_1 generation had the second highest mean value in the F_2 (82.7 gm, Table 5). The array means (Table 8) show that the F_2 's derived from BTS and SB gave the highest and second highest array means respectively (69.2, 65.5 gm). Tables 7 and 8 show that the array means were decreasing in the F_2 generations due to a decrease in heterozygosity of the F_2 populations.

Figure 26 shows the W_r/V_r graph of the 5 x 5, F_2 . The regression line is significantly different from 0 but not from 1 ($b = 1.06 \pm .11$). The line intersects the W_r axis below the origin but not significantly different from 0 ($a = -18.12 \pm 3.38$). The $\sqrt{H_1/D}$ value is 2.75. The evidence on balance suggests that the prevailing mode of gene action is in the complete to over-dominant range.

The position of the array points show that strain 72-7427 contains a preponderance of dominant genes. BTS and SB apparently contained a lower proportion of dominant genes than strain 72-7427. Strain 0674 appears to contain a preponderance of recessive genes and SEA contains a lower proportion of recessive genes than strain 0674.

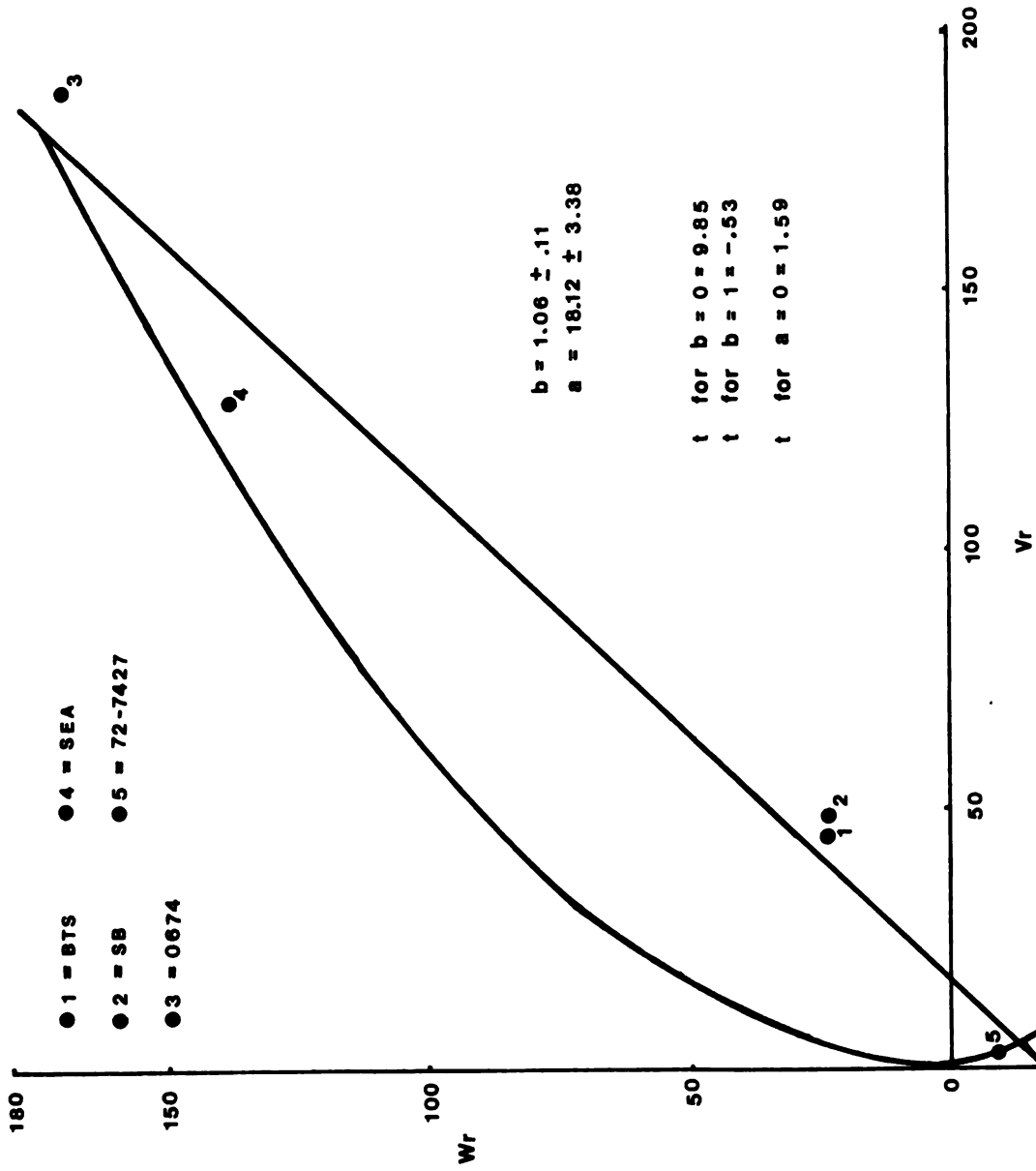


Figure 26. Pod dry weight per plant in gm (5×5 , F_2).

The calculated value of $F = -6.13$, indicates an excess of recessive genes among the parental lines. However, the position of the array points of 3 out of the 5 parents are on the dominant side. Therefore the evidence for suggesting a slight excess of recessive genes is not reliable. The heritability estimate is 8% which is low. The prediction of results in future generations regarding this trait, therefore, cannot be made with accuracy.

Number of Seeds Per Pod

5 x 5, F_1

In the analysis of variance (Table 2), no significant differences were found among the replicates but highly significant differences were found among the genotypes. BTS gave the highest mean number of seeds per pod of 5.4. SEA, strain 0674, strain 72-7427 and SB gave mean values of 4.1, 3.8, 3.6 and 3.6 respectively. Nine out of 10 F_1 hybrids examined had mean values exceeding mid-parent values. The hybrid derived from BTS x SB gave a mean value lower than the mid-parent value (Table 1). The hybrid derived from BTS x 0674 gave the highest mean number of seeds per pod.

Figure 27 presents the W_r/V_r graph of the 5 x 5, F_1 . The regression of W_r on V_r is significantly different from zero but not from 1; ($b = .86 \pm .81$) it

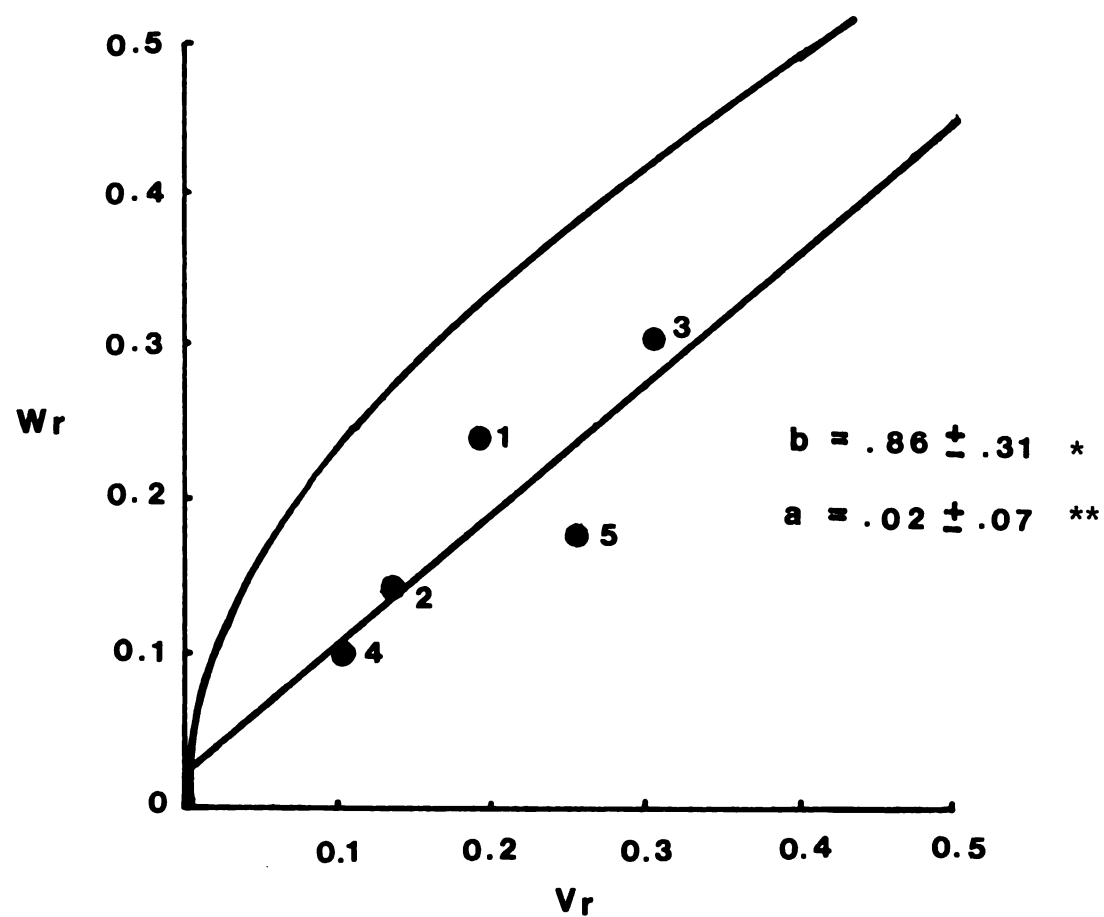
● 1 = BTS

● 2 = SB

● 3 = 0674

● 4 = SEA

● 5 = 72-7427



* t for $b = 0 = 2.75$ and t for $b = 1 = .46$

** t for $a = 0 = .30$

Figure 27. Number of seeds per pod (5 x 5, F_1).

intersects slightly above the origin on the W_r axis ($a = 0.02 \pm .007$) which is not significantly different from 0. The $\sqrt{H_1/D}$ value is 0.77. On balance the evidence suggests partial to complete dominance. The position of the points seems to fit the regression line very well. SEA and SB appear to contain a higher proportion of dominant than recessive genes. BTS and strain 72-7427 contain a balance of dominant and recessive genes. Only strain 0674 appears to contain a high proportion of recessive genes. This agrees well with the "F" value of .16 which indicates a slight excess of dominant genes among the parental inbred lines.

The heritability estimate for this trait in the 5 x 5, F_1 is 29%.

8 x 8, F_1

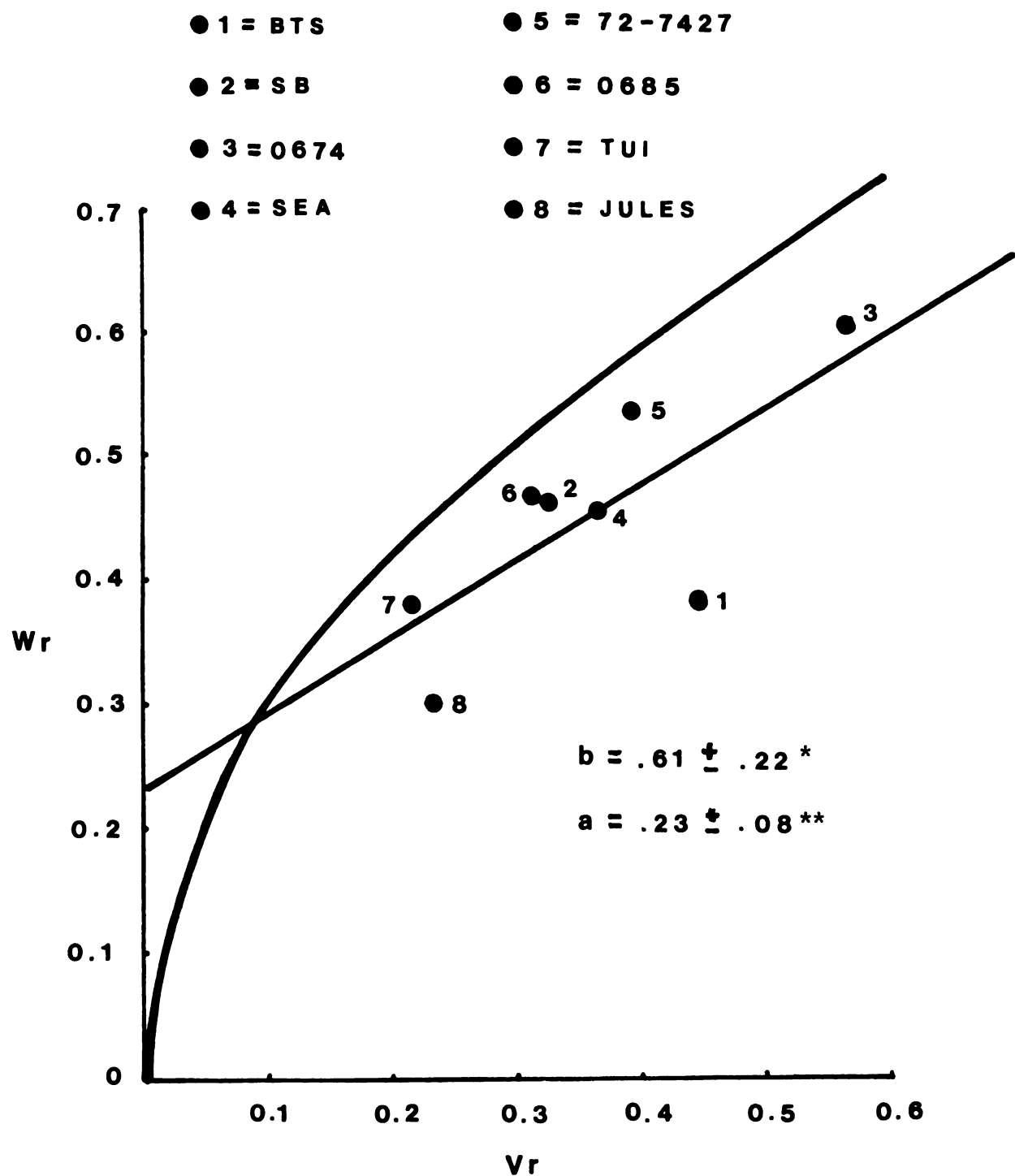
Two out of 3 indeterminate types used in the 1974 trial gave the highest mean number of seeds per pod. Tui and BTS gave mean values of 5.9 and 5.8 respectively. Jules, which is another indeterminate type, ranked 4th and gave a mean value of 4.6. Strain 0685 ranked 1st among the determinate type giving a mean value of 4.6. SB gave the lowest mean value of 3.3. Twenty-five out of 28 F_1 hybrids examined had mean values exceeding mid-parent values. The 3 crosses that gave hybrids with mean values lower than the mid-parent values were:

BTS x Jules = 4.8, SB x Jules = 3.9 and SEA x Jules = 3.6

(Table 3). The hybrids resulting from BTS x Tui and its reciprocal gave the highest mean value. The analysis of variance indicated that there were significant differences both among the replicates and among the genotypes (Table 4).

Figure 28 presents the W_r/V_r graph of the 8 x 8, F_1 . The regression line is significantly different from zero but not from a unit slope ($b = .61 \pm .22$) and it intersects the W_r axis significantly above the origin ($a = .23 \pm .08$). The $\sqrt{H_1/D}$ value is 0.74. The evidence suggests again that the gene system controlling this trait is partially dominant. Since the array point representing Tui is closest to the point of intersection between the regression line and the parabola, it indicates that Tui carries a preponderance of dominant genes. Strain 0674 carries a preponderance of recessive genes. SB, SEA, strains 72-7427 and 0685 seem to carry a balance of dominant and recessive genes. BTS and Jules, which were the indeterminate types, behaved differently from the others. Both array points of BTS and Jules are below the regression line. Jules is located close to the point of intersection of the regression line and the parabola indicating that it contains a higher level of dominant genes than BTS which is at the center.

The estimate of " h^2 " is 44%. The excess of recessive alleles was indicated by $F = -.06$.



* t for $b = 0 = 2.75$ and t for $b = 1 = 1.73$

** t for $a = 0 = 2.76$

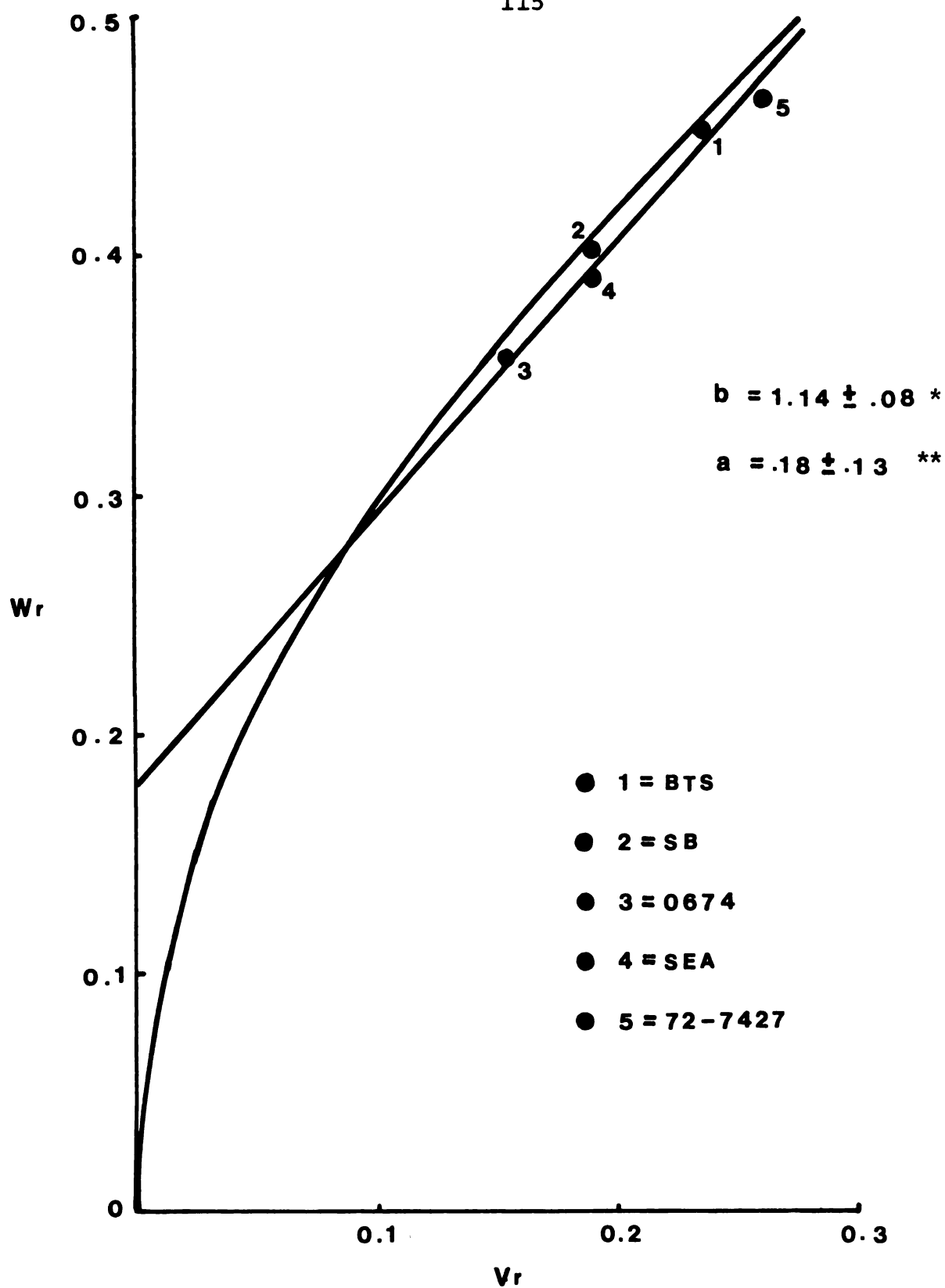
Figure 28. Number of seeds per pod (8 x 8, F_1).

5 x 5, F₂

In the 1974 trial of the 5 x 5, F₂, BTS still gave the highest mean number of seed per pod (Table 5) and SB still gave the lowest mean. The analysis of variance shows highly significant differences among the replicates and among the genotypes. Out of the 10 F₂ populations examined all had the mean values exceeding the mid-parent values but only 2 crosses had mean values exceeding the mean of the high parent.

The Wr/Vr graph presented in Figure 29 shows that the regression line differs significantly from slope $b = 0$ but not from $b = 1$ ($b = 1.14 \pm .08$). The regression line intersects the Wr axis above the origin and significantly different from 0 ($a = .18 \pm 13.5$). The genes affecting this trait behave as though they were in the additive to partially dominant range. We can observe that the regression line is very close to the parabola. This relationship suggests also that the dominance is only partial. This observation also agrees well with the $\sqrt{H_1/D}$ value of .38. The relationship of the regression line and the parabola suggests that dominance plays a small part in determining this trait.

According to the position of the array points, strain 0674 seems to contain the highest level of dominant genes, BTS and strain 72-7427 contain the highest level of recessive genes and SB and SEA seem



* t for $b = 0 = 13.73$ and t for $b = 1 = 1.70$

** t for $a = 0 = 10.40$

Figure 29. Number of seeds per pod (5×5 , F_2).

to have a balance of dominant and recessive genes. The "F" value of .22 suggests a slight excess of dominant genes among the inbred parents. The heritability estimate of 90% indicates that number of seeds per pod is highly heritable. Since the gene system is additive to partially dominant, it is reasonable to believe that the parents which gave the highest array mean would give progenies with high number of seeds per pod in the later generations.

100-Seed Weight

5 x 5, F₁

The New York kidney type of strain 72-7427 gave the highest mean 100-seed weight of 55.2 gm. SB, a large-seeded bean, gave the second highest mean value of 39.5. BTS, SEA and strain 0674 gave mean values of 17.3, 13.9 and 12.7 respectively (Table 1). Significant differences among the genotypes were found in the analysis of variance (Table 2).

Out of the 10 F₁ hybrids examined, there was only one, resulting from the cross BTS x SEA, which gave a mean value greater than the mid-parent value, exceeding the mean value of the larger parent. Two gave mean values exceeding mid-parent value but smaller than the larger parent. Seven gave mean values smaller than mid-parent values. The crosses between the large-seeded

parents tended to give large-seeded F_1 hybrids but the mean 100 seed weight was not necessarily greater than that of the mid-parent values.

Figure 30 presents the W_r/V_r graph of the 5 x 5, F_1 . The regression of W_r on V_r is significantly different from $b = 0$ but not from $b = 1$ ($b = .87 \pm .14$) indicating an additive gene system for this trait. The intercept on the W_r axis is significantly above the point of origin ($a = 80.66 \pm 15.36$). The calculated value of " D " = 349.32 confirmed that there are strong additive effects. The interception on the W_r axis is above the origin and is significantly different from 0 ($a = 80.66 \pm 15.36$) suggesting that the dominance, if any, is partial. This is also confirmed by the $\sqrt{H_1/D}$ value of .47. However, there is evidence that the gene system controlling this trait in dry bean is strongly additive. The consistency of the regression lines in 5 x 5, F_1 , and 8 x 8, F_1 and 5 x 5, F_2 all strongly support the hypothesis of additivity of this trait.

The position of the points indicates that strain 0674 and SEA contain a preponderance of dominant genes. Strain 72-7427 contains a preponderance of recessive genes. BTS and SB contain a lower proportion of recessive genes than strain 72-7427.

The " F " value of 35.20 indicates that there is an excess of dominant genes among the parental lines. The

● 1 = BTS

● 2 = SB

● 4 = SEA

● 3 = 0674

● 5 = 72-7427

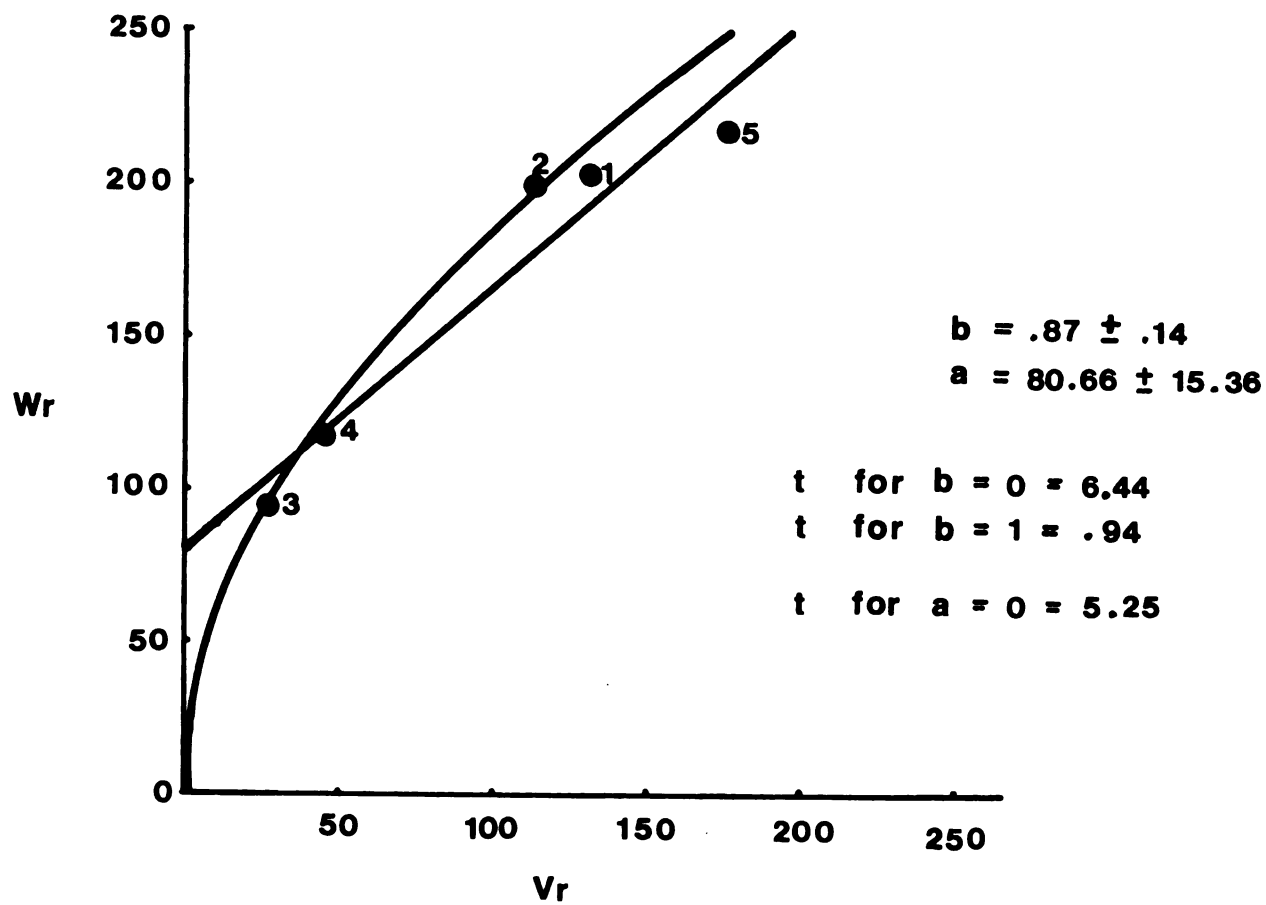


Figure 30. 100-seed weight in gm (5 x 5, F_1).

heritability estimate of 82% suggests that 100-seed weight is highly heritable and further confirms that the gene system is essentially an additive one.

8 x 8, F_1

The 1974 data confirmed 1973 data that strain 72-7427 and SB were the two highest in mean 100-seed weight (Table 3). SEA, however, in 1974, gave a slightly higher mean value than BTS. Jules gave mean value of 36.0 which was highest among the three new varieties and ranked 3rd of all the 8 varieties tested. Tui, which was about as late in maturing as strain 0685, gave the lowest mean value among the 3 new varieties (17.9, Table 3) and ranked 7th among the 8 varieties. Strain 0685 gave a slightly higher mean value than that of BTS and SEA. Strain 0674 had the lowest mean 100-seed weight (14.66, Table 3) among the 8 varieties.

Out of 28 F_1 hybrids examined, 12 had mean values exceeding the mid-parent values and only 2 hybrids (0674 x Tui and SEA x Tui) gave mean values exceeding the mean of the parent with greater mean 100-seed weight (Table 3). Fifteen had mean values smaller than that of mid-parent values.

It was observed that the strain 72-7427 when crossed with other parents, on the average would give hybrids with highest mean values. SB would give hybrids

with the second highest mean values in the same series. Strain 0674 would generally produce hybrids with the lowest mean values except in 2 series of crosses where 0685 x BTS and Tui x BTS would give the lowest mean values.

The W_r/V_r graph in Figure 31 shows that the regression line is significantly different from $b = 0$ but not from $b = 1$ ($b = .88 \pm .08$) indicating additive effects for this trait. The intercept on the W_r axis is above the origin and significantly different from 0 ($a = 48.56 \pm 5.25$) indicating partial dominance. The closeness of the regression line to the parabola suggests that dominance plays a small part in the determination of 100-seed weight (Whitehouse et al., 1958). As the array points of Tui, strains 0674, 0685 and Jules are closest to the lower intersection of the regression line and the parabola, they possess a preponderance of dominant genes. SEA possesses a lower proportion of dominant genes than the above mentioned 4 parents. SB and BTS contain a preponderance of recessive genes. Strain 72-7427, the outlier, has its array point below the regression line and away on the high V_r value side. Strain 72-7427, which is the red kidney type of dry bean, has the highest mean 100-seed weight. It is the only variety that behaves differently from the others. It is interesting to observe that the W_r/V_r graph of 100-seed weight, 8×8 , F_1 has a similar picture to

that of the length of pod 8 x 8, F_1 (Figure 22). The changing position of strain 0674 in Figure 22 to the position in Figure 31 is believed to be a consequence of susceptibility to ozone injuries of strain 0674. Ozone injuries did not affect length of pod but it did affect 100-seed weight.

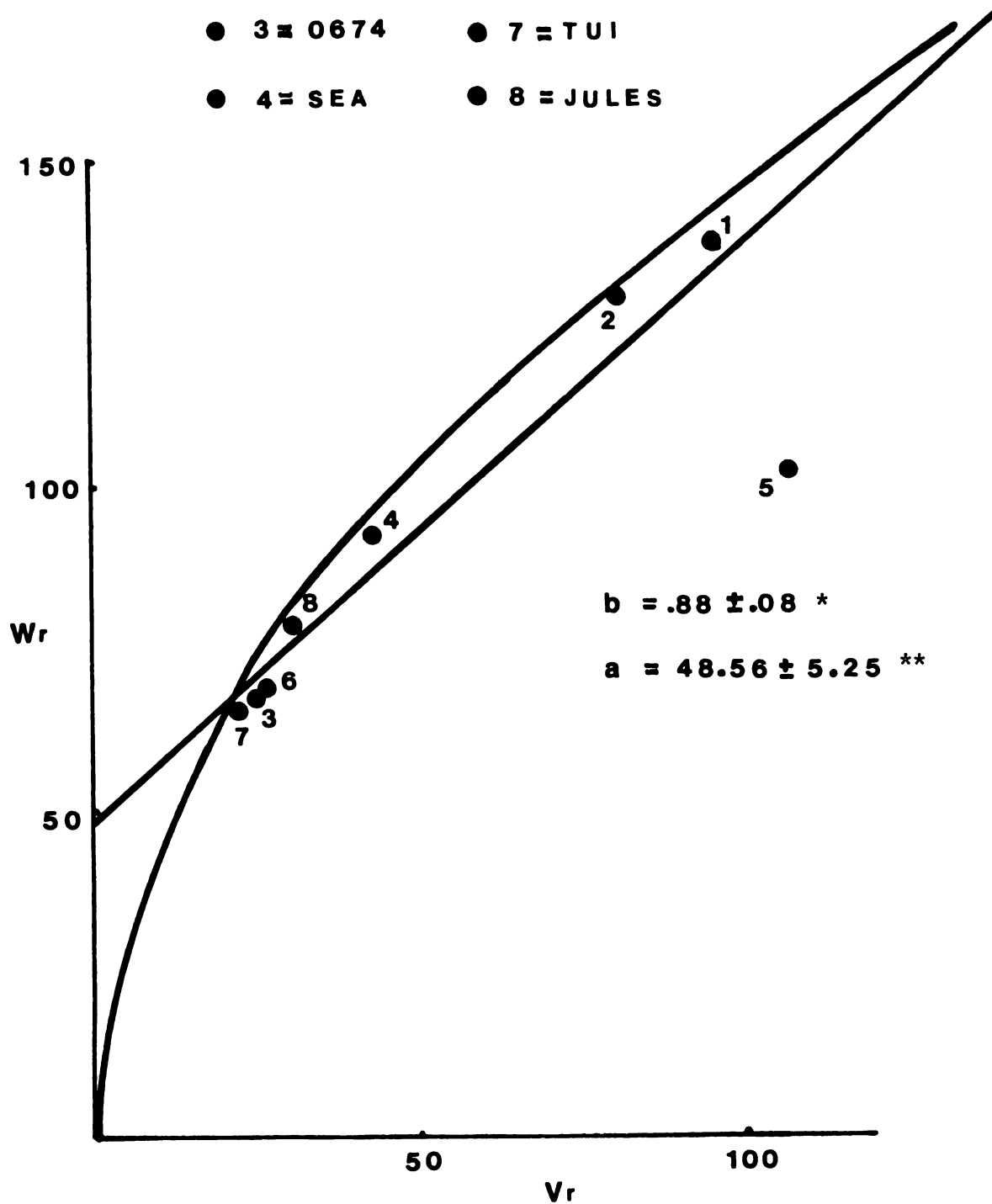
The heritability estimate of 100-seed weight is 90% suggesting that this trait is highly heritable similar to length of pod. The "D" value of 210.89 indicates the presence of substantial additive genetic variance. It is, therefore, to be expected that the parents with high array means will produce progenies with high 100-seed weights.

The correlation between length of pod and 100-seed weight of plants in the 8 x 8, F_1 was calculated and had the value of 0.47 which is highly significant. The evidence from the correlation and W_r/V_r graphs suggested that these two traits might result from action of the same gene system.

5 x 5, F_2

The ranking of the mean 100-seed weight in the F_2 (Table 5) is the same as those reported in the 8 x 8, F_1 section, namely, strain 72-7427 gave the highest mean value and strain 0674 the lowest. Four of 10 F_2 populations examined had mean values greater than the

- 1 = BTS ● 5 = 72-7427
- 2 = SB ● 6 = 0685
- 3 = 0674 ● 7 = TUI
- 4 = SEA ● 8 = JULES



* t for $b = 0 = 10.58$ and t for $b = 1 = 1.45$

** t for $a = 0 = 9.26$

Figure 31. 100-seed weight in gm (8 x 8, F_1).

mid-parent values. Six F_2 populations had mean values smaller than the mid-parent values. Two out of the 4 F_2 populations which had the mean exceeding the mid-parent value involved the crosses between BTS x 0674 and BTS x SEA. The other 2 F_2 populations involved the cross between 0674 x SEA and SB x 72-7427. BTS x 0674, BTS x SEA and SB x 7427 also showed heterosis in the 5 x 5, F_1 .

The W_r/V_r graph presented in Figure 32 shows that the regression line is significant ($b = 1.01 \pm .06$) and it intersects significantly above the origin ($a = 69.61 \pm 2.44$). As far as the relationship between the regression line and the parabola is concerned, it takes the same form as in the 8 x 8, F_1 . Dominance plays only a minor part in the determination of 100-seed weight.

The position of the points show that BTS, strain 0674 and SEA possess a preponderance of dominant genes. Strain 72-7427 contains a preponderance of recessive genes. SB seems to contain a balance of dominant and recessive genes.

The "F" value of 147.11 indicates that there is an excess of dominant genes among the parents. This agrees very well with the position of the 3 parents being closest to the point of intersection of the regression and parabola. The "D" value of 320.42 and the high value of h^2 of 81% indicate that the gene system is additive and the trait is highly heritable. Evidence from the

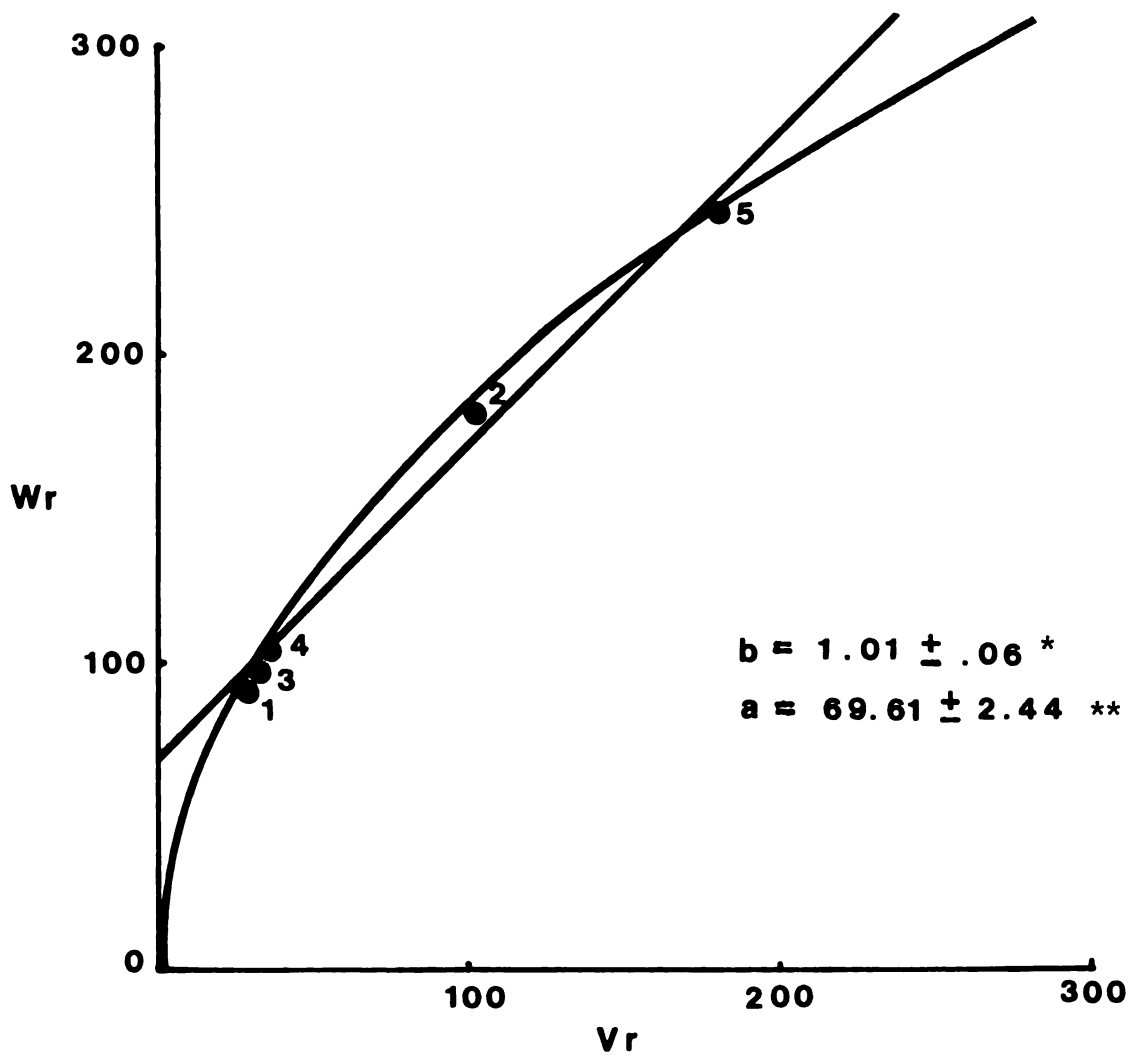
● 1 = BTs

● 2 = SB

● 4 = SEA

● 3 = 0674

● 5 = 72-7427



* t for $b = 0 = 16.24$ and t for $b = 1 = -.11$

** t for $a = 0 = 11.65$

Figure 32. 100-seed weight in gm (5 x 5, F_2).

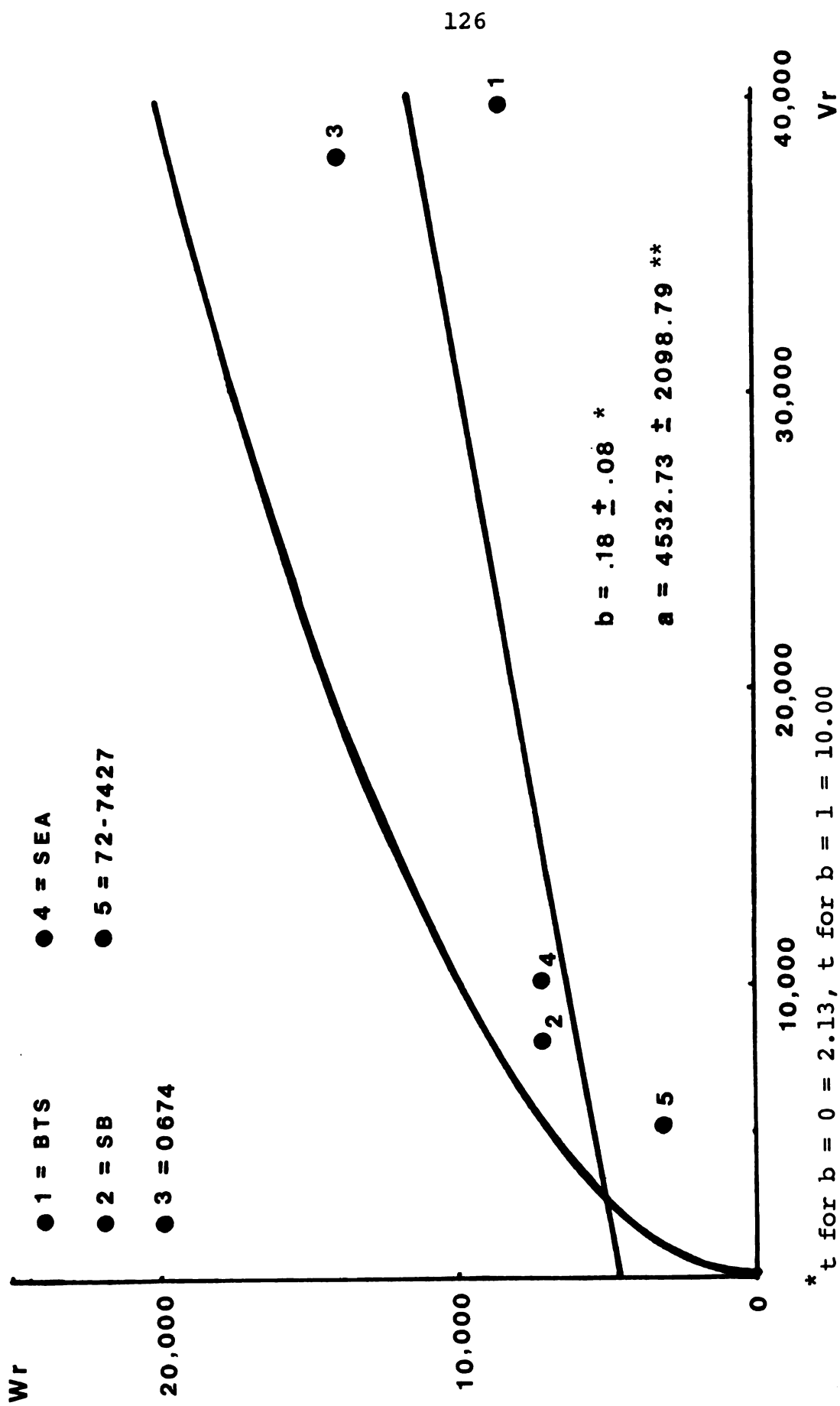
three graphs strongly suggests that the gene system controlling 100-seed weight in dry bean is additive and the trait is highly heritable.

Number of Seeds Per Plant

5 x 5, F₁

BTS had the highest mean number of seeds per plant (338.9, Table 1) and strain 72-7427 had the lowest mean of 85.6. SEA, strain 0674 and SB had mean values of 235.9, 201.7 and 109.7, respectively. Eight out of 10 F₁ hybrids examined had mean values exceeding that of mid-parent values and 2 hybrids had the mean values smaller than mid-parent values. The hybrid with the highest mean value derived from BTS x 0674 which gave a mean of 720.9 (Table 1). The lowest mean value came from the hybrid of 72-7427 x BTS which gave a mean value of 62.3.

It was disturbing that the computed "D" value had a negative value of -11798.58. The high error variance (E = 23580.39) coupled with the low variance of the parental arrays resulted in a very high negative "D" value. The regression is not significantly different from 0 but significantly different from 1 ($b = .18 \pm .08$) (Figure 33). The line intersects above the origin but not significantly different from 0 ($a = 4532.73 \pm 8098.79$). Further interpretation is not valid.



* t for b = 0 = 2.13, t for b = 1 = 10.00

** t for a = 0 = 2.16

Figure 33. Number of seeds per plant (5 x 5, F₁).

Number of seeds per plant is a complex trait. Several factors can influence the variation in this trait. It is strongly influenced by number of pods per plant (X) and number of seeds per pod (Y). In turn, "X" and "Y" themselves are strongly influenced by environmental factors. Inter-plant competition can easily cause variation in "X." Once the pods are formed there may be intraplant competition if environmental stress is imposed. Although "X" may not have any direct genetic influence on "Y," nevertheless, developmentally it has an indirect effect on "Y" (Adams, 1967). The interactions between X and Y and between these two components with the environment may cause "D" to be negative. It is, therefore, not reliable to make further interpretation of this set of data.

8 x 8, F₁

In the 1974 trial, BTS still showed its superiority in this trait over the other 7 lines. It had a mean value of 318.9, as compared to the lowest mean value of 82.2 for 72-7427 (Table 3). Twenty-three out of 28 F₁ hybrids examined showed heterosis, having mean values greater than that of mid-parent values. Only 5 hybrids had mean values smaller than that of mid-parent values. The F₁ hybrid derived from BTS x 0685 gave the highest mean value of 662.2; the smallest mean came from the hybrid SB x 72-7427 (103.5).

Figure 34 presents the picture of the W_r/V_r graph of 8×8 , F_1 . The regression coefficient has the value of $.24 \pm .05$. This is significantly different from $b = 0$ and $b = 1$. Genic interaction is indicated for this trait. The intercept on the W_r axis is above the origin ($a = 3377.79 \pm 580.07$) and it is significantly different from 0. Strain 72-7427, Jules, SB, Tui and SEA seem to contain a preponderance of dominant genes. BTS contains a preponderance of recessive genes. Strains 0674 and 0685 seem to have a balance of dominant and recessive genes.

Even though the calculated value of "D" is 2968.64 which indicates additivity of the gene system, genic interaction should be postulated for this trait according to the evidence of the regression line.

The heritability is low ($h^2 = 5\%$).

5 x 5, F_2

Seven out of 10 F_2 populations examined had mean values greater than that of the mid-parent values (Table 5). The F_2 population derived from the cross BTS x SEA gave the highest mean value of 303.5. Three of the F_2 's gave mean values lower than that of mid-parent values and the lowest mean value belongs to the cross derived from SB x 72-7427 (92.2, Table 5).

The regression of W_r on V_r (Figure 35) is significantly different from $b = 0$ but not from $b = 1$

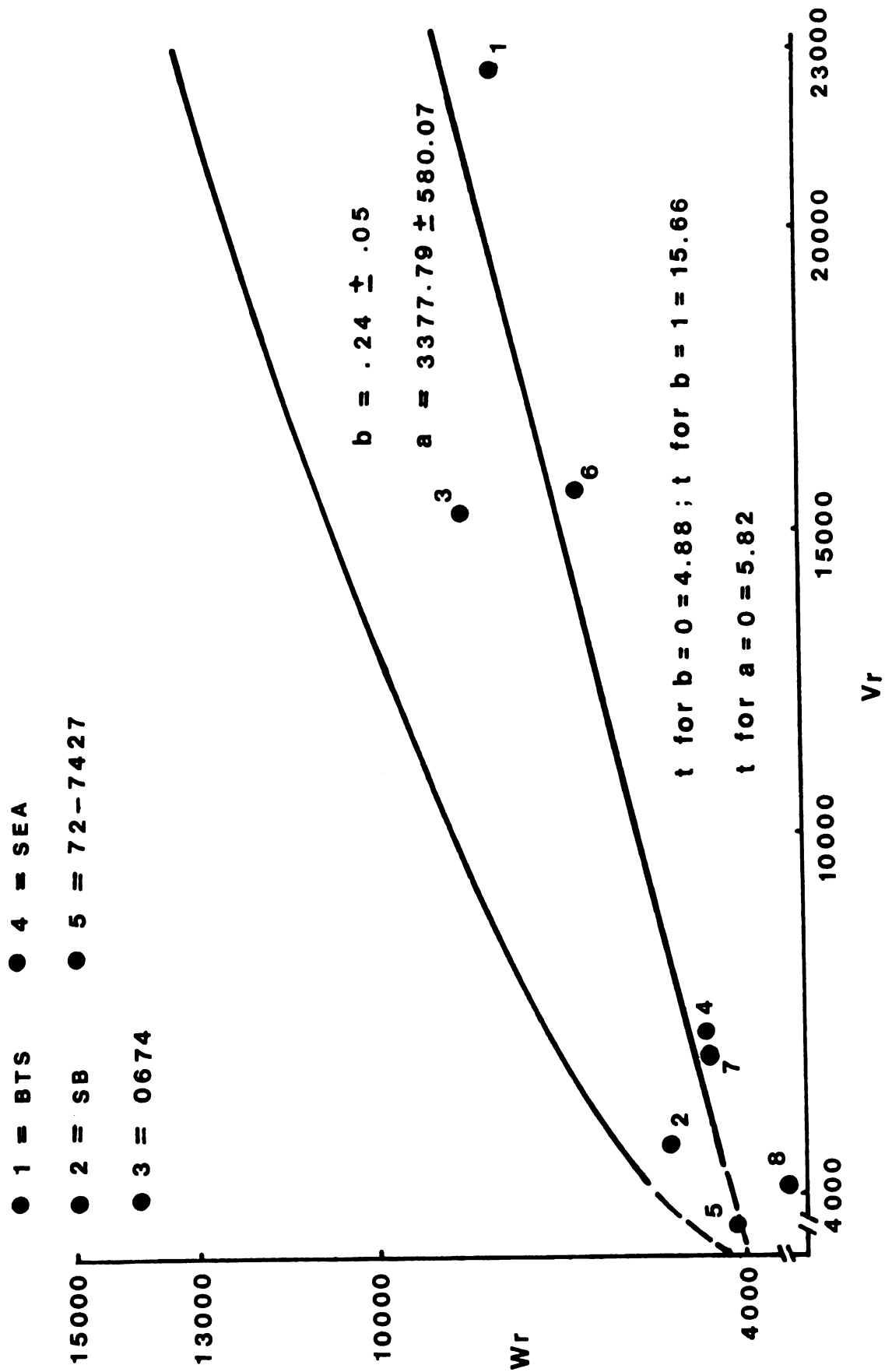
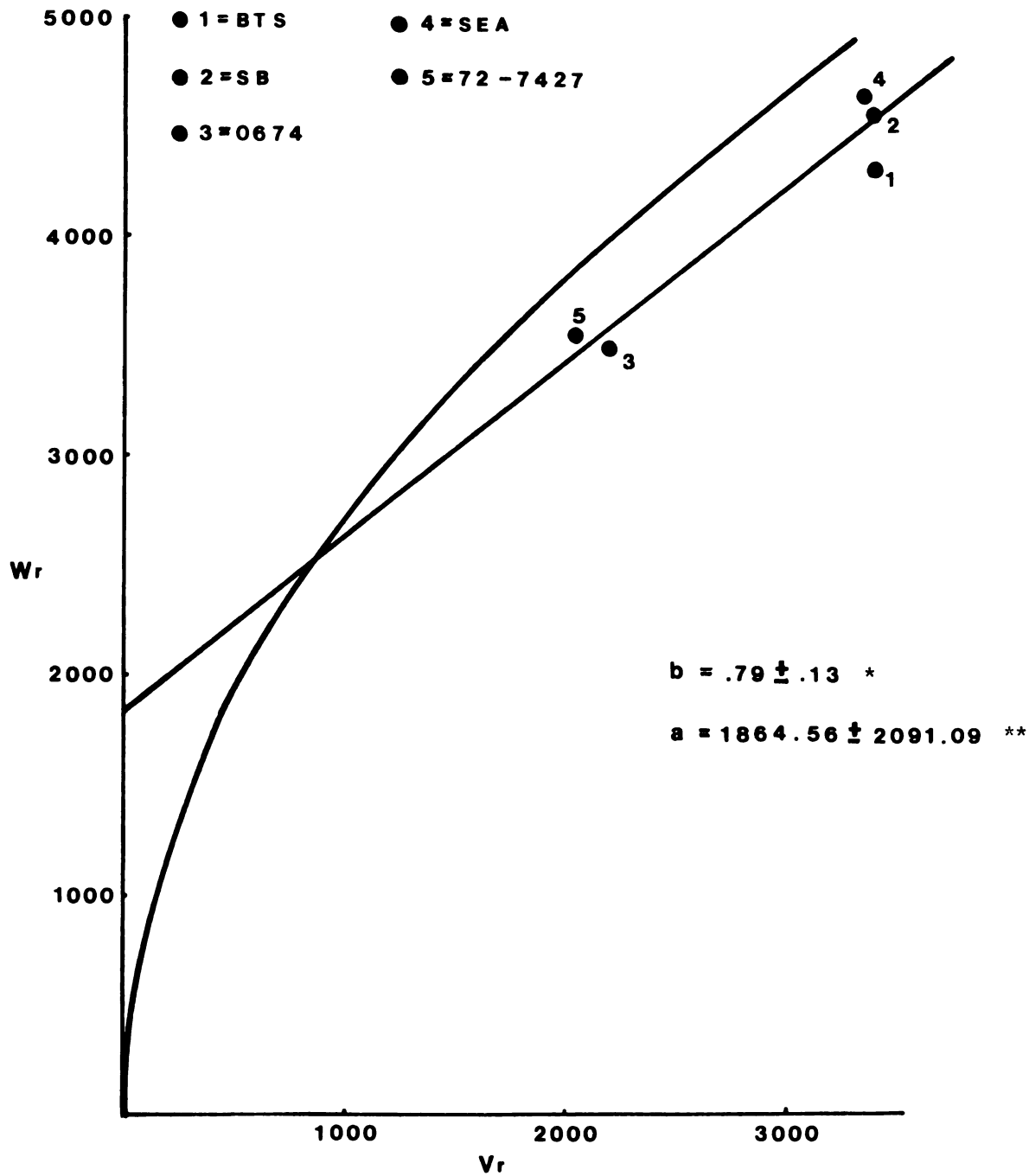


Figure 34. Number of seeds per plant (8×8 , F_1).



* t for $b = 0 = 6.21$ and t for $b = 1 = 1.69$

** t for $a = 0 = 10.40$

Figure 35. Number of seeds per plant (5 x 5, F_2).

($b = .79 \pm .13$). This agrees well with the "D" value of 737.13. The regression line intersects the W_r axis significantly above the origin ($a = 1864.56 \pm 374.39$). The $\sqrt{H_1/D}$ value is 0.58. The evidence suggests partial dominance.

The position of BTS, SB and SEA indicate that they contain a preponderance of recessive genes and that strains 0674 and 72-7427 contain a higher proportion of dominant genes. The "F" value of 328.01 suggests an excess of dominant genes among the parents. The heritability estimate is 90%.

Seed Dry Weight Per Plant

5 x 5, F_1

It appears in Table 1 that BTS gave the highest mean seed dry weight of 58.7 gm. Strain 72-7427 gave the second highest mean value of 46.2 gm. SB gave a mean value of 42.9 gm and ranked third. SEA and 0674 gave mean values of 33.2 and 25.2, respectively (Table 1). It can also be seen from the same table that BTS gave the highest mean values of number of pods per plant and number of seeds per pod. Even though it did not give the highest mean 100-seed weight it did give a reasonably high mean value of that trait according to its seed size. Analysis of variance shows significant differences among the genotypes.

Nine out of 10 F_1 hybrids examined showed heterosis with mean values exceeding mid-parent values and in most cases exceeding the mean of the parent with high mean seed weight. There was only one cross 0674 x SEA, which gave an F_1 mean value lower than that of the mid-parent.

The F_1 hybrids derived from the cross BTS x 0674 and its reciprocal gave the highest mean seed dry weight. The 0674 x SEA F_1 had the lowest mean seed dry weight. The cross between the two largest seed size lines, SB x 72-7427, did not give F_1 progenies with highest mean seed dry weight. On the contrary the cross between BTS x 0674 which gave the lowest 100-seed weight in that series gave F_1 progenies with the highest mean seed dry weight (111.8, Table 1). The array means in the F_1 also indicate that BTS had the highest array mean of 76.9 (Table 7). SB apparently gave the second highest array mean of 66.0. SEA, strains 0674 and 72-7427 gave array means of 63.1, 58.6 and 50.9, respectively.

Figure 36 shows the W_r/V_r graph of the 5 x 5, F_1 . The regression line is neither significantly different from $b = 0$ nor $b = 1$ ($b = 48 \pm .29$). It intersects the W_r axis below the point of origin ($a = -184.91 \pm 261.01$) but not significantly different from 0. It is interesting to observe that the position of the 5 array points are very similar to those in total plant weight (Figure 7)

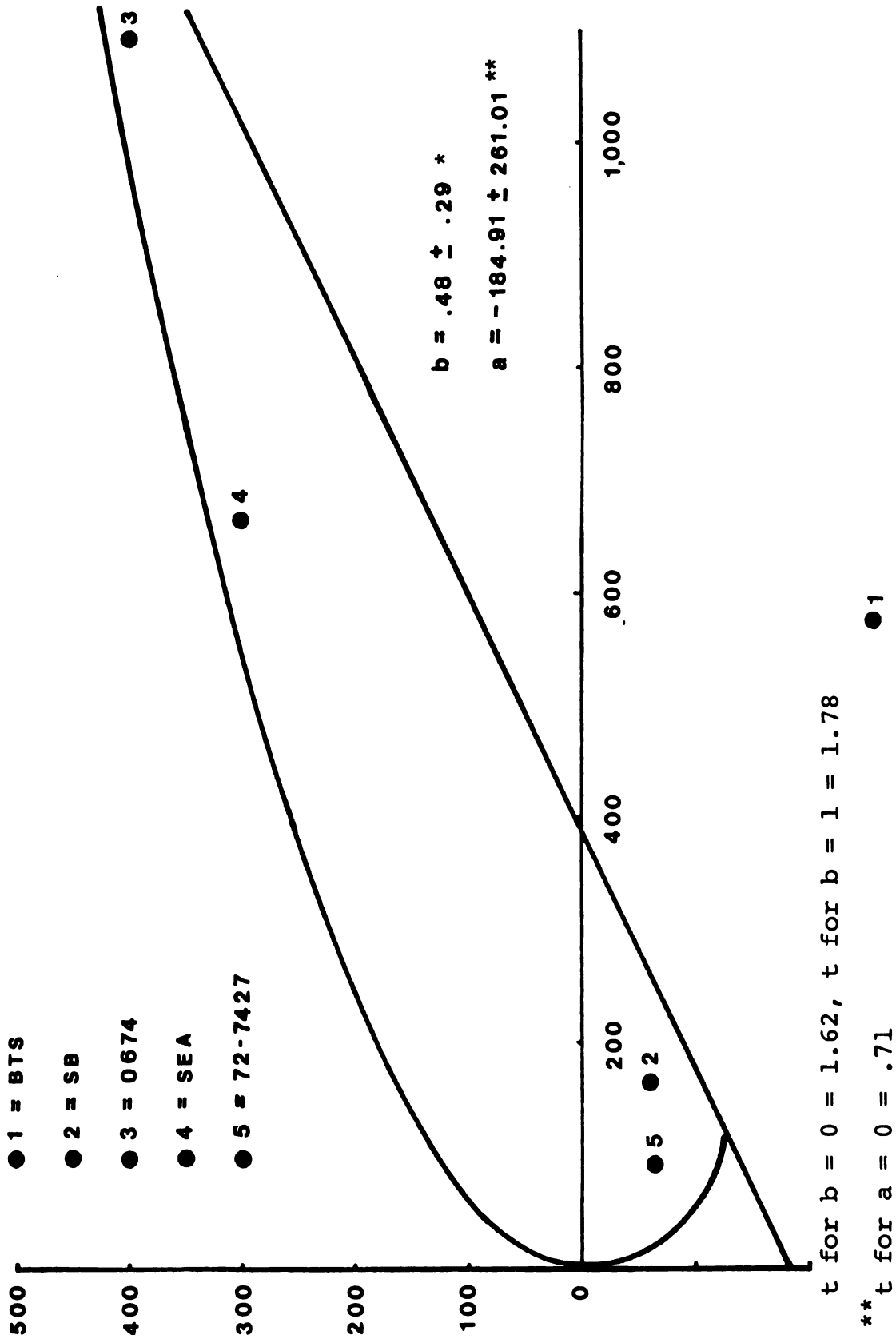


Figure 36. Seed dry weight per plant, in gm (5 x 5, F₂).

and total pod dry weight (Figure 16). The consistency of the position of these array points suggests that the gene systems controlling these three traits are similar. And also due to the same reason, SB and strain 72-7427 contained a preponderance of dominant genes, strain 0674 contained a preponderance of recessive genes, and SEA contained a slightly higher proportion of recessive than dominant genes. BTS is the outlier as described in "Pod Dry Weight." SB and strain 72-7427 which have several phenotypic characters in common as mentioned earlier under some traits, are believed to have similar dominant genes controlling total seed weight as well as weights of pods and whole plant. Strain 0674 and SEA which are also very similar phenotypically, unexpectedly are located far apart from each other. It is believed that different responses to ozone injuries and the interaction between strain 0674 with the environment later in the season after it resumed its second stage of growth were the main causes for this difference. BTS, being the only indeterminate type among the 5 parents, has a unique gene system controlling seed dry weight.

Because "D" had a negative value of -721.3585, no reliable interpretation of the genetic component of variations can be expected. Since seed dry weight or seed yield (W) is a complex trait, interactions

between the yield components are expected. Therefore, the assumption of no gene interaction is not valid in this case.

8 x 8, F₁

Among the 8 parental lines used in 1974, Jules gave the highest mean seed dry weight of 67.2 gm. Strain 0685, Tui, BTS, SB, strain 72-7427, SEA and strain 0674 gave mean values of 58.8, 57.6, 56.7, 51.9, 45.9, 40.4 and 31.6 gm respectively (Table 3). The analysis of variance (Table 4) showed that there were highly significant differences among replicates and among genotypes.

Twenty-five hybrids had mean values exceeding the means of the parent with higher seed weight. The cross SB x 72-7427 gave a hybrid with mean values smaller than the mean of the parent with higher seed weight (Table 3). The hybrid resulting from the crosses 0674 x SEA and Tui x Jules gave mean values smaller than their mid-parent values. The hybrid derived from Jules x 0685 gave the highest mean value of 113.2 gm. Other hybrids which had mean values exceeding 100 gms per plant were those derived from Jules x SB (112.4), BTS x 0685 (109.8) and 0685 x Jules (109.1). The cross which produced a hybrid with the lowest mean value was 0674 x SEA (34.9). It has been noticed that the crosses involving the parents with contrasting plant type such as Jules x 0685 and

BTS x 0685 resulted in hybrids with very high degree of heterosis (high seed yield). The cross involving similar plant types such as 0674 x SEA produced poor seed yield.

The array means in Table 8 show that Jules had the highest value of 85.4 and strain 0674 again had the lowest value of 60.4.

Figure 37 presents the W_r/V_r graph of the 8×8 , F_1 . The regression line is significantly different from zero but not from $b = 1$ ($b = .64 \pm .19$). It intersects the W_r axis below the point of origin but not significantly different from 0 ($a = -80.58 \pm 105.78$). The $\sqrt{H_1/D}$ has the value of 2.77. The evidence suggests complete to over-dominance; but interaction still may play a role, since some of the components of seed dry weight/plant appeared to be influenced by genic interaction.

5 x 5, F_2

Seven out of 10 F_2 populations still have mean seed dry weights greater than that of their mid-parent values. Three F_2 populations had the mean value less than that of the mid-parent value. They were derived from the crosses BTS x 0674, BTS x 72-7427 and SB x 72-7427 (Table 5). The F_2 populations which had the highest mean value was derived from BTS x SB (66.8) and that with the lowest mean value was derived from

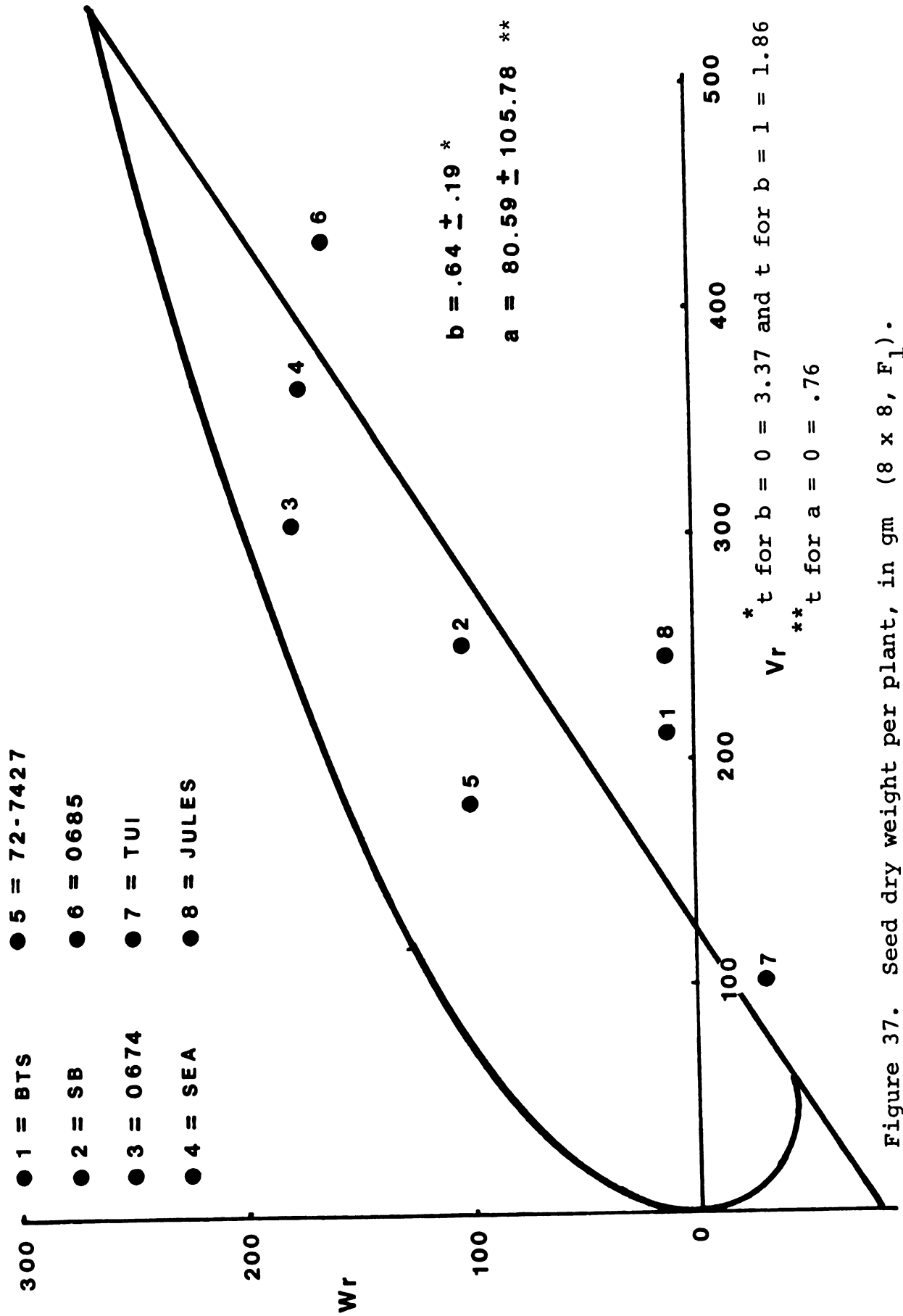


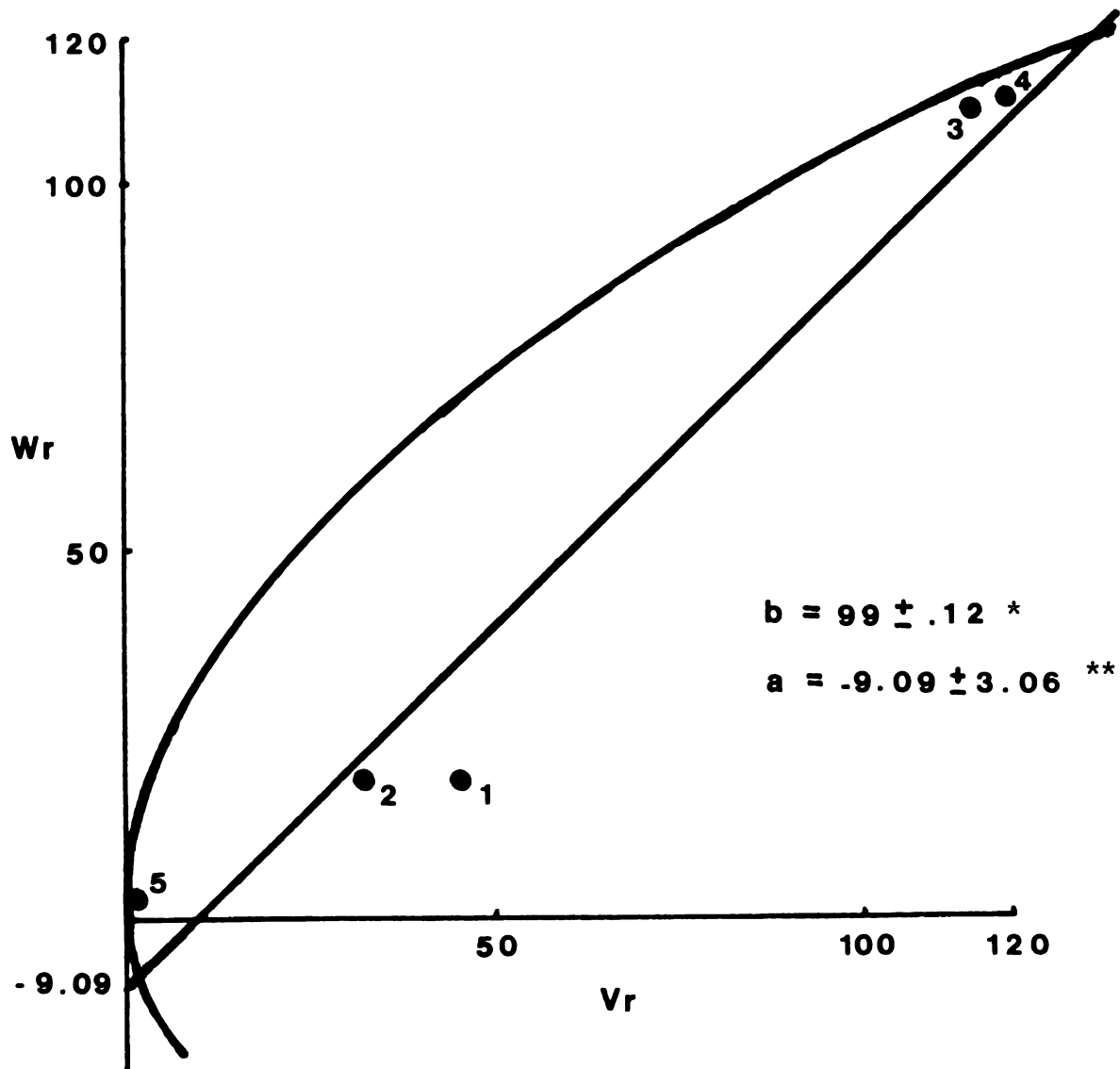
Figure 37. Seed dry weight per plant, in gm (8 x 8, F_1).

SEA x 0674 (31.1). The analysis of variance (Table 6) showed that there were highly significant differences among replicates and among genotypes.

Figure 38 shows that the regression of W_r on V_r is significantly different from $b = 0$ but not from $b = 1$ ($b = .99 \pm .12$). The regression line intersects the W_r axis below the origin but not significantly different from 0 ($a = -9.09 \pm 3.06$) indicating complete dominance. This result does not agree with the $\sqrt{H_1/D}$ value of 2.41 which indicates over-dominance. On balance the evidence from the graph and the $\sqrt{H_1/D}$ value, suggests complete to over-dominance.

The position of the points indicate that strain 0674 and SEA contain a preponderance of recessive genes. Strain 72-7427 contains a preponderance of dominant genes. SB and BTS contain a lower proportion of dominant genes than strain 72-7427. The calculated "F" value of -28.67 indicates that there is an excess of recessive genes among the parental lines. The heritability estimate of 10% suggests that total seed weight is of low heritability. It is not expected that total seed weight or seed yield (W) per se will be transferred to the next generation effectively. It has been understood that "yield" is a complex trait. "W" is very much influenced by other components i.e. X, Y and Z. Any factor affecting these components would ultimately effect "W."

- 1 = BTS ● 4 = SEA
- 2 = SB ● 5 = 72-7427
- 3 = 0674



* t for $b = 0 = 8.28$ and t for $b = 1 = .06$

** t for $a = 0 = .97$

Figure 38. Seed dry weight per plant, in gm (5 x 5, F_2).

Harvest Index5 x 5, F₁

The variety SB had the highest mean harvest index among the 5 parental lines tested in 1973. Its mean value was .63. Strain 0674 had the lowest mean harvest index of .50 (Table 1). Eight out of 10 F₁ hybrids examined had the mean harvest index greater than that of the mid-parent values and two smaller. BTS x SB produced the hybrid with the highest mean value of .64 and SB x 0674 gave the hybrid with the smallest mean value of .50. The analysis of variance shows that there were significant differences among the genotypes.

Due to the very small value of variances and covariances it was difficult to construct a W_r/V_r graph for this trait. However, according to the calculation, it was found that the regression coefficient had the value of $b = .96 \pm .15$ and it was not significantly different from $b = 1$ but significantly different from $b = 0$. This suggests that either an additive or dominant gene system, without the complication of genic interactions, controls this trait. The "F" value of -.0026 indicated that there was slightly an excess of recessive genes among the parental lines. The heritability estimate was 7%. This indicates that harvest index probably is not highly heritable. It is a complex trait and depends on several other factors. The plant dry weight

or the biological yield of the plant which is the denominator is heavily dependent on other traits and environmental factors. The total seed yield which is the numerator for harvest index is a complex trait by itself and influenced by the interactions of the yield components (X, Y and Z). Harvest index is a ratio of seed yield to total plant weight and thus expresses the efficiency of partition. As such it is useful in selection, but it does not by itself indicate the highest yielding lines.

8 x 8, F_1

Table 3 shows the mean H.I. of the 8 x 8, F_1 . SB still had the highest mean value of .66 among the 8 parental lines tested in 1974. Strain 0685 appears to have the lowest mean value of .44. Seventeen out of 28 crosses gave F_1 hybrids with mean values greater than that of the mid-parent values and 11 F_1 hybrids had mean values smaller than that of the mid-parent values. SB x Jules appeared to give the hybrid with the highest mean value of .70 and the lowest mean value came from the hybrid derived from SB x 0685 which had the value of .45.

It is shown in Table 8 that Jules had the highest array mean of .65 and strain 72-7427 the lowest of .51.

SB and SEA had the next highest array means of .59. The lowest array mean belongs to the strain 72-7427 (.51).

5 x 5, F_2

Eight out of 10 F_2 crosses had the mean harvest index smaller than that of the mid-parent values. The F_2 derived from BTS x 0674 and 0674 x 72-7427 had the smallest mean value of .52 (Table 5). Only 2 F_2 crosses had mean values greater than that of the mid-parent values. They were those derived from SB x 72-7427 and 0674 x SEA which had mean values of .61 and .56 respectively. However, these 2 crosses appeared to give the smallest mean seed yield (43.4 and 39.3, Table 5). On the other hand, BTS x SB, which gave a H.I. of .60 and is lower than the mid-parent value, had the highest mean seed yield of 66.8 (Table 5). Therefore, harvest index is not a reliable trait in predicting the yield.

DISCUSSION

At the outset of this thesis it had not been determined which morphological traits were most important in constructing an ideotype for high yield. Consequently a rather large group of characteristics had to be included in the analysis. Denis (1971) did a factor analysis of plant-type variables related to yield of dry beans. A Weight-factor and a Number-factor, typified by pod weight and number of pods, respectively, identified as two major factors or patterns for high yielding bean plant type. A third factor, a Display-factor, was inferred, based on upper internode length and leaf size.

The genetic complexity of the traits proposed for investigation here have not been thoroughly studied. A quick assessment of certain aspects of the traits, e.g. gene action, etc., is necessary. One would want to know when he is building an ideotype, how the gene system of these traits will interact or recombine. The diallel cross was thought to be an appropriate method for this investigation. Generally we can get reliable information in a rather short time. While we are using the parental materials making the cross for genetic studies, we also

generate populations for selection of potential new varieties. These new varieties may provide details in genetic analysis. In order to assure that a wider base of genetic differences would be expressed for these characteristics among parental lines involved, the size of the diallel in this study was extended from 5 in 1973 to 8 in 1974.

There are limitations in the diallel methods. Firstly, it is understood that in dealing with single plant data, large errors of estimation are expected. Secondly, with a small number of parents in a diallel set, one extreme parent can have a disproportionate influence on the slope of the regression line. This will lead to genetic interpretation that are valid only for that particular set of parents (5 x 5) and may not be valid for another set of 8 parents. In this study it can be seen in Figures 8, 14, 24, and 36 that parent 1 (BTS) behaved as an outlier in the 5 x 5, either in the F_1 or F_2 generations. This is because BTS has a contrasting plant type and, presumably, genotype as compared with others in the same set of parents. In some cases, the strain 0685 joined BTS as the outliers. This can be seen in Figures 13 and 25. Here again, even though strain 0685 is a determinate type, its morphological characters are much different from other determinate types among the 8 parental lines. Therefore, both BTS and strain 0685

behaved differently from the others in some of the traits. They tend to have low covariances and high variances. This may have caused the slope of the regression line to deviate significantly from 1, thus influencing the interpretation to be genic interaction.

For the purpose of building an ideotype, we must have appropriate genetic recombinations. One can obtain preliminary information about recombination in the F_2 generation by correlation of the traits under investigation. The degree of association of the traits in the F_2 has to be observed.

High heritability was indicated for some traits, namely; number of seeds per pod and number of seeds per plant in the 5 x 5, F_2 , 100-seed weight in all 3 sets of data, and length of pod in the 8 x 8, F_1 . This can be used partly as evidence of additivity of gene action. In several cases, however, low h^2 values were indicated together with evidence of genic interaction. In the case of days-to-first-flower, for example, in 5 x 5, F_1 and 8 x 8, F_1 , apparent partial to complete dominance was indicated. In the 5 x 5, F_2 , however, genic interaction was indicated. Genic interaction as deduced from the W_r/V_r graph, would obscure the manifestation of genic additivity or dominance if these were present. It does not, in itself, exclude them. These kinds of gene action may, in fact, be operating in the expression of this

trait, but simultaneous presence in two or more parents of genes that interact in a nonadditive way with each other, leads to regression slope less than unity. And it is on the slope evidence that genic interaction is inferred. Often, it will turn out that, by omitting one or possibly two arrays from consideration in the makeup of the W_r/V_r graph, the slope value will return to unity, and the genetic interpretation of simple additivity or dominance will be indicated (Dickson, 1967). Therefore, the deduction of genic interaction in some of the traits in this investigation does not mean that additivity or dominance are thereby excluded.

Some of the more important characteristics we want to investigate, e.g., are size and number characteristics. These traits seemed to be more complex in their genic behavior. In some cases they showed additivity such as length of pod, number of seeds per pod (5 x 5, F_2) and 100-seed weight. In other cases, they show genic interaction such as length of internode (8 x 8, F_1), number of seeds per plant and seed weight per plant. One of the most important components of yield, number of pods per plant, showed genic interaction in the 5 x 5, F_1 and 8 x 8, F_1 . In the 5 x 5, F_2 complete dominance was indicated. It can be seen that some of the important traits are not simple genetically. However, number of seeds per pod and 100-seed weight were found to have high

heritability and their gene system is additive. It would be extremely lucky for a breeder to find that all the major traits contribute to high yield are highly heritable and also have additive gene systems. One would generally find that one of these traits have a low h^2 value and genic interaction may be involved. It is also very common to find that these three important traits, namely; number of pods per plant, number of seeds per pod and 100-seed weight, usually have negative correlations (Adams, 1967). This, of course, makes it more difficult for plant breeders to create an ideal plant type for high yield.

Overall, it has not been found very promising in this investigation for all the traits investigated. This is due to the fact that most of the traits do not have an additive gene system. Genic interaction seemed to be a major feature of the genetic behavior of several traits. It appeared likely that this was caused, in part, by the inclusion in the diallel of particular parents (e.g. BTS). In any case, genic interaction does not exclude additivity or dominance. The final test would be to conduct multiple-trait selection experiments in advanced generations, wherein genic heterozygosity would be minimal and where reliable mean values could be obtained.

SUMMARY AND CONCLUSIONS

Inheritance of morphological characteristics of field beans (Phaseolus vulgaris L.) was studied in (1) a 5 x 5, F_1 and F_2 diallel, and (2) an 8 x 8, F_1 diallel. The parental materials were hand pollinated in the greenhouse in the winter of 1972 and 1973 to produce the necessary crosses. The parental and F_1 seeds of the 5 x 5 diallel were space planted in the field in East Lansing in the summer of 1973. The parental, F_1 of the 8 x 8 and F_2 of the 5 x 5 were space planted in the adjacent field in the summer of 1974.

Data collection, either on living plants in the field or subsequent determination after harvesting was done on a per plant basis. Some of the missing data were replaced by figures calculated according to Snedecor and Cochran's (1976) method. For the late maturing plants which some of whose pods had been damaged by frost yield components (X, Y and Z) were determined from the fully matured pods of that plant.

The results of this investigation are summarized in the following paragraphs.

1. An additive gene system was not found for the trait number-of-days-to-first-flower for the 5 x 5, F_1 and an apparent partial to complete dominance was indicated for the 8 x 8, F_1 . Even though the evidence from the 5 x 5, F_2 graph indicated genic interaction for this trait, this does not mean that additivity or dominance were excluded from the gene system. The majority of the F_1 hybrids showed heterosis. The cross involving two determinate parents, SB x 72-7427, gave hybrids with the earliest flowering date and one indeterminate (BTS) x determinate (0685) cross gave hybrids with the latest flowering date. The heritability was found to be low (29%).

2. BTS was found to have the shortest duration-of-flowering among the 5 varieties tested in 1973. The longest duration-of-flowering of strain 0674 appeared to be abnormal due to ozone injury in an early growth stage which induced a resumption of growth and reproduction in a delayed later stage. The heritability estimate was 15%. Genic interaction was involved in controlling this trait.

3. The earliest maturing variety was SEA with a mean of 74.77 days. Strain 0674 with a mean of 92.63 days was found to be the latest in maturity. However, the delay in maturity of strain 0674 was probably due to ozone injury and the resumption of its growth later in

the season. Genic interaction was found in the 5 x 5, F_1 . In the 8 x 8, F_1 multiple alleles was found to control this trait. Whereas in the 5 x 5, F_2 complete dominance was indicated. It could be hypothesized from the F_2 data that late maturity is controlled largely by dominant and early maturity by recessive genes. Heritability was found to be low in all three sets of data (7%, 29%, 14%).

4. BTS and strain 0685 had the highest mean plant weight in the 5 x 5, and 8 x 8 diallels respectively. Strain 0674 had the lowest mean plant weight in both years. It was noticed that parents with similar plant type, e.g. strain 0674 and SEA, when crossed, gave hybrids with poor mean plant weight. On the other hand, crosses between parents with contrasting plant types, e.g. BTS x 0674 or BTS x 0685, gave hybrids with largest mean plant weights (Table 1 and 3). Genic interactions as well as genic dominance effects were believed to be involved in determining this trait. The heritability was very low (4%).

5. Strain 0674 produced the highest number of main stem branches among the 5 parents tested in 1973 and SB the lowest. Eight out of 10 hybrids in the 5 x 5 diallel showed heterosis. However, when parents of similar phenotype, e.g., 0674 and SEA, were crossed, the hybrid did not show heterotic effects. This trait showed great response to plant density, and to differential

vigor within plots attributable to legitimate genetic segregation (in the F_2). Consequently, the errors associated with its estimation were large, tending seriously to bias estimates of any genetic effects that might have been present. The estimate of "D," in the 5×5 , F_1 was in fact negative. Accordingly, no attempt was made in 1974 to measure number of branches.

6. BTS had the highest mean number of main stem nodes among the 5 parents tested in 1973. Seven out of 10 F_1 hybrids showed heterosis for this trait. All the parents except BTS appeared to contain a preponderance of recessive genes. The estimate of $F = -24.36$ seemed to agree with this interpretation. However, the estimate of "D" was negative (-17.24) and it was decided that no valid interpretation could be reached based upon the 5×5 , F_1 data of 1973.

7. Strain 0685 gave the highest mean total number of nodes among the 8 parents tested in 1974. BTS x 0685 gave the hybrid with the highest mean value of 196.50. Eight out of 10 F_2 populations from the 5×5 had mean values exceeding the mid-parent values. Genic interactions were indicated for this trait in the 8×8 , F_1 . In the 5×5 , F_2 , genic interaction was indicated as the prevailing mode of genic action when heterozygosity was

reduced to that of the F_2 level. An excess of recessive genes among the parents was also suggested ($F = -24.36$). The heritability for this trait was very low (3-4%).

8. The determinate type appeared to have average internode lengths longer than the indeterminate type. Strain 0685 had the longest internode length. Seventeen of 28 hybrids showed heterotic effects in the 8×8 , F_1 . The hybrid with the longest internode length was derived from 0685 x SB and the shortest was from Tui x Jules. Genic interaction was suggested for length of internode in the 8×8 , F_1 . The F_2 population with the longest internode was derived from 0674 x 72-7427 and the F_2 with the shortest internode resulted from BTS x 0674. A partial to complete dominance was suggested for length of internode in the 5×5 , F_2 . Since all the indeterminate varieties had array points near the origin in both the 8×8 , F_1 and 5×5 , F_2 graphs it can be hypothesized that short internodes are controlled by dominant genes. The positions of the determinate varieties on the graphs also suggested that long internodes were controlled by recessive genes. Heritability was 22% in the 8×8 , F_1 and 14% in the F_2 .

9. Strain 0685 was found to have the highest number of racemes among the 8 parental lines. The hybrid derived from BTS x 0685 gave the highest number of

racemes. Additive genetic variance was not detected. The W_r/V_r graph indicated genic interaction. However, if 0674, 0685 and BTS were omitted and a new regression line drawn, the remaining array points would fit the regression line quite well, implying for the remaining parental arrays an additive to partially dominant system. Nine out of 10 F_2 populations retained heterosis for number of racemes. The F_2 with the highest mean value was derived from BTS x SEA. The evidence from the graph and $\sqrt{H_1/D}$ in the 5 x 5, F_2 is strongly suggestive of complete to slight over-dominance. All the parents seemed to contain a higher proportion of recessive genes. The negative value of "F" supported this observation. The heritability estimate in the F_2 for this trait was 11%.

10. BTS and 0685 had the highest mean number of pods per plant (X) in the 5 x 5 and 8 x 8 diallels respectively. The only hybrid in the 5 x 5, F_1 , 0674 x SEA which did not show a heterotic effect was probably adversely influenced by ozone injury. BTS when crossed with 0674 in the 1973 and with 0685 in 1974 gave the hybrids with largest mean number of pods per plant. The parent with large pod size, 72-7427, when crossed with the others, tended to give hybrids with small

number of pods per plant. Genic interaction was found both in the 5 x 5, F_1 and 8 x 8, F_1 . Complete dominance was found to control number of pods per plant in the F_2 . An excess of recessive genes among the parents was indicated for all populations tested. The heritability estimates were negligibly low in 5 x 5, F_1 and 8 x 8, F_1 whereas it was 21% in the 5 x 5, F_2 .

11. Strain 72-7427 had the longest pod length among the 8 parents. BTS x 7427 gave the hybrid with the longest pod in 8 x 8, F_1 but in the F_2 , the family derived from SB x 72-7427 had the longest pod. Additivity was indicated in both 8 x 8, F_1 and 5 x 5, F_2 . There was an excess of dominant genes in the 8 x 8, F_1 whereas an excess of recessive genes was indicated in the 5 x 5, F_2 . Heritability was 100% in 8 x 8, F_1 and 31% in the F_2 . The closeness of the regression line to the parabola in both graphs indicated that dominance plays only a minor role in determining length of pod.

12. As in number of pods per plant, BTA and strain 0685 had the highest mean pod dry weight in 1973 and 1974, respectively. The hybrids with highest mean pod dry weight were those derived from BTS x 0674 in 1973, and 0685 x BTS in 1974. These hybrids were the results of crosses between parents with contrasting plant types. Both the 5 x 5, and 8 x 8, F_1 gave a

negative value of "D" which follows from the large error variances associated with estimates of pod dry weight, and the low estimates of additive genetic variance associated with differences among array means. The W_r/V_r graph suggested that the genetic variance observed was generated mostly by genic interaction. However, in the F_2 , complete to over-dominance was indicated. The F_2 generation with the highest mean pod dry weight was derived from BTS x SB. The heritability was low (8%). A slight excess of recessive genes among the common parents in the F_2 was also suggested.

13. BTS and Tui gave the highest means number of seeds per pod in 1973 and 1974, respectively. BTS x O674 gave the hybrid with highest mean number of seeds per pod in 5 x 5, F_1 and BTS x Tui gave the highest in 8 x 8, F_1 . Partial to complete dominance was indicated in the 5 x 5, F_1 . Partial dominance was indicated in the 8 x 8, F_1 . The evidence from the graph suggested that dominance played a minor role in the 5 x 5, F_2 . It followed that an additive gene system was suggested. Heritability was 29% in the 5 x 5, F_1 , 44% in the 8 x 8, F_1 and 90% in the 5 x 5, F_2 .

14. Strain 72-7427 had the highest mean 100-seed weight among all parents tested. The hybrid derived from SB x 72-7427 had the highest mean 100-seed weight in both years. The W_r/V_r graphs of the 5 x 5, F_1 , 8 x 8,

F_2 and 5 x 5, F_2 indicated that the gene system controlling 100-seed weight is highly additive which agrees well with the positive value of "D" in all 3 graphs. The heritability was high, ranging from 82% for 5 x 5, F_1 , 90% for 8 x 8, F_1 and 81% for 5 x 5, F_2 . On balance, the evidence from all 3 sets of data strongly indicates additivity with minimal dominance effect. It was inferred from the "F" value that there were an excess of dominant genes in all 3 sets of data. The correlation test showed that 100-seed weight was significantly correlated with length of pod ($r = .4663$, $df = 54$) and they probably have the same gene system.

15. BTS had the highest mean number of seeds per plant. The hybrid with the highest mean number of seeds per plant in the 5 x 5, F_1 was derived from BTS x 0674. In the 8 x 8, F_1 , the hybrid derived from BTS x 0685 gave the highest number of seeds per plant. The F_2 generation derived from BTS x SEA gave the highest mean value of this trait. No additive genetic variance was detected for this trait. Genic interaction was indicated in the 5 x 5 and 8 x 8, F_1 . Partial dominance was suggested for the 5 x 5, F_2 .

16. BTS gave the highest mean seed dry weight in the 5 x 5, F_1 and Jules gave the highest mean in the 8 x 8, F_1 . The hybrid derived from BTS x 0674 gave the highest seed yield in 1973 and the hybrid derived from

Jules x 0685 gave the highest in 1974. Additive variance was not found for this trait. Gene interaction is believed to be involved but the evidence is not compelling. In the 5 x 5, F_2 , however, partial dominance was indicated. The F_2 derived from BTS x SB had the highest seed yield. An excess of recessive genes among this set of parents was indicated in F_2 . The heritability in the 5 x 5, F_1 and 8 x 8, F_1 was negligible because of negative "D" values, whereas it was 10% in the F_2 .

17. BTS was found to be a promising variety to be used in a breeding program for improving seed yield. Tui may be an alternate choice.

APPENDIX

Table 9. Genetic component of variations (5 x 5, F₁).

	D	F	H ₁	H ₂	E	$\sqrt{H_1/D}$	h ²
Days to 1st Flower	15.22	-37.43	47.18	40.01	8.76	1.76	0.11
Duration of Flowering	10.40	5.19	26.01	23.39	9.83	1.58	0.15
Days to Maturity	22.97	-10.11	111.62	100.05	41.17	2.20	.07
Plant Dry Wt.	-3385.36	-4182.51	4153.88	5440.68	3961.49	--	--
# Main Stem Branches	-.20	-1.53	4.02	3.34	3.50	--	--
# Main Stem Nodes	-17.24	-24.36	-10.24	-5.31	19.61	--	--
# Pods/Plant (X)	-471.05	-1194.24	547.07	742.67	823.30	--	--
Pod Dry Wt./Plant	-1262.99	-1738.42	1152.82	1801.20	1677.99	--	--
# Seeds/Pod (Y)	0.50	0.16	0.29	0.29	0.27	0.77	0.29
100-Seed Wt. (Z)	349.32	35.20	76.06	68.58	8.59	0.47	0.82
# Seeds/Plant	-11798.52	-37621.51	21637.57	27189.58	23580.39	--	--
Seed Dry Wt./Plant (W)	-721.36	-989.43	736.35	1111.95	941.05	--	--

Table 10. Genetic component of variations (8 x 8, F₁).

	D	F	H ₁	H ₂	E	$\sqrt{H_1/D}$	h ²
Days to 1st Flower	46.89	-20.38	57.42	53.50	4.98	1.11	0.32
Days to Maturity	61.53	-20.65	78.15	80.13	13.27	1.13	0.29
Plant Dry Wt.	-325.96	-1375.10	3235.30	3152.17	875.10	--	--
Total Number of Nodes	139.41	-720.46	2495.57	2348.79	213.46	4.23	0.03
Length of Internode	1173.40	1386.33	1712.56	1462.54	252.96	1.21	0.22
# Racemes/Plant	-2.86	-80.78	155.73	163.74	35.02	--	--
# Pods/Plant (X)	37.91	-303.97	439.05	439.03	124.77	3.40	0.03
Length of Pod	475.57	158.42	73.99	53.53	10.01	0.39	1.10
Pod Dry Wt./Plant	-282.39	-822.31	1239.16	1327.05	485.23	--	--
# Seeds/Pod (Y)	0.79	-0.06	0.43	0.37	0.13	0.74	0.44
100-Seed Wt. (Z)	210.89	35.90	42.54	37.26	4.09	0.45	0.90
# Seeds/Plant	2968.64	-14858.78	21810.21	21192.18	4841.99	2.71	0.05
Seed Dry Wt./Plant (W)	-94.08	-449.56	723.53	779.53	245.64	--	--

Table 11. Genetic component of variations (5 x 5, F₂).

	D	F	H ₁	H ₂	E	$\sqrt{H_1/D}$	h ²
Days to 1st Flower	21.70	-27.32	49.80	55.25	12.35	1.52	0.15
Days to Maturity	42.38	43.42	269.36	246.41	6.81	2.52	0.14
Plant Dry Wt.	93.54	-215.70	1534.62	1542.87	176.33	4.05	0.04
Total Number of Nodes	75.30	-417.18	1211.45	1056.34	53.01	4.01	0.04
Length of Internode	668.16	-743.48	2614.26	2163.40	201.05	1.98	0.14
# Racemes/Plant	23.14	-39.65	109.30	102.85	8.77	2.17	0.11
# Pods/Plant (X)	162.21	-187.31	266.32	246.17	41.08	1.28	0.21
Length of Pod	6732.63	-5609.24	4748.85	4514.69	1144.49	0.84	0.31
Pod Dry Wt./Plant	100.34	-6.13	761.23	296.27	99.01	2.75	0.08
# Seeds/Pod (Y)	0.87	0.22	0.12	0.10	0.05	0.38	0.90
100-Seed Wt. (Z)	320.42	147.11	214.99	186.05	2.34	0.82	0.81
# Seeds/Plant	737.13	328.01	247.34	160.15	39.65	0.58	0.90
Seed Dry Wt./Plant (W)	74.13	-28.67	430.57	393.41	59.44	2.41	0.10

Table 12. Days to flowering: array covariances, variances, and their differences (5x5, F_1).

	Wr	Vr	Wr-Vr
	12.8048	23.4551	-10.6503
	18.8084	18.5549	.2535
	4.6747	5.1593	-.4846
	25.3686	35.2405	-9.8719
	16.3206	17.5254	-1.2048
Tot al	77.9770	99.9352	-21.9582

Necessary statistics for plotting limiting parabola.

Wr	Vr
22.962	23.455
20.423	18.555
10.769	5.159
28.145	35.241
19.848	17.525

- \bar{V}_p - (variance of the parents) = 22.479
 \bar{W}_r - (the mean covariance of the parents and the arrays) = 15.595
 \bar{V}_r - (the mean variance of the arrays) = 19.987
 V_r - (the variance of the means of the arrays) = 11.005

Table 13. Days to flowering: array covariances, variances and their differences (8×8 , F_1).

Wr	Vr	Wr-Vr
37.2017	36.3169	0.8848
51.3766	50.5102	0.8663
28.6434	22.6990	6.0444
39.2315	34.5062	4.7253
51.7221	51.3769	0.3452
26.5031	28.9868	-2.4837
16.8240	12.9861	3.8379
15.1304	8.9996	6.1308
Total 266.6328	246.2818	20.3510

Necessary statistics for plotting limiting parabola.

Wr	Vr
48.312	36.317
56.976	50.510
38.111	22.599
47.092	34.506
57.467	51.377
43.162	28.987
28.890	12.986
24.050	9.000

\bar{V}_p - (variance of the parents) = 64.269

\bar{W}_r - (the mean covariance of the parents and the arrays) = 33.329

\bar{V}_r - (the mean variance of the arrays) = 30.785

V_r - (the variance of the means of the arrays) = 18.192

Table 14. Days to flowering: array covariances, variances,
and their differences (5x5, F_2).¹⁶³

	Wr	Vr	Wr-Vr
	15.7880	20.4957	-4.7077
	15.1306	14.9696	.1610
	20.5226	21.1779	-.6553
	23.2061	18.4337	4.7725
	15.8980	16.3349	-.4369
Total	90.5453	91.4118	-.4369

Necessary statistics for plotting limiting parabola.

Wr	Vr
26.235	20.496
22.421	14.970
26.668	21.178
24.880	18.434
23.421	16.335

\bar{V}_p - (variance of the parents) = 33.580
 \bar{W}_r - (the mean covariance of the parents and the arrays) = 18.109
 \bar{V}_r - (the mean variance of the arrays) = 18.282
 \bar{V}_r - (the variance of the means of the arrays) = 11.091

Table 15. Duration of flowering: array covariances, variances, and their differences (5×5 , F_1).

	Wr	Vr	Wr-Vr
	4.2163	2.9153	1.3010
	9.6751	14.1254	-4.4503
	3.4009	19.1637	-15.7628
	-3.0415	9.3287	-12.3702
	2.2319	3.8662	-1.6342
Total	16.4827	49.3992	-32.9166

Necessary statistics for plotting limiting parabola.

Wr	Vr
4.828	2.915
10.627	14.125
12.378	19.164
8.636	9.329
5.560	3.866

V_p - (variance of the parents) = 7.995

\bar{W}_r - (the mean covariance of the parents and the arrays) = 3.297

\bar{V}_r - (the mean variance of the arrays) = 9.880

V_r - (the variance of the means of the arrays) = 2.159

Table 16. Days to maturity: array covariances, variances and their differences (5×5 , F_1).

Wr	Vr	Wr-Vr
.5119	49.0775	-48.5656
19.6605	15.2323	4.4282
37.4017	54.8509	-17.4492
40.9315	69.6673	-28.7358
15.2037	6.1551	9.0486
Total 113.7093	194.9831	-81.2738

Necessary statistics for plotting limiting parabola.

Wr	Vr
48.825	49.077
27.201	15.232
51.617	54.851
58.172	69.667
17.291	6.155

\bar{V}_p - (variance of the parents) = 48.573

\bar{W}_r - (the mean covariance of the parents and the arrays) = 22.742

\bar{V}_r - (the mean variance of the arrays) = 38.997

V_r - (the variance of the means of the arrays) = 14.506

Table 17. Days to maturity: array covariances, variances and their differences (8×8 , F_1).

	Wr	Vr	Wr-Vr
	12.7977	39.1711	-26.3735
	47.9942	72.7896	-24.7953
	63.6142	78.6827	-15.0685
	52.6734	48.9027	3.7707
	34.7439	37.1858	-2.4419
	37.4036	35.6818	1.7217
	24.3398	14.0462	10.2935
	30.2754	24.2070	6.0685
Total	303.8422	350.6669	-46.8248

Necessary statistics for plotting limiting parabola.

Wr	Vr
53.546	39.171
72.992	72.790
75.889	78.683
59.829	48.903
52.171	37.186
51.105	35.682
32.064	14.046
42.093	24.207

V_p - (Variance of the parents) = 73.195
 $\bar{W}r$ - (the mean covariance of the parents and the arrays) = 37.980
 $\bar{V}r$ - (the mean variance of the arrays) = 43.833
 $V\bar{r}$ - (the variance of the means of the arrays) = 20.746

Table 18. Days to maturity: array covariances, variances and their differences (5×5 , F_2).

Wr	Vr	Wr-Vr
.9034	11.1937	-10.2903
1.9365	9.1586	-11.0951
48.8392	54.5959	-5.7568
38.8037	33.2354	5.5683
-4.1837	3.8818	-8.0655
Total 82.4259	112.0654	-29.6394

Necessary statistics for plotting limiting parabola.

Wr	Vr
22.824	11.194
20.645	9.159
50.407	54.596
39.328	33.235
13.441	3.882

V_p - (variance of the parents) = 46.539

\bar{W}_r - (the mean covariance of the parents and the arrays) = 16.485

\bar{V}_r - (the mean variance of the arrays) = 22.413

$V_{\bar{r}}$ - (the variance of the means of the arrays) = 6.876

Table 19. Plant dry weight: array covariances, variances, and their differences (5x5, F₁).

	Wr	Vr	Wr-Vr
	-713.3178	2287.1513	-3000.4691
	-240.9623	628.3488	-869.3111
	1147.0317	3727.0787	-2580.0471
	791.8640	1833.7598	-1041.8958
	-265.3427	261.9819	-527.3246
Total	719.2728	8738.3204	-8019.0476

Necessary statistics for plotting limiting parabola.

Wr	Vr
950.938	2287.151
498.431	628.349
1213.918	3727.079
851.483	1833.760
321.840	261.982

V_p - (variance of the parents) = 395.376

\bar{W}_r - (the mean covariance of the parents and the arrays) = 143.855

\bar{V}_r - (the mean variance of the arrays) = 1747.664

$V_{\bar{r}}$ - (the variance of the means of the arrays) = 141.692

Table 20. Plant dry weight: array covariances, variances, and their differences (8x8, F_1).

Wr	Vr	Wr-Vr
257.5814	1803.9777	-1546.3963
259.5286	724.0860	-464.5574
558.5417	1153.4891	-594.9474
378.6945	936.3962	-557.7017
294.8829	613.4682	-318.5853
251.9716	1669.7756	-1417.8041
-18.1539	439.6740	-457.8279
192.0286	716.9851	-524.9565
2175.0753	8057.8520	-5882.7766

Necessary statistic for plotting limiting parabola.

Wr	Vr
822.565	1803.978
521.134	724.086
657.751	1153.489
592.831	936.396
479.679	613.468
791.377	1669.776
406.088	439.674
518.573	716.985

V_p - (variance of the parents) = 375.067

\bar{W}_r - (the mean covariance of the parents and the arrays) = 371.884

\bar{V}_r - (the mean variance of the arrays) = 1007.231

V_r - (the variance of the means of the arrays) = 249.792

Table 21. Plant dry weight: array covariances, variances, and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	13.9006	76.8356	-62.9350
	8.7019	104.0901	-95.3883
	259.7898	345.1188	-85.3290
	250.0065	285.2190	-35.2124
	-38.2374	26.8669	-65.1043
Total	494.1614	838.1304	-343.9690

Necessary statistics for plotting limiting parabola.

Wr	Vr
130.304	76.836
151.664	104.090
276.161	345.119
251.054	285.219
77.052	26.867

\bar{V}_p - (variance of the parents) = 220.982

\bar{W}_r - (the mean covariance of the parents and the arrays) = 98.832

\bar{V}_r - (the mean variance of the arrays) = 167.626

\bar{V}_r - (the variance of the means of the arrays) = 52.765

Table 22. Number of main stem branches: array covariances, variances, and their differences (5×5 , F_1).

	Wr	Vr	Wr-Vr
	.5330	.5637	-.0307
	2.1284	4.0740	-1.9457
	-.3316	3.1058	-3.4373
	-.1918	.2371	-.4290
	.9712	1.0927	-.1216
Total	3.1091	9.0735	-5.9644

Necessary statistics for plotting limiting parabola.

Wr	Vr
.859	.564
2.309	4.074
2.016	3.106
.557	.237
1.196	1.093

V_p - (variance of the parents) = 1.309

\bar{W}_r - (the mean covariance of the parents and the arrays) = .622

\bar{V}_r - (the mean covariance of the arrays) = 1.815

V_r - (the variance of the means of the arrays) = .515

Table 23. Number of main stem nodes: array covariances, variances and their differences (5x5, F_1).

	Wr	Vr	Wr-Vr
	.4411	.3640	.0771
	1.1018	1.1899	-.0881
	.9919	1.0924	-.1005
	1.4052	1.2930	.1122
	1.1143	.8216	.2927
Total	5.0542	4.7608	.2934

Necessary statistics for plotting limiting parabola

Wr	Vr
.770	.364
1.393	1.190
1.334	1.092
1.452	1.293
1.157	.822

V_p - (variance of the parents) = 1.630

\bar{W}_r - (the mean covariance of the parents and the arrays) = 1.011

\bar{V}_r - (the mean variance of the arrays) = .952

$V_{\bar{r}}$ - (the variance of the means of the arrays) = .669

Table 24. Total number of nodes: array covariances, variances, and their differences (8×8 , F_1).

	Wr	Vr	Wr-Vr
	422.8405	1891.4584	-1468.6179
	338.8424	420.8217	-81.9793
	306.7417	952.9258	-646.1841
	257.5169	546.7503	-289.2333
	334.5537	444.8759	-110.3222
	401.3598	1781.1960	-1379.8362
	-8.6904	253.3750	-262.0654
	80.9154	343.3929	-262.4775
Total	2134.0800	6634.7960	-4500.7159

Necessary statistics for plotting limiting parabola.

Wr	Vr
803.436	1891.458
378.967	420.822
570.272	952.926
431.964	546.750
389.648	444.876
779.666	1781.196
294.059	253.375
342.333	343.393

\bar{V}_p - (variance of the parents) = 341.276
 \bar{W}_r - (the mean covariance of the parents and the arrays) = 266.760
 \bar{V}_r - (the mean variance of the arrays) = 829.349
 V_r - (the variance of the means of the arrays) = 347.593

Table 25. Total number of nodes: array covariances, variances and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	54.5366	154.3764	-99.8397
	117.2463	125.1923	-7.9460
	103.9059	177.3033	-73.3974
	146.5915	230.8118	-84.2203
	80.4161	83.6692	-3.2531
Total	502.6964	771.3530	-268.6565

Necessary statistics for plotting limiting parabola.

Wr	Vr
138.122	154.376
124.383	125.192
148.024	177.303
168.889	230.812
101.685	83.669

\bar{V}_p - (variance of the parents) = 123.580
 \bar{W}_r - (the mean covariance of the parents and the arrays) = 100.539
 \bar{V}_r - (the mean variance of the arrays) = 154.271
 V_r - (the variance of the means of the arrays) = 82.889

Table 26. Length of internode: array covariances, variances, and their differences (8×8 , F_1).

	Wr	Vr	Wr-Vr
	681.5488	558.2203	123.3285
	1387.0026	1992.3983	-605.3937
	1272.0288	1606.1485	-334.1197
	985.3777	988.3466	-2.9690
	954.3713	1182.6354	-228.2640
	1170.5062	1668.3578	-497.8516
	391.4162	164.8066	-226.6096
	636.3754	375.4472	-260.9282
Total	7478.6270	8536.3607	-1057.7337

Necessary statistics for plotting limiting parabola.

Wr	Vr
875.903	558.220
1654.784	1992.398
1485.751	1606.149
1165.488	988.347
1274.907	1182.635
1514.251	1668.358
475.927	164.807
718.336	375.447

\bar{V}_p - (variance of the parents) = 1374.379
 \bar{W}_r - (the mean covariance of the parents and the arrays) = 934.828
 \bar{V}_r - (the mean variance of the arrays) = 1067.045
 V_r - (the variance of the means of the arrays) = 676.769

Table 27. Length of internode: array covariances, variances and their differences (5x5, F_2).

	Wr	Vr	Wr-Vr
	206.4770	104.2895	102.1875
	320.7211	446.1704	-125.4494
	684.4725	708.3345	-23.8620
	518.2200	397.6907	120.5293
	460.0102	599.8999	-139.8898
Total	2189.9007	2256.3851	-66.4844

Necessary statistics for plotting limiting parabola.

Wr	Vr
280.427	104.290
580.030	446.170
730.835	708.335
547.612	397.691
672.573	599.900

\bar{V}_p - (variance of the parents) = 754.050

\bar{W}_r - (the mean covariance of the parents and the arrays) = 437.980

\bar{V}_r - (the mean variance of the arrays) = 451.277

$V_{\bar{r}}$ - (the variance of the means of the arrays) = 289.059

Table 28. Number of racemes per plant: array covariances, variances, and their differences (8×8 , F_1).

	Wr	Vr	Wr-Vr
	35.1979	97.2443	-62.0465
	30.4382	44.8403	-14.4021
	33.8718	65.1401	-31.2683
	22.8495	68.5184	-45.6689
	31.4680	48.4628	-16.9948
	23.8738	78.7383	-54.8645
	2.5745	31.3446	-28.7700
	10.5664	38.9633	-28.3969
Total	190.8400	473.2520	-282.4120

Necessary statistics for plotting limiting parabola.

Wr	Vr
56.595	97.244
38.431	44.840
46.320	65.140
47.506	68.518
39.953	48.463
50.925	78.738
32.131	31.345
35.824	38.963

\bar{V}_p - (variance of the parents) = 32.937

\bar{W}_r - (the mean covariance of the parents and the arrays) = 23.855

\bar{V}_r - (the mean variance of the arrays) = 59.156

V_r - (the variance of the means of the arrays) = 18.071

Table 29. Number of racemes per plant: array covariances, variances and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	13.8801	15.7573	-1.8772
	24.5333	24.7781	-.2448
	12.5687	14.3410	-1.7723
	19.0418	20.9910	-1.9491
	20.5889	18.4717	2.1172
Total	90.6128	94.3391	-3.7262

Necessary statistics for plotting limiting parabola.

Wr	Vr
21.314	15.757
26.727	24.778
20.334	14.341
24.600	20.991
23.077	18.472

- V_p - (variance of the parents) = 28.830
 \bar{W}_r - (the mean covariance of the parents and the arrays) = 18.123
 \bar{V}_r - (the mean variance of the arrays) = 18.868
 V_r - (the variance of the means of the arrays) = 11.443

Table 30. Number of pods per plant: array covariances, variances and their differences (5x5, F_1).

	Wr	Vr	Wr-Vr
	411.3968	1309.9542	-898.5573
	264.7316	293.7758	-29.0442
	239.5299	1000.3238	-760.7939
	100.0836	169.8571	-69.7735
	144.3925	174.6483	-30.2558
Total	1160.1344	2948.5591	-1788.4247

Necessary statistics for plotting limiting parabola.

Wr	Vr
614.975	1309.954
291.231	293.776
537.403	1000.324
221.448	169.857
224.549	174.648

\bar{V}_p - (variance of the parents) = 288.708
 \bar{W}_r - (the mean covariance of the parents and the arrays) = 232.027
 \bar{V}_r - (mean variance of the arrays) = 589.712
 V_r - (the variance of the means of the arrays) = 205.585

Table 31. Number of pods per plant: array covariances, variances, and their differences (8x8, F_1).

	Wr	Vr	Wr-Vr
	150.9662	328.5792	-177.6131
	133.2383	147.4411	-14.2027
	119.2898	221.0860	-101.7962
	46.8678	144.6902	-97.8224
	128.0412	125.0402	3.0010
	83.3472	228.3354	-144.9881
	98.6967	144.3408	-45.6440
	112.7087	182.6606	-69.9518
Total	873.1559	1522.1733	-649.0174

Necessary statistics for plotting limiting parabola.

Wr	Vr
226.230	328.579
151.544	147.441
185.571	221.086
150.124	144.690
139.558	125.040
188.589	228.335
149.942	144.341
168.675	182.661

\bar{y}_p - (variance of the parents) = 155.761
 \bar{w}_r - (the mean covariance of the parents and the arrays) = 109.144
 \bar{v}_r - (the mean variance of the arrays) = 190.272
 \bar{v}_r - (the variance of the means of the arrays) = 82.560

Table 32. Number of pods per plant: array covariances, variances, and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	109.4022	85.2360	24.1662
	157.1892	148.2594	8.9298
	59.1199	52.5758	6.5441
	94.2196	69.1782	25.0414
	113.6461	78.3462	35.2999
Total	533.5771	433.5956	99.9814

Necessary statistics for plotting limiting parabola.

Wr	Vr
125.243	85.236
165.179	148.259
98.364	52.576
112.831	69.178
120.075	78.346

V_p - (variance of the parents) = 184.029

\bar{W}_r - (the mean covariance of the parents and the arrays) = 106.715

\bar{V}_r - (the mean variance of the arrays) = 86.719

V_r - (the variance of the means of the arrays) = 63.657

Table 33. Length of pod: array covariances, variances, and their differences (8×8 , F_1).

	Wr	Vr	Wr-Vr
	282.1517	172.1475	110.0042
	187.1875	77.1015	110.0860
	298.0238	194.0591	103.9648
	208.7491	96.0566	112.6925
	195.1987	145.4165	49.7823
	157.5953	57.6305	99.9647
	141.0955	49.2912	91.8043
	180.0945	72.0393	108.0551
Total	1650.0961	863.7423	786.3538

Necessary statistics for plotting limiting parabola.

Wr	Vr
287.751	172.148
192.574	77.102
305.515	194.059
214.946	96.057
264.468	145.416
166.492	57.631
153.975	49.291
186.145	72.039

\bar{V}_p - (variance of the parents) = 480.986

\bar{W}_r - (the mean covariance of the parents and the arrays) = 206.262

\bar{V}_r - (the mean variance of the arrays) = 107.968

V_r - (the variance of the means of the arrays) = 89.988

Table 34. Length of pod: array covariances, variances, and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	211.2778	78.5769	132.7008
	359.3604	218.9639	140.3966
	301.0073	160.0556	140.9517
	246.7677	105.0833	141.6844
	313.8754	192.3400	121.5353
Total	1432.2885	755.0197	677.2688

Necessary statistics for plotting limiting parabola.

Wr	Vr
215.301	78.577
359.405	218.964
307.279	160.056
248.980	105.083
336.847	192.340

\bar{V}_p - (variance of the parents) = 589.923

\bar{W}_r - (the mean covariance of the parents and the arrays) = 286.458

\bar{V}_r - (the mean variance of the arrays) = 151.004

V_r - (the variance of the means of the arrays) = 139.924

Table 35. Pod dry weight per plant: array covariances, variances, and their differences (5x5, F_1).

	Wr	Vr	Wr-Vr
	-483.7266	1070.2868	-1554.0134
	-66.9011	238.8275	-305.7287
	740.7012	1985.1808	-1244.4797
	544.9569	1088.7864	-543.8294
	-136.3319	125.3896	-261.7215
Total	598.6985	4508.4712	-3909.7728

Necessary statistics for plotting limiting parabola.

Wr	Vr
576.099	1070.287
272.138	238.828
784.597	1985.181
581.056	1088.786
197.187	125.390

V_p - (variance of the parents) = 310.094

\bar{W}_r - (the mean covariance of the parents and the arrays) = 119.740

\bar{V}_r - (the mean variance of the arrays) = 901.694

V_r - (the variance of the means of the arrays) = 90.423

Table 36. Pod dry weight per plant: array covariances, variances, and their differences (8×8 , F_1).

	Wr	Vr	Wr-Vr
	25.0364	536.7740	-511.7375
	121.0250	351.8647	-230.8397
	273.6165	580.3621	-306.7456
	224.4278	533.3928	-308.9650
	139.5937	278.7339	-139.1402
	158.5120	645.6067	-487.0947
	-69.0218	160.9872	-230.0090
	34.9289	316.4985	-281.5696
Total	908.1185	3404.2199	-2496.1014

Necessary statistics for plotting limiting parabola.

Wr	Vr
208.951	536.774
250.139	351.865
321.250	580.362
307.976	533.393
222.632	278.734
338.826	645.607
169.196	160.987
237.235	316.499

V_p - (variance of the parents) = 177.822

\bar{W}_r - (the mean covariance of the parents and the arrays) = 113.515

\bar{V}_r - (the mean variance of the arrays) = 425.527

V_r - (the variance of the means of the arrays) = 95.067

Table 37. Pod dry weight per plant: array covariances, variances, and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	23.7799	45.8021	-22.0223
	23.0879	48.7255	-25.6376
	170.4483	188.5391	-18.0908
	138.7417	128.0535	10.8882
	-9.6865	2.6532	-12.3397
Total	346.5712	413.7734	-67.2022

Necessary statistics for plotting limiting parabola.

Wr	Vr
87.199	45.802
89.938	48.725
176.916	188.539
145.802	128.054
20.987	2.653

V_p - (variance of the parents) = 166.010
 \bar{W}_r - (the mean covariance of the parents and the arrays) = 69.314
 \bar{V}_r - (the mean variance of the arrays) = 82.755
 $V_{\bar{r}}$ - (the variance of the means of the arrays) = 34.618

Table 38. Number of seeds per pod: array covariances, variances, and their differences (5×5 , F_1).

	Wr	Vr	Wr-Vr
	.2485	.1982	.0503
	.1419	.1410	.0009
	.3086	.3116	-.0030
	.0972	.1089	-.0118
	.1798	.2595	-.0797
Total	.9760	1.0192	-.0432

Necessary statistics for plotting limiting parabola.

Wr	Vr
.342	.198
.289	.141
.429	.312
.254	.109
.391	.259

V_p - (variance of the parents) = .591

\bar{W}_r - (the mean covariance of the parents and the arrays) = .195

\bar{V}_r - (mean variance of the arrays) = .204

V_r - (the variance of the means of the arrays) = .081

Table 39. Number of seeds per pod: array covariances, and their differences (8×8 , F_1).

	Wr	Vr	Wr-Vr
	.3867	.4483	-.0617
	.4652	.3234	.1418
	.6061	.5688	.0373
	.4548	.3611	.0937
	.5338	.3918	.1420
	.4681	.3188	.1492
	.3802	.2121	.1681
	.3029	.2374	.0655
Total	3.5977	.2374	.7360

Necessary statistics for plotting limiting parabola.

Wr	Vr
.628	.448
.533	.323
.708	.568
.564	.361
.587	.392
.530	.319
.432	.212
.457	.237

\bar{V}_p - (variance of the parents) = .880

\bar{W}_r - (the mean covariance of the parents and the arrays) = .450

\bar{V}_r - (the mean variance of the arrays) = .358

V_r - (the variance of the means of the arrays) = .248

Table 40. Number of seeds per pod: array covariances, variances, and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	.4556	.2350	.2206
	.4040	.1919	.2121
	.3574	.1568	.2007
	.3933	.1907	.2026
	.4678	.2571	.2108
Total	2.0782	1.0314	1.0468

Necessary statistics for plotting limiting parabola.

Wr	Vr
.460	.235
.416	.192
.376	.157
.415	.191
.481	.257

\bar{V}_p - (variance of the parents) = .902

\bar{W}_r - (the mean covariance of the parents and the arrays) = .416

\bar{V}_r - (the mean variance of the arrays) = .206

V_r - (the variance of the means of the arrays) = .193

Table 41. 100-seed weight: array covariances, variances and their differences (5×5 , F_1).

	Wr	Vr	Wr-Vr
	202.5222	131.7357	70.7865
	199.9750	114.0080	85.9670
	94.6029	28.3491	66.2538
	121.0468	45.8792	75.1676
	217.9625	176.2460	41.7165
Total	836.1094	496.2180	339.8915

Necessary statistics for plotting limiting parabola.

Wr	Vr
216.376	131.736
201.291	114.008
100.375	28.349
127.692	45.879
250.275	176.246

- V_p - (variance of the parents) = 355.398
 \bar{W}_r - (the mean covariance of the parents and the arrays) = 167.222
 \bar{V}_r - (mean variance of the arrays) = 99.244
 V_r - (the variance of the means of the arrays) = 80.813

Table 42. 100-seed weight: array covariance, variances, and their differences (8x8, F_1)

Wr	Vr	Wr-Vr
137.3270	95.5322	41.7947
129.9318	81.2738	48.6580
67.3029	25.0819	42.2210
92.3470	43.2586	49.0883
129.8178	106.4716	23.3462
69.5279	27.5020	42.0259
65.1596	22.9448	42.2147
78.6573	31.7742	46.8831
770.0712	433.8393	336.2319

Necessary statistics for plotting limiting parabola.

Wr	Vr
142.972	95.532
131.872	81.274
73.258	25.082
96.208	43.259
150.398	106.472
76.711	27.502
70.068	22.945
82.454	31.774

\bar{V}_p - (variance of the parents) = 213.968

\bar{W}_r - (the mean covariance of the parents and the arrays) = 96.259

\bar{V}_r - (the mean variance of the arrays) = 54.230

V_r - (the variance of the means of the arrays) = 44.126

Table 43. 100-seed weight: array covariances, variances and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	93.8971	30.3831	63.5141
	184.6897	103.1299	81.5598
	99.1678	30.8048	68.3630
	106.5742	34.7113	71.8628
	246.1807	180.8131	65.3675
Total	730.5095	379.8423	350.6672

Necessary statistics for plotting limiting parabola.

Wr	Vr
101.034	30.383
186.143	103.130
101.733	30.805
107.991	34.711
246.473	180.813

V_p - (variance of the parents) = 335.975

\bar{W}_r - (the mean covariance of the parents and the arrays) = 146.102

\bar{V}_r - (the mean variance of the arrays) = 75.968

V_r - (the variance of the means of the arrays) = 64.484

Table 44. Number of seeds per plant: array covariances, variances, and their differences (5×5 , F_1).

	Wr	Vr	Wr-Vr
	8567.44	39929.99	-31362.55
	7387.96	8203.13	-815.17
	14150.35	38103.55	-23953.20
	7003.41	10019.62	-3016.22
	3387.42	5153.76	-1766.34
Total	40496.58	101410.05	-60913.47

Necessary statistics for plotting limiting parabola.

Wr	Vr
20399.95	39929.99
9246.33	8203.13
19927.94	38103.55
10218.93	10019.63
7328.95	5153.76

V_p - (variance of the parents) = 10422.19

$\bar{W}r$ - (the mean covariance of the parents and the arrays) = 8099.316

$\bar{V}r$ - (mean variance of the arrays) = 20282.010

$V\bar{r}$ - (the variance of the means of the arrays) = 7024.339

Table 45. Number of seeds per plant: array covariances, variances, and their differences (8×8 , F_1).

	Wr	Vr	Wr-Vr
	8051.27	22634.37	-14583.10
	5365.11	4880.91	484.19
	8612.49	15345.70	-6733.21
	4772.83	6704.89	-1932.05
	4237.89	3496.28	741.60
	6739.55	15798.86	-9059.32
	4753.22	6342.66	-1589.44
	3342.64	4153.08	-809.45
Total	45875.98	79356.75	-33480.77

Necessary statistics for plotting limiting parabola.

Wr	Vr
13075.85	22634.37
6072.06	4880.91
10766.61	15345.70
7116.75	6704.89
5139.13	3496.28
10924.43	15798.86
6921.84	6342.66
5601.07	4153.08

\bar{V}_p - (variance of the parents) = 7553.909

\bar{W}_r - (the mean covariance of the parents and the arrays) = 5734.498

\bar{V}_r - (the mean variance of the arrays) = 9919.594

V_r - (the variance of the means of the arrays) = 4622.845

Table 46. Number of seeds per plant: array covariances, variances, and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	4321.90	3412.52	909.38
	4659.35	3423.64	1235.71
	3500.61	2206.07	1294.54
	4660.36	3394.40	1265.97
	3569.40	2061.17	1508.23
Total	20711.62	14497.79	6213.83

Necessary statistics for plotting limiting parabola.

Wr	Vr
4992.160	3412.519
5000.285	3423.636
4013.842	2206.067
4978.886	3394.396
3879.787	2061.170

V_p - (variance of the parents) = 7303.010

\bar{W}_r - (the mean covariance of the parents and the arrays) = 4142.324

\bar{V}_r - (the mean variance of the arrays) = 2899.558

V_r - (the variance of the means of the arrays) = 2400.653

Table 47. Seed dry weight per plant: array covariances, variances, and their differences (5×5 , F_1).

	Wr	Vr	Wr-Vr
	-269.3118	573.9881	-843.2999
	-61.3609	165.8638	-227.2247
	403.2444	1093.4786	-690.2342
	308.3806	663.6575	-355.2768
	-69.3422	98.3472	-167.6894
Total	311.6102	2595.3352	-2283.7250

Necessary statistics for plotting limiting parabola.

Wr	Vr
306.253	573.988
164.628	165.864
422.702	1093.479
329.307	663.657
126.768	98.347

V_p - (variance of the parents) = 163.402

$\bar{W}r$ - (the mean covariance of the parents and the arrays) = 62.322

$\bar{V}r$ - (mean variance of the arrays) = 519.067

$V\bar{r}$ - (the variance of the means of the arrays) = 46.819

Table 48. Seed dry weight per plant: array covariances, variances, and their differences (8×8 , F_1).

	Wr	Vr	Wr-Vr
	10.4517	210.5904	-200.1387
	102.0296	251.7684	-149.7388
	178.2754	206.8470	-128.5716
	174.7507	367.3232	-192.5725
	103.1487	181.9810	-78.8322
	161.9645	430.4944	-268.5299
	-36.8704	101.2156	-138.0860
	13.7114	247.0833	-233.3718
Total	707.4617	2097.3033	-1389.8416

Necessary statistics for plotting limiting parabola.

Wr	Vr
166.054	210.590
181.564	251.768
200.443	306.847
219.308	367.323
154.363	181.981
237.418	430.494
115.121	101.266
179.867	247.083.

\bar{V}_p - (variance of the parents) = 130.936

\bar{W}_r - (the mean covariance of the parents and the arrays) = 88.433

\bar{V}_r - (the mean variance of the arrays) = 262.163

V_r - (the variance of the means of the array) = 66.675

Table 49. Seed dry weight per plant: array covariances, variances, and their differences (5×5 , F_2).

	Wr	Vr	Wr-Vr
	19.9308	45.5948	-25.6640
	19.8373	32.9696	-13.1322
	110.2897	114.7157	-4.4260
	110.9398	118.9813	-8.0415
	3.9887	.4656	3.5232
Total	264.9863	312.7269	-47.7406

Necessary statistics for plotting limiting parabola.

Wr	Vr
71.936	45.595
61.171	32.970
114.104	114.716
116.206	118.981
7.269	.466

\bar{V}_p - (variance of the parents) = 113.496

\bar{W}_r - (the mean covariance of the parents and the arrays) = 52.997

\bar{V}_r - (the mean variance of the arrays) = 62.545

V_r - (the variance of the means of the arrays) = 29.046

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