QUANTITATIVE INHERITANCE STUDIES IN THE GARDEN PEA (*Pisum sativum* L.)

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ABSTRACT

A quantitative inheritence study of leaf form in the garden pea, *Pisum sativum* L., was carried out using an eight parent F_1 half diallel cross. The inheritance of yield and its components were also studied.

The parental lines used for the diallel contained combinations of the following genes which act in the homozygous recessive condition = *af* converts normal pea leaflets to tendrils, *tl* converts normal pea tendrils to leaflets and *st* reduces the size of the stipule. A combination of *af* and *tl* together results in a mass of small leaflets.

The characters measured included length, width, areas and weights of leaflets, stipules and tendrils and the components of yield. The data from the twenty-eight F_1 crosses and their eight parents were analysed with Hayman-Jinks diallel method. The adequacy of the additive-dominance model was determined by the relationships of Wr and Vr: the analysis of variance of (Wr - Vr), the Wr on Vr regression analysis and the WrVr graphical analysis.

The results indicated the predominance of additive genetic variance for the vegetative characters although dominance variance and non-allelic interactions were important. The inheritance of yield and its components were mainly attributable to additive genetic variance while the type of dominance varied from partial to complete for both types of characters. Heritabiity was high for the vegetative characters and medium to low for the components of yield.

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INTRODUCTION

Peas, together with green beans, broadbeans, chickpeas and lentils are some of the more important types of edible temperate legumes. Peas provide a source of human dietary protein which complements the carbohydrate component of the cereals (Duckworth 1966).

Although the early history and the early progenitors of peas are not known, the cultivation of the pea is considered to be as ancient as that of wheat and barley (Zohary and Hopf 1973). Probable centres of origin have been suggested by Vavilov (1949) and these include: Ethiopia, the Mediterranean and Central Asia, with a secondary centre of diversity in the New East.

Traditionally the pea has been used as a fresh vegetable or in the form of the dry seed, either as split peas for soup or canned. In recent years the use of the crop has changed. A portion of the world pea crop, mainly in the developed countries is now harvested at an immature stage and frozen. This product has become one of the more important modern convenience foods (Pate 1977).

In New Zealand, the "garden pea", *Pisum sativum* L. is the most widely grown of all horticultural crops with 8000 hectares under production annually (Anon 1981). The bulk of the crop is processed by quick freezing and small proportions are canned or utilised as a fresh vegetable. As an export crop, frozen peas are valuable. They earned $6.2 million in foreign exchange in 1979-80 (Bolland 1981). The "field" or "dried" pea, *Pisum arvense* L. makes up the largest proportion of the New Zealand pea crop, producing $14 million in export returns in 1980 while seed peas were worth slightly less (Anon 1981).

The main requirement for the production of peas suited to the freezing industry is the necessity for harvesting

all peas at a given stage of maturity. As the optimum time of harvest is confined to a period of hours rather than days, the efficiency of the harvesting operation is important. Part of this efficiency is determined by the through-put of peas through a mobile pea viner. Through-put is decreased by excessive vegetative growth (Snoad 1974). Excessive vegetative growth however, is not a serious problem with the use of the "pod picker" harvesting machinery.

Another problem which may arise is that the pea crop is prone to lodging or the collapsing of the canopy (Davies 1977a). Prior to harvest the increase in weight of the pea pod will almost invariably cause the plants to collapse. This is due to the weakness of the basal region of the stem in relation to the weight of the upper part of the plant. This can result in an increase in humidity within the crop, leading to pathogen attack and to a reduction in quality of the peas through the pods contact with the soil. Also a yield reduction may occur because of a restriction in assimilate transport through the stem.

Recent research has attempted to solve these problems by altering the morphology of the pea plant, particularly the leaves and stipules. This work has been reviewed by Davies (1977b) and Snoad (1980). The objective of this study was to estimate the quantitative inheritance of the vegetative structures, the leaves, stipules and tendrils, using different foliage types. Quantitative inheritance of the yield components of these altered phenotypes was also investigated.

REVIEW OF LITERATURE

1.1 The pea crop

The pea crop has two important defects: its proneness to lodging or collapsing of the canopy and the excessive amounts of vegetative growth produced (Snoad *et al* 1971, Snoad 1973, 1975, Davies 1977a). This can effect pea yield and quality, and the efficiency of the harvesting operation.

In recent years pea breeders have overcome some of these problems. This has been achieved with the incorporation of genes which can modify the morphology of the plant, particularly leaves and stipules (Snoad *et al* 1971, Snoad 1973, Snoad *et al* 1974, Ali 1980).

1.2 Pea genetics

1.2.1 The Normal Pea leaf

The normal pea leaf is compound, usually pinnate with one or more pairs of leaflets. The petiole has two large stipules at its base and ends in several tendrils (Blixt 1974, Sutcliffe and Pate 1977). During ontogenesis the leaf goes through a series of metamorphoses (Blixt 1974). The scale leaves are followed by approximately three simpler leaves with one pair of leaflets and one terminal tendril. Full complexity is reached at about the time of appearance of the seventh leaf; the number and combination of leaflets and tendrils being characteristic for a particular genotype. Blixt (1972) notes at the end of ontogenesis there is a slight tendency to return to greater simplicity.

1.2.2 Foliage Mutants

The morphology of the normal pea leaf is subject to modification by a number of genes (Blixt 1972, 1974). Genes which have an effect on the foliage of the plant include: "latum", *lat*[1], (Lamm 1957) increasing foliage area; "elongata", *elo* (Kellenbarger 1952); "folia oblonga", *fo* (Harstedt 1950); *y* (Brotherton 1923) reduces foliage width; "maximo-reductus", *mare* (Blixt 1972) foliage is thread like and reduced; "narrow rouge", *nr* (Blixt 1972) foliage narrow with pointed apex; "reductus", *red* (Lamprecht 1948) and "tenuifolius", *ten* (Lamprecht 1949) result in narrow leaflets; "unipetiole", *up* (Rosen 1944, Lamprecht 1963, Snoad and Davies 1972) has only one pair of leaflets; "Rogue" *X* (Mathews 1970, Brotherton 1923) foliage and pods narrow with pointed apices; sinuate leaf, *Sil* (Marx 1977); notched leaf, *nol*, (Sharma 1972b); and "insectus", *ins* (Lamprecht 1959) causes a deeply incised leaflet apex.

The "clavicula" gene, *tl*, produces the "acacia" phentotype where tendrils are replaced by leaflets (Vilmorin 1910, Vilmorin and Bateson 1912, White 1917, Lamm 1957). Wellensiek (1959) has produced this phenotype by neutron radiation. In the heterozygous form the tendrils are slightly strap-shaped (Sverdrup 1927, Nilsson 1933). Another allele at the *tl* locus was reported by Lamm (1957). This type of acacia phenotype, tl^{pet}, has extended petioles and is recessive to the short petioled form, tl^{w} (= *tl* earlier) (Solovjeva 1958, Khangildin 1966). The acacia type has been shown to be linked with wrinkled seed (Pellew 1913, Vilmorin 1910, Vilmorin and Bateson 1912). A recombination fraction of 0.0159 was reported by Vilmorin and Bateson (1912).

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1 NOTE: Throughout the text capitalized gene symbols indicate that the mutant in question is dominant and the lower-case symbols refer to genes that are recessive to the normal.

1.2.3 Stipules

A number of separate genes can influence stipules. Blixt (1972) reports cases where stipules may become longer, increased in size or narrower than normal. The gene, *st*, results in a reduction in stipule size (Pellew and Sverdrup 1923). Other genes affecting stipules include the "Cochleata" gene, *coch*, which results in spoon-shaped stipules on a long petiole (Wellensiek 1959, 1962, Marx and Mishanec 1970); "stipula imminata", *stim*, (Lamprecht 1960) causes stipula to be narrow and diamond shaped; and *cist* (Kumar and Sharma 1975) results in a circular stipule.

Several genes affect both the size of leaflets and stipules. The gene "tenuifolius", *ten*, produces narrower leaflets and stipules than the normal type (Lamprecht 1949, Yarnell 1962); "Lathyroides", *lath*, results in leaflets and stipules which are pointed and narrow (Lamprecht 1959b). Genes which increase length and breadth ratios of leaflets have similar effects on stipules. Four independent genes are involved, these are *fo*, *fob*, *fol* and *Fom* (Yarnell 1962).

The reduced stipule form, *st*, is recessive to the normal (Pellew and Sverdrup 1923, Sverdrup 1927), however Brotherton (1923) found dominance for a similar smaller form. This was the result of using the "rogue" pea (Bateson and Pellew 1915, 1920) which always behaves as a dominant, giving a very peculiar form of segregation.

1.2.4 Tendrils

The action of the "afila" gene, *af*, results in the leaflets of a pea plant being transformed into tendrils (Kujala 1953, Solovjeva 1958). The recessive condition of afila in the presence of the acacia, *tl*, background (*afaftltl* genotype) results in a mass of small leaflets (Goldenberg

1965) and can cause in an increase in total leaf area (Harvey 1972). Another gene, the tendrilled acacia, *tac*, produces a leaf with tendrils and an apical leaflet (Sharma 1972a, Sharma and Arabindan 1972, Sharma *et al* 1972).

Marx (1977) reports a pea phenotype where adventitous tendrils arise from clefts in the tips of stipules. This occurs when the sinuate leaf mutant, *sil*, is in combination with the afila background.

1.3 Modified plant types

1.3.1 Agronomic aspects

Of all the genes which can modify the pea plant, three have received considerable attention during the last decade. These are the *af*, *st* and *tl* types. They form the genetic basis of the "leafless", *afst* , and "semi-leafless", *af* forms.

Yield evaluations[2] have shown that pea cultivars containing these genes have yields equivalent to those of the conventional types (Snoad 1974, Snoad and Gent 1975, 1976, Goldberg 1973). Solovjeva (1958) has reported increased yields with semi-leafless cultivars. Snoad *et al* (1977) in describing the fruiting characteristics of one normal and three recessive foliar mutants showed the recessive genes individually had little effect upon yield. However in combination they caused a significant reduction in the yield of a single plant. Similar results were obtained by Harvey (1978) and Harvey and Goodwin (1978). Gritton (1972) recorded lower yields with leafless and semileafless types compared with the normal, however he was dealing with heterozygous plants within heterogeneous populations. Snoad (1981) also obtained lower yields, although the leafless type had a higher harvest index.

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[2] NOTE: Yield results discussed in this section include both green pea and dry pea yields.

The reasons given for differences in yield between conventional and modified leaf types include the variation in the adaptation of the genotype to environment and the genetic background of the cultivar. Lafond *et al* (1981) using near-isogenic lines from two different genetic backgrounds have shown the importance of the genetic background.

The single plant yield reductions observed can be overcome by increasing plant density through the use of higher seeding rates. Hedley and Ambrose (1979) studied the effect of shading on the yield components of different leaf genotypes. They showed there was no source limitation to the yield of these types at normal light intensities. Further work with a range of plant densities (Hedley and Ambrose 1980) showed conventional peas only outyielded the other types at lower densities but not at higher densities. These observations could suggest that the contrasting yield trial results have arisen from competition effects.

1.3.2 Physiological Studies

Physiological studies carried out on leafless and semileafless peas (Harvey 1972, 1974) have shown that these types have a similar photosynthetic efficiency to the conventional pea in relation to carbon dioxide uptake per unit area of leaf or tendril. The pattern of translocation is also similar (Harvey 1974).

In terms of seed production per plant the normal stipules of the semileafless phenotype can virtually compensate for the reduced photosynthetic area. Similarly the leaves appear to be able to compensate for the genetic reduction in stipule area (Snoad *et al* 1977, Harvey 1978). The components of yield have also been examined (Harvey 1978, Harvey and Goodwin 1978). In considering the water requirements in relation to seed production, Harvey (1980) showed that leafless phenotypes utilized less water and correspond-

ingly produced a lower total seed dry-weight than the conventional pea. Wilson *et al* (1981) found that semi-leafless peas made more efficient use of water under dry conditions than the normal pea type. The results from all these physiological studies indicated that the altered plant types are not radically different physiologically to the normal types.

1.4 Components of Yield

A knowledge of the factors which determine yield and the environmental effects influencing it are necessary for an understanding of the inheritance of the components of yield.

Handwick and Milbourn (1967) have partitioned the final yield of a green pea plant into the following components:

$$\text{Yield} = \begin{matrix}\text{Number of}\\\text{Podding Nodes}\end{matrix} \times \begin{matrix}\text{Pods per}\\\text{Node}\end{matrix} \times \begin{matrix}\text{Peas per}\\\text{Pod}\end{matrix} \times \begin{matrix}\text{Weight}\\\text{per pea}\end{matrix}$$

Another component, the lateral branch is considered relatively unimportant as it contributes to only a small fraction of the total yield under commercial conditions (Snoad 1981b). Pods formed on the lateral branches are usually less mature than those on the main stem. Higher plant densities will decrease the number of branches (Kruger 1977).

1.4.1 Number of podding nodes

Flowering of peas commences after the shoot apex switches to the production of flower primordia in the leaf axil and the development of primordia into mature open flowers (Murfet 1977). The flower initials develop in the axils

of successive leaves until the senescence of the apical meristem (Hole and Hardwick 1976). This senescence is a result of developing fruits (Lockhart and Gottschalk 1961) and also to flower inhibitors produced by the *Sn* gene (Reid 1980). A longer vine length can provide more fruiting nodes and this may contribute to an increased yield. However a lengthy vine is an undesirable characteristic for processing peas. It results in a wider range of maturity, decreases the harvesting efficiency due to the greater through-put required through the viner, increases lodging and reduces light transmission through the canopy (Snoad 1974).

1.4.2 Number of pods per node

The inflorescence of the pea plant is a raceme. The number of flowers on each inflorescence varies from one to several (Blixt 1972). However the eventual number of pods per node at harvest depends on a series of developmental processes. The maxiumum number of flowers is characteristic of a particular genotype (Yarnell 1962) and the actual number depends on the environmental condition at flower initiation (Hole and Hardwick 1976). A reduction in the number of flowers or pods formed can occur with either flower abortion or pod abscission (Meadley and Milbourn 1970).

1.4.3 Number of peas per pod

Terasvouri (1915) reported the number of ovules per ovary in the pea ranges from four to twelve. Most cultivars have between seven and nine ovules per ovary.

Environmental conditions influence ovule number although it is less sensitive than seed number (Manner 1958, Linck 1961). Linck (1961) studying embryo failure in the cultivar *Alaska* found a third of the embryos failed to

develop. Failure was most frequent with the ovules in the end positions of the pod. Similar results were reported by Manner (1958). Lack of fertilization was not considered to be the cause of embryo mortality. Pate and Flinn (1977) observed high frequencies of abortion of ovules in peas grown under adverse environmental conditions.

1.4.4 Weight per pea

The weight of green peas per pod is controlled by the maturity of the pea and to a lesser extent by its size. This may be influenced by management practices such as irrigation.

Anderson and White (1974b) and also Maurer *et al* (1968) studied the effect of plant density and irrigation on pea size. Irrigation of plants grown at lower densities resulted in more podding nodes which were less mature and smaller in size than those grown at higher densities.

With the onset of maturity there is an accumulation of starch in the pea seed. Pate and Flinn (1977) found up to 45 percent of the total dryweight in round seeded types and 35 percent total dryweight in wrinkled pea types was starch. The increase in yield over the stage at which peas are harvested as a function of time is a non-linear relationship (Anderson and White 1974a). Lynch and Mitchell (1953) have shown that quality changes over this period, it reaches an optimum level then declines. Sykes (1953) considered the quality factors of tenderness and flavour to be strongly dependant upon the stage of maturity of the pea.

1.4.4.1 Pea Maturity

A number of methods have been used to estimate the level of maturity of the pea. Many of these are discussed by Lynch and Mitchell (1953) and by Torfason *et al* (1956).

The more common methods used are;

(i) the tenderometer (Martin 1937),
(ii) the maturometer (Lynch and Mitchell 1953) and
(iii) the alcohol insoluble-solids content (Kertesz 1934, 1935).

The tenderometer measures the resistance of a constant volume of peas to the shearing forces of two grids; the tougher the peas, the greater the resistance and hence the higher the maturity. The maturometer measures the mass resistance of peas to puncturing by steel pins, the more resistant, the more mature. The alcohol insoluble-solids test is a chemical analysis which measures starches, hemicelluloses, fibre and proteins, the sugars are dissolved. The proportion of the insoluble compounds increases with the advancement of maturity. Comparisons between the different methods have been discussed by Sayre (1954), Adam (1957) and Ottoson (1968). A good correlation exists between the alcohol soluble solids chemical method and that of the widely used tenderometer.

1.5 Quantitative Genetics

1.5.1 Introduction

Quantitative genetics has been defined by Falconer (1981) as the study of the inheritance of continuous characters. Quantitative genetics is based on the assumption that continuous characters are determined by genes which behave in the same way as the genes of major effect which control discrete characters. However the distinct classes of the classical mendelian methods do not occur.

1.5.2 Partitioning genetic variance

The basis of quantitative genetics is the partitioning of the phenotypic value of a character for an individual

into components attributable to the influence of the genes and of the environment (Johannsen 1903, 1909).

$$P = G + E$$

where P is the phenotypic value, G is the genotypic value and E is the environmental deviation.

The genotypic value can be further divided into three components (Kempthorne 1954, 1955, Cockerham 1954):

$$G = A + D + I$$

where A is the sum of the additive effects of genes at all loci or the average gene effect; D is the sum of dominance deviations (or intra-locus interaction effects) and I is the sum of the inter-loci interactions or epistatic effects of genes at two or more loci.

The additive genetic component arises from the differences of a pair of corresponding homozygotes (Mather and Jinks 1971, 1977). It is the departure of one of the homozygotes from the midparent or origin. It is positive for the homozygote with the increasing allele and negative for that with the decreasing allele.

The dominance component results from the departure of the heterozygote from the mean of the corresponding pair of homozygotes (Mather and Jinks 1971, 1977). It is positive when the heterozygote is similar to the higher homozygote and negative when it is more like the lower homozygote.

Non-allelic interaction arises from the modification of the additive and dominance effects at one locus resulting from allelic substitution at other loci.

The variances of these values are the parameters estimated from quantitative genetic experiments (Fisher *et al* 1932, Mater 1949).

$$\sigma^2_P = \sigma^2_G + \sigma^2_E$$

and

$$\sigma^2_G = \sigma^2_A + \sigma^2_D + \sigma^2_I$$

The epistatic effects can be further partitioned (Cockerham 1954).

$$\sigma^2 I = \sigma^2 AA + \sigma^2 AD + \sigma^2 DD$$

Where $\sigma^2 AA$ is the additive x additive variance, $\sigma^2 AD$ the additive x dominance interaction and $\sigma^2 DD$ the dominance x dominance variance. The environmental variance, $\sigma^2 E$, can be partitioned in other ways also, depending upon experimental design (Le Clerg *et al* 1962, Comstock and Moll 1963).

1.5.3 Experimental designs

The simplest of the experimental mating designs used to obtain estimates of genetical components are the basic generations and random biparental matings.

The basic generation consist of F2, first backcrosses B1 and B2 and an F1 for a cross between a pair of pure-breeding lines P1 and P2 (Mather and Vines 1952, Opsahl 1956, Hayman 1958b, 1960b, 1960c). The means and variances of the six families permit the estimation of the additive and genetic components D, H and F, and the environmental component, E. Their determination is known as the generation means analysis. This also detects: non-allelic interaction, genotype x environment interaction and reciprocal differences.

The random biparental mating (RBIP) design involves crossing parents in pairs to produce full sib families (Kearsey 1965, Mather and Jinks 1971). Mather (1949) discusses using F3's produced from intercrossing pairs of F2's.

Total variation can be subdivided into the variation between full sib family means (full sib covariance) and the mean variation within full sib families.

The random biparental design is limited to only two degrees of relationship among progeny, either full sibs or unrelated. Other degrees of relationship require families with only one parent in common. For example, half sibs among offspring of a randomly mating population includes the North Carolina 1 and 2 designs and diallels.

The North Carolina 1, or hierarchical, design is where a random sample of males is mated to a number of different females (Comstock and Robinson 1948, 1952a, Kempthorne 1957). The males being common parents to a number of progeny families. Morley (1960) has extended this design by the inclusion of genotype x environment interaction.

The North Carolina 1 design has made no allowance for either common family environmental effects or maternal effects (Mather and Jinks 1971). This bias has been removed with the North Carolina 2 design in which half sib families have a common mother as well as a common father (Comstock and Robinson 1948, 1952a, Kempthorne 1957). This has been achieved by a systematic crossing programme in which n_1 males are crossed with n_2 females in turn to produce $n_1 n_2$ progeny, i.e. a factorial mating design where the males and females are different.

Other methods have been proposed for investigating randomly mating populations. These include:

1. Inbreeding a random sample of the population (Mather and Jinks 1971, Kearsey 1970, Hillel *et al* 1972).

2. Making test crosses to purebreeding lines or their F1's (Comstock and Robinson 1952b, Kearsey and Jinks 1968).

3. The triple test cross (Kearsey and Jinks 1968, Jinks and Perkins 1970, Pooni and Jinks 1976, 1978), where a random sample of individuals from a population are crossed to three testers (two inbred lines and their F1).

4. Combining the generation means analysis with the triple test cross (Jinks and Perkins 1969, Perkins and Jinks 1970).

Although these multiple mating designs were developed for the analysis of random mating populations, they are also applicable to other kinds of populations including inbred and F2 populations.

1.6 Diallels

The diallel cross is a mating system in which a set of inbred lines is crossed in all possible combinations. It was first introduced by Schmidt (1919) to denote all possible crosses among a collection of male and female animals. The diallel can be regarded as a special case of the North Carolina 2 or factorial design where the N_1 males and N_2 females are identical (Cockerham 1963).

1.6.1 Diallel cross designs

Diallel cross designs may be classified into a number of types:

1. designs involving P monoecious individuals or inbred lines (after Griffing 1956a, 1956b). These include designs with and without parents and with and without reciprocal crosses.

2. Partial diallels. These designs overcome the constraint of the large number of crosses required when the number of parents increases (Gilbert 1958, Kempthorne and Curnow 1961, Curnow 1963, Fyfe and

Gilbert 1963, England 1974, Mathur and Narain 1976).

3. Two level designs which contain a diallel cross of individuals within a diallel cross of a population (Hinkelmann 1974).

4. Triallels. Rowlings and Cockerham (1962a) have extended the diallel to analyse three-way hybrids, a cross between an inbred line and an unrelated F1 hybrid. They have presented a model for the estimation of additive and dominance variance components.

5. Partial triallel cross designs have been developed as an extension of the triallel (Hinkelmann 1965).

6. Four way mating designs or the tetra-allel cross design for analysing double cross hybrid populations have been discussed by Rawlings and Cockerham (1962b). Hinkelmann (1968) has presented a partial diallel cross design for this model. It considers a sample of all possible four-way crosses to determine combining abilities. However prediction formulae are available for determining the outcome of double crosses from the performance of single crosses (Jenkins 1934, Eberhart *et al* 1964).

1.6.2 Analysis of diallel cross data

Early methods for the analysis of diallel crosses involved the use of regression techniques (Hull 1946), and factorial analyses (Yates 1947). These were later followed by the Hayman-Jinks analysis (Jinks and Hayman 1953, Jinks 1954, Hayman 1954a). This method was based on an idea introduced by Fisher (1918) and later developed by Fisher *et al* (1932) and Mather (1949). It was basically an extension of Mather's (1949) method for crosses between two inbred lines.

Alternative methods of diallel analyses were developed by Kempthorne, Gardner, Griffin and Wearden. Kempthorne (1956) analysed the diallel in terms of variances of inbred parents, crossbred progeny and the covariance between parents and progeny. Gardner (Gardner and Eberhart 1966, Eberhart and Gardner 1966) gave a model to provide the genetic expectations of means of a fixed set of random-mating parents in a diallel cross while Wearden (1964) discussed the diallel cross replicated in a randomised block design. Griffin (1956a, 1956b) (See Section 1.6.4) estimated combining ability effects from a diallel cross.

The Hayman-Jinks analysis involves the partitioning of the second degree statistics, Variance (Vr) and Covariance (Wr) of parental arrays. It can be separated into:

1. The analysis of variance of the diallel table (Hayman 1954b, Walters and Gale 1977). This later being extended to the half-diallel (Jones 1965, Walters and Morton 1978) and F2 and backcrosses (Hayman 1958a, Jinks 1956).

2. The analysis of variance of (Wr-Vr), the difference of the array covariance and variance.

3. The WrVr graphical analysis. This shows:

   (a) a test of the adequacy of the additive-dominance model

   (b) a measure of the average level of dominance

   (c) the distribution of dominant to recessive genes among the parents

   (d) the presence of non-allelic gene interaction (Hayman and Mather 1955, Hayman 1957, Mather 1967, Coughtrey and Mather 1970).

4. The estimation of the genetical components D, H1, H2 and F and their derived statistics. D measures additive gene effects, H1 and H2 measure dominance

effects and F measures the relative frequencies of dominant and recessive alleles. From Falconer (1960), when parents are inbred lines (f = 1), D = $2\sigma^2A$, where σ^2A is the additive genetic variance of a random mating population and H1 = $4\sigma^2D$ where σ^2D is the dominance variance of a random mating population. The derived statistics will give direct estimates of the degree of dominance, the ratio of dominant to recessive alleles, the symmetry of gene distribution, number of effective factors and estimates of heritability.

1.6.3 Genetical assumptions

The interpretation of the genetical components depends on the validity of a number of assumptions (Hayman 1954a). These are:

1. diploid segregation
2. no differences between reciprocal crosses
3. independent action of non-allelic genes and in the diallel cross
4. absence of multiple allelism
5. homozygous parents
6. independent distribution of genes between parents.

The validity of the assmptions are tested by the homogeneity of the (Wr-Vr) variance, a significant Wr on Vr regression and a non-significant deviation of the regression line from unity (Jinks and Hayman 1953, Hayman 1954a).

If the assumptions fail, Hayman and Jinks have recommended removing arrays from the diallel table until the assumptions can be satisfied. This procedure has been severely criticised (Gilbert 1958, Kempthorne 1956, Baker 1978, Sokol and Baker 1977). Kempthorne (1956) considered that with the removal of arrays, the parents were no longer a random sample from the population of inference. He insisted parents must be a random sample of inbred lines which are the result of unselected inbreeding from a random mating population rather than just a set or even sample of inbred

lines. Kempthorne's comments are not justified in this context as his remarks have only beenmade in terms of cross-pollinated crops.

1. Diploid Segregation

The assumption of diploid segregation is usually made (Cockerham 1963) because knowledge concerning gene action is with reference to diploid species. However certain polyploids do behave as diploids during meiosis thus fulfilling this assumption (Strickberger 1968). An example is common wheat, a hexaploid with a diploiding gene (McFadden and Sears 1947).

2. Reciprocal differences

Differences between reciprocal crosses can occur and are usually assumed to be the result of maternal effects. Cockerham (1963) reported for many species of plants reciprocal effects have not been found to be significant. Many results for peas have shown an absence of reciprocal differences (Krarup and Davis 1970a, 1970b; Ibarbia and Bienz 1970a; Kumar 1973; Pandey and Gritton 1975, Gritton 1975) however Davies (1975) found a reciprocal difference for seed size.

3. Non-allelic interaction

The assumption of non-allelic interaction or lack of epistasis is considered by Sokol and Baker (1977) to be biologically unrealistic as the absence of epistasis cannot be assumed when dealing with quantitative characters (Mather 1943, Horner *et al* 1955, Gilbert 1958, Cockerham 1959). It is usual to assume lack of epistasis. However if epistasis is present, a fraction of the additive comonent of the epistatic variance will be confounded with both the additive genetic variance and the dominance variance.

4. Multiple alleslism

The assumption of no multiple allelism has been included by Hayman (1954a) in an effort to remove the complicat-

ing effects which could occur. Most practical situations consist of a comparison between two alleles per locus, so this is not an unreasonable assumption.

5. Homozygous parents

The use of homozygous parents is assumed when dealing with self pollinated crops. Heterozygous parents can be used as demonstrated by Oakes (1967). He investigated the effect of non-homozygosity and multiple allelism in parental lives and showed that most of the information obtained using homozygous parents could still be extracted if the parents were heterozygous. Dickinson and Jinks (1956) have presented an analysis for the use of heterozygous parents.

6. Independent distribution

The failure of the assumption of independent distribution of genes between parents can effect the WrVr graphical anlaysis in the estimation of dominance (Hayman 1954a). Sokol and Baker (1977) consider independent distribution will be assumed only if the parents of the diallel are chosen as a random sample.

1.6.4 Combining ability diallel analysis

A second approach to the analysis of the diallel cross is the combining ability analysis (Griffing 1956a, 1956b). The concepts of general and specific combining ability have been defined by Sprague and Tatum (1942). General combining ability, GCA, is the average performance of a line in hybrid combination. Specific combining ability, SCA, is defined as the deviation of a hybrid from its expectation based on the average performane of its parents.

Griffing (1956b) has outlined procedures for analysing four types of diallels. These include combinations of the presence and absence of parents and reciprocal crosses.

The inclusion of parents in the analysis was considered by Griffing to bias the results. With the combining ability diallel the interest is usually in the performance of the F1 crosses.

The GCA and SCA variances, σ^2GCA and σ^2SCA, can be related to covariance among relatives (Griffing 1956a).

$$\sigma^2 GCA = COV\ (HS)$$
$$\sigma^2 SCA = COV\ (FS) - 2\ COV(HS)$$

Where COV(HS) and COV(FS) are the half sib and full sib covariances respectively.

Kempthorne (1957) has defined these covariances:

$$COV(FS) = \frac{1 + F}{2}\sigma^2_A + \left(\frac{1 + F}{2}\right)^2 \sigma^2_D + \left(\frac{1 + F}{2}\right)^2 \sigma^2_{AA} + \left(\frac{1 + F}{2}\right)^3 \sigma^2_{AD} + \left(\frac{1 + F}{2}\right)^4 \sigma^2_{DD} + \cdots$$

$$COV(HS) = \frac{1 + F}{4}\sigma^2_A + \left(\frac{1 + F}{4}\right)^2 \sigma^2_{AA} + \cdots$$

Where F is the inbreeding coefficient. With self-fertilization F = 1, then

$$\sigma^2_{GCA} = \tfrac{1}{2}\sigma^2_A + \tfrac{1}{4}\sigma^2_{AA}$$

and $$\sigma^2_{SCA} = \sigma^2_D + \tfrac{1}{2}\sigma^2_{AA} + \sigma^2_{AD} + \sigma^2_{DD}$$

These genetic variances can be used to calculate heritability ratios.

Griffing's combining ability model has been extended to permit analysis over a number of environments (Singh 1973a, 1973b, Dhillon and Singh 1977).

1.7 Quantitative Genetics in Peas

A number of quantitative genetic studies have been reported for peas. These include the use of the generation means analysis for the inheritance of yield components (Johnson 1957, Marx and Mishanc 1962, Ibarbia and Bienz 1970a, 1970b, Singh and Singh 1979, Chandel and Joshi 1979). Diallels have also been widely used for yield components (Krarup and Davis 1970a, 1970b, Snoad and Arthur 1973a, 1973b, 1974, Singh and Singh 1970, Koranne and Singh 1974, Pandey and Gritton 1975, Davies 1975, Gritton 1975, Singh *et al* 1980, Srivastava and Sachar 1975, Kumar and Das 1974, 1975a, 1975b, Brahmappa and Singh 1977, Dahiya *et al* 1977, Sharma *et al* 1977, Weber 1976, Singh *et al* 1975, Bhullar *et al* 1976). Flowering has been considered by Rowlands (1964) and Watts *et al* (1970) while leafroll virus resistance has been examined by Crampton and Watts (1968). Most of these quantitative genetic studies have shown that the components of yield are controlled by an additive genetic system.

Very few studies in quantitative inheritance have been carried out for the vegetative characters. However Guzhov (1976) examined the connection between type of leaf and yield while Lichter (1959) considered the length-width ratio of leaflets and found this character to be under the control of additive gene action although non-allelic genes had only a small effect.

MATERIALS AND METHODS

2.1 Experimental Outline

The study involved producing hybrid and selfed pea seed under glasshouse conditions during the winter, and the evaluation of the progeny in a replicated field trial during the spring and summer. The mating design was an eight parent half diallel with the parental lines being included in the field trial.

Reciprocal crosses were not included in the experiment. Previous research (Krarup and Davis 1970a; Kumar 1973) showed no significant differences with reciprocal crosses for yield components. No differences have been reported for leaf characters.

2.2 Crossing Programme

The parental lines used were a stratified random selection of three different foliage type genes (See Table 2.1). These genes were sometimes separate and sometimes in combination. The genes involved included the following all of which act in the homozygous recessive condition:

af converts normal leaflets to tendrils (Kujala 1953)

tl converts normal tendrils to leaflets (Vilmorin 1910, Vilmorin and Bateson 1912)

st reduces the size of stipules (Pellew and Sverdrup 1923, Sverdrup 1927)

The normal type was the cultivar Kuru, while all the other types were isogenic lines from the cultivar New Season (See Plates 1 to 6). Kuru is a commercial New Zealand green pea cultivar and has been described by Sparks (1979). New Season is a garden pea cultivar from Australia (Goulden *pers com*).

TABLE 2.1: PARENTAL LINES

Code Number	Genotype	Description
1	AfAfStStTlTl	Normal leaflets, stipules and tendrils
2	AfAfStSt*tltl*	acacia leaf
3	AfAf*stst*TlTl	Normal leaflets, reduced stipules
4	*afaf*StStTlTl	tendrillate
5	AfAf*ststtltl*	acacia leaf, reduced stipules
6	*afaf*StSt*tltl*	minute leaflets
7	*afafstst*TlTl	tendrilate, reduced stipules
8	*afafststtltl*	minute leaflets, reduced stipules

PLATE 1:
Normal genotype
(AfAfStStTlTl)

PLATE 2:
Acacia leaf genotype
(AfAfStSt$tltl$)

PLATE 3:
Tendrillate genotype (*af af*StStTlTl)

PLATE 4:
Acacia leaf with reduced stipules (AfAf*ststtltl*)

PLATE 5:
Tendrillate with reduced stipules (*afafstst*TlTl)

PLATE 6:
Minute leaflets with reduced stipules (*afafststltl*)

2.2.1 Cross pollination programme

The twenty eight crosses which were produced are described in Table 2.2. Cross pollinations were made by hand under glass during the winter of 1980. The glasshouse was held at an average air temperature of 20°C. Plants were grown in a peat-sand media, 2 to 5 ratio, with nutrients supplied by NFT nutrient solution (Cooper 1979) at weekly intervals together with osmocote in the growing media.

Pea flowers are hermaphroditic with preanthesis self-pollination ("bud pollination") occurring (Frankel and Galun 1977). Under normal conditions the anthers dehisce in the bud with pollen accumulating at the top of the keel. With the growth of the pistil the pollen becomes deposited on the stigma and self-fertilization is assured. The time of pollen shedding is about the tight bud stage, between stages 0.1 and 0.2 on the Maurer scale of pea floral development (Maurer *et al* 1966).

The procedure used for hand pollinating was similar to the method outlined by Wellensiek (1925). Using forceps the lower part of the calyx enclosing the keel was removed. Then the suture of the corina-leaves or wings was split upwards making the interior of the flower accessible. Ten stamen had to be removed. The stigma is usually receptive for immediate pollination. This was carried out by dusting pollen which was deposited on the stigma of a freshly shed flower on to the stigma of an emasculated flower. Flowers were not bagged or covered after crossing, the wing petals were closed back together to protect the stigma.

Pods were harvested after they had dried off on the plant. Prior to sowing all seed were treated with a slurry of a combination of the fungicide VITAFLO[1] and the bird repellant METHOCARB[2] (Porter 1977, Burgmans 1979).

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1 VITAFLO: 200g/litre Carboxin and 200g/litre thiram in form of a suspension

2 METHOCARB: 75% a.i. Mesurol [4-(methylthio)-3,5-xylyl N-methyl-carbamate]

TABLE 2.2: PROGENY

Progeny Number	Cross Number ♀	♂	Genotype
1	1	2	+
2	1	3	+
3	1	4	+
4	1	5	+
5	1	6	+
6	1	7	+
7	1	8	+
8	2	3	+
9	2	4	+
10	2	5	*tl*
11	2	6	*tl*
12	2	7	+
13	2	8	*tl*
14	3	4	+
15	3	5	*st*
16	3	6	+
17	3	7	*st*
18	3	8	*st*
19	4	5	+
20	4	6	*af*
21	4	7	*af*
22	4	8	*af*
23	5	6	*tl*
24	5	7	*st*
25	5	8	*st tl*
26	6	7	*af*
27	6	8	*af tl*
28	7	8	*af st*

2.3 Field trial

The twenty eight crosses and the eight parental lines were sown on 18 November 1980. The experiment was laid out as a randomised complete block design in three blocks with two ranges or tiers per block. Seeds were sown by hand into single row plots, two metres long at a spacing of 10cm within the row by 50cm between rows (See Plates 7 and 8). They were grown as spaced plants so that individual plant measurements and recordings could be made. End plants of each plot were used as guards and the perimeter of the trial was surrounded by guard rows.

2.3.1 Crop husbandry

The soil type of the trial area was Karapoti brown sandy loam and it had been in pasture the previous year. No fertilzer was applied. The method of weed control was by hand. The site was irrigated with 10mm water at the midflowering stage, 12 January 1981. During the growing period the crop was treated for a minor outbreak of downy mildew using RIDOMIL[3], 1kg/ha, and for leaf miner using ACEPHATE[4] at 0.2kg/ha.

2.4 Data Collection and Measurements

Ten plants at random from each plot were used. These plants were destructively harvested at the green pea stage, commencing on 28 January, to sample both leaf characters and components of yield. Green plant material was stored at 5°C in polythene bags prior to evaluation.

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3 RIDOMIL: 250g/kg [metalaxyl ((±)-methyl N-(2-methoxyacetyl)-N-(2,6-xylyl alaninate)]

4 ACEPHATE: [O,S-Dimethyl acetylphosphora midothioate]

PLATE 7:
Field trial at early growth stage

PLATE 8:
Field trial at flowering stage

2.4.1 Vegetative data

One leaf was sampled from each plant: the leaf at the first podding node. This leaf was considered to be representative of a fully developed leaf (Blixt 1974). It is also the primary source of carbohydrate for the first pod (Linck and Sudia 1962, Flinn and Pate 1970, Harvey 1974).

The character measured included: leaflet number, area, weight, length and width; stipule area, weight, length and width; tendril area and weight.

Area measurements were determined with a photoelectric planimeter. This gives a suitable estimate of the area of the upper surface of leaflets and stipules but it underestimates tendril area, the upper surface, by a factor of $\pi/2$. However it can not be assumed that the photosynthetic area of a tendril is restricted to half the total surface area (Snoad 1981a) as with leaflets, therefore tendril area was not adjusted. Leaflet, stipule and tendril weights were determined on a dry weight basis using an oven temperature of 80°C (Evans 1972) for 24 hours.

2.4.2 Components of yield

Flowering time was determined as the number of days from sowing for 50 percent of the plants to reach full bloom at the first flowering node. This is defined as the 0.5 stage on Maurer's floral development scale (Maurer *et al* 1966).

The other yield components measured were as follows:

(i) Number of podding nodes
(ii) Pod weight per plant (grams)
(iii) green pea weight (grams)
(iv) Number of pods per node
(v) Number of seeds per pod

2.4.3 Maturity assessment

Peas have a continuous increase in fresh weight during the immature green pea stage. In an effort to standardise the maturity level at harvest, plots were harvested on two occasions 48 hours apart and the yields were interpolated to a common value of maturity (Nelder 1963), as follows.

The method used for determining the maturity level was the alcohol insoluble solids technique (Kertesz 1934, 1935). This involves the maceration in a blender for 3 minutes of a 20 gram sample of peas in 50cm³ of 80 percent ethanol (by volume). This was then boiled for 30 minutes in a further 200cm³ ethanol, filtered, oven dried overnight at 80°C, cooled in a desicator and the insoluble portion weighed.

The relationship between the yield of shelled peas per plant and the maturity level (Salter 1963, Berry 1966) is a curvilinear relationship. Berry (1963) fitted the following equation:

$$Y = \left(\frac{T - T_0}{W}\right)^{\theta} = A + B\,(T - T_0)$$

where W = yield of shelled peas per plant

T = maturity value measured in terms of tenderometer units

To = base maturity level at which yield is zero

A, B, and θ are constants (θ = 1.0)

The interpolation based on the previous equation is given by:

$$W' = \frac{(T_2 - T_1)(T' - T_0)\,W_2W_1}{(T' - T_1)(T_2 - T_0)W_1 + (T_2 - T')(T_1 - T_0)W_2}$$

Where W_1 and W_2 are the yields at maturity levels T_1 and T_2 respectively and W' is the interpolated yield at maturity level T'. The alcohol insoluble solids content was used

for the maturity value in Berry's equation. This was reasonable because a high correlation has been reported between the alcohol insoluble solids content and tenderometer reading (Walls and Kemp 1939, Sayre 1954).

For the constants T_0 and T' the arbitrary values 7.40 and 21.40 were used. T_0 of 7.40 corresponds with Berry's (Berry 1966) base maturity value while T' value was the A.I.S. mean for the experiment. For the diallel analysis of maturity, the data used were the means of the alcohol insoluble solids contents for both harvests.

2.5 Statistical Analysis

Prior to the analysis of the diallel cross data, an analysis of variance was carried out on plot means for both parents and their progeny. The computer programme PHANIE (Gordon unpublished) was used. This follows the model described by Gordon *et al* (1972) based on Le Cerg *et al* (1962), Comstock and Robinson (1952b) and Comstock and Moll (1963).

Genotype differences were tested with Duncan's multiple range test (Balaam 1963). The symbols used for significant differences in this study were: NS = $P > 0.10$, (NS) = $0.10 \geq P > 0.05$, * = $0.05 \geq P > 0.01$, ** = $0.01 \geq P \geq 0.005$, *** = $0.005 \geq P > 0.001$, **** = $P \leq 0.001$.

Characters which showed significant genotype differences were analysed by the Hayman-Jinks diallel method (Jinks and Hayman 1953, Jinks 1954, Hayman 1954a, Mather and Jinks 1971). The analysis of variance of the diallel table (Hayman 1954b) was not carried out following Hayman's comments (Hayman 1960a) that although the analysis of variance can estimate and test the significance of specific components of variation they can not supply a complete set either of the estimates or tests of significance. Hence they have limited value.

2.5.1 Hayman-Jinks diallel analysis

The adequacy of the additive-dominance model was determined by considering the relationship of Wr and Vr. Wr represents the covariance of the offspring of each parent with its non-recurrent parent and Vr represents the variance of all offspring of each parent. Other statistics calculated included Vp, the variance of the parents; $\bar{Vr}$, the variance of array means; $\overline{Wr}$, the mean covariance and $\overline{Vr}$ the mean variance of arrays.

The relationships between these statistics and the genetical components of variation, D, H_1, H_2 and F are as follows:

$$Vp = D + Ep$$

$$\bar{Vr} = \tfrac{1}{4}D + \tfrac{1}{4}H_1 - \tfrac{1}{4}H_2 - \tfrac{1}{4}F + \frac{1}{n^2}(Ep + (n-1)Ef)$$

$$\overline{Wr} = \tfrac{1}{2}D - \tfrac{1}{4}F + \frac{1}{n}Ep$$

$$\overline{Vr} = \tfrac{1}{4}D - \tfrac{1}{4}F + \tfrac{1}{4}H_1 + \frac{1}{n}(Ep + (n-1)\,Ef)$$

where n is the number of parents, Ep and Ef are the environmental components of the parents and progeny respectively. In this anlaysis a pooled environmental component was used. Observation between the two components did not show marked differences. The environmental component used was the block x genotype (Error) mean square from the initial analysis of variance (Mather and Jinks 1971). The above formulae for the second degree statistics have been modified for use in the half diallel analysis (See Appendix I for derivation of formulae).

The adequacy of the additive-dominance model was tested by:

(i) the analysis of variance of (Wr-Vr). This tests the homogeneity of the (Wr-Vr) variance by considering the conistency of (Wr-Vr) over arrays.

(ii) Wr on Vr regression analysis. The slope of regression line was tested for its significance from zero and

unity by a two tailed t-test (Draper and Smith 1966).

(iii) The graphical analysis involving a plot of Wr on Vr and also the parabola $Wr^2 = VrVp$.

If the model was considered adequate the genetical components were calculated, otherwise the offending array or arrays were removed from the diallel table and the model reanalysed. The presence of non-additive genetic variation was determined by an analysis of variance of (Wr + Vr).

2.5.2 Components of Variation

The genetical components D, H_1, H_2 and F were calculated from least squares estimates of the previous equation of $\overline{Wr}$, $\overline{Vr}$, Vp and $V\bar{r}$.

$$D = Vp - Ep$$

$$F = 2Vp - 4\overline{Wr} - \frac{2}{n}(n-2)Ep$$

$$H_1 = Vp - 4\overline{Wr} + 4\overline{Vr} - Ep - \frac{4}{n}(n-1)Ef$$

$$H_2 = 4\overline{Vr} - 4V\bar{r} - \frac{4}{n^2}(n-1)Ep - \frac{4}{n^2}(n^2 - 2n + 1)Ef$$

These and previous calculations were made with the aid of a series of B6700 Fortran Computer programmes. From the components of variation the following ratios were determined:

$\sqrt{H_1/D}$ — The dominance ratio, for complete dominance it equals 1, with over dominance it is greater than 1 and with partial dominance is less than 1.

$\frac{1}{4}H_2/H_1$ — This estimates the average value of uv over all loci, showing whether positive and negative alleles are present in equal proportions.

$\frac{\frac{1}{2}F}{\sqrt{D(H_1 - H_2)}}$ This measures the extent to which the dominance level varies from one locus to another.

$\frac{KD}{KR} = \frac{\sqrt{4DH_1} + F}{\sqrt{4DH_1} - F}$ This estimates the ratio of the numbers of dominant to recessive genes over all parents.

$K = M / H_2$ K is an estimate of the number of gene groups or effective factors which control the character, and which exhibit dominance to some degree. M is the difference between the progeny mean and the parental mean and has an environmental component $n-1[(n-1)Ep + Ef] / n^3$ (Hayman 1954).

2.5.3 Heritability

Narrowsence heritability (Mather and Jinks 1971) was estimated as:

$$h^2ns = \frac{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{2}H_2 - \frac{1}{2}F}{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{4}H_2 - \frac{1}{2}F + E}$$

and broadsence heritability as:

$$h^2bs = \frac{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{4}H_2 - \frac{1}{2}F}{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{4}H_2 - \frac{1}{2}F + E}$$

where E is the pooled environmental component.

2.5.4 Direction of dominance

A comparison was made between (Wr + Vr) and $\overline{P}$, the parental mean. This enables estimates to be made of the correlation between the dominance order and the parental order of magnitude, i.e. whether the distribution of the dominant to recessive alleles is correlated with the phenotype of

the common parent. A positive correlation implies that the recessive genes are mostly positive (increasing) while a negative correlation shows dominant genes are mostly positive. A non-significant correlation suggests that equal proportions of dominant genes are positive and negative, dominance being ambidirectional.

RESULTS AND DISCUSSION

3.1 Phenotypic analysis

The means for each genotype, the 28 crosses and 8 parents are presented in Tables 3.1.1 to 3.1.19. Also included are the results from the analyses of variance carried out on plot means.

Significant genotype differences at the 0.1 percent level were obtained for all characters with the exception of adjusted pea yield. The coefficients of variation for most characters ranged from 4 to 16 percent. Levels of this magnitude are considered to be acceptable for biological and agricultural data (Balaam 1972). The coefficients of variation for leaflet number, tendril area and weight, and adjusted pea yield were of a higher magnitude. Some of the tendril variability can be accounted for by the inaccuracy of the measuring equipment and the sample size; and the variability in leaflet number by the variation in numbers of the minute leaflet (*afaftltl*) forms.

The adjustment of pea yield for maturity level using the method of Nelder (1963) resulted in a decrease in the level of significance, and an increase in the standard error and coefficient of variation. No advantage appeared to have been obtained (Tables 3.1.15 and 3.1.16).

3.2 Hayman-Jinks diallel analysis

As the genotypic variances were significant for the characters studied the Hayman-Jinks analysis was conducted. The variances (Vr) and Covariances (Wr) for each array (averaged over blocks) are presented in Tables 3.2.1 to 3.2.19. These tables also contain the analysis of variance for testing the consistency of (Wr-Vr) over arrays; the test for the non-additive genetic variation, the analysis of variance of (Wr + Vr) and the regression analysis of Wr on Vr.

TABLE 3.1: Genotype means and analysis of variance

TABLE 3.1.1 : LEAFLET NUMBER

GENOTYPE MEANS

		MALES						
		1	2	3	4	5	6	7	8
F	1	5.43	5.63	5.27	4.90	5.63	5.43	4.87	5.40
E	2		13.07	5.40	5.23	13.10	12.97	5.10	13.23
M	3			4.80	4.43	5.60	4.97	4.23	5.50
A	4				0.00	5.17	0.00	0.00	0.00
L	5					13.07	13.60	5.17	13.47
E	6						660.00	0.00	672.93
S	7							0.00	0.00
	8								596.70

CHARACTER MEAN	58.90
PARENT MEAN	161.63
HYBRID MEAN	29.54

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	2364.15	2.57	(NS)
GENOTYPES	35	96115.11	104.36	****
ERROR	70	920.96		

STANDARD ERROR	17.521
COEFFICIENT OF VARIATION	0.515

TABLE 3.1.2 : LEAFLET LENGTH (mm)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	59.67	56.00	61.67	56.33	60.00	58.00	61.00	58.67
E 2		51.67	55.67	54.00	50.33	49.67	59.33	52.33
M 3			54.00	55.00	57.33	56.00	60.00	57.33
A 4				0.00	56.67	0.00	0.00	0.00
L 5					54.67	53.00	59.67	57.00
E 6						6.00	0.00	6.67
S 7							0.00	0.00
8								7.00

CHARACTER MEAN	41.24
PARENT MEAN	29.13
HYBRID MEAN	44.17

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	28.398	4.60	*
GENOTYPES	35	1861.059	301.65	****
ERROR	70	6.170		

STANDARD ERROR	1.434
COEFFICIENT OF VARIATION	0.060

TABLE 3.1.3 : LEAFLET WIDTH (mm)

GENOTYPE MEANS

		MALES						
		1	2	3	4	5	6	7	8
F	1	39.00	36.00	38.67	35.33	38.67	36.67	38.67	37.00
E	2		32.00	34.00	32.00	31.67	29.33	34.67	31.00
M	3			32.00	32.67	36.00	34.00	34.00	33.33
A	4				0.00	33.33	0.00	0.00	0.00
L	5					34.00	32.33	34.33	34.33
E	6						3.67	0.00	4.33
S	7							0.00	0.00
	8								3.67

CHARACTER MEAN	25.19
PARENT MEAN	18.04
HYBRID MEAN	27.23

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	17.509	5.32	**
GENOTYPES	35	701.628	213.25	****
ERROR	70	3.290		

STANDARD ERROR	1.047
COEFFICIENT OF VARIATION	0.072

TABLE 3.1.4 : LEAFLET AREA (cm^2)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	59.53	59.17	64.83	57.00	65.83	59.20	61.47	59.87
E 2		69.80	53.13	49.30	72.03	60.90	56.70	71.80
M 3			44.03	45.30	59.47	55.80	49.40	53.80
A 4				0.00	53.47	0.00	0.00	0.00
L 5					74.87	72.43	54.93	80.63
E 6						43.60	0.00	53.33
S 7							0.00	0.00
8								55.63

CHARACTER MEAN	47.52
PARENT MEAN	43.43
HYBRID MEAN	48.69

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	272.736	8.19	****
GENOTYPES	35	1897.822	57.01	****
ERROR	70	33.290		

STANDARD ERROR	3.331
COEFFICIENT OF VARIATION	0.121

TABLE 3.1.5 : LEAFLET WEIGHT (mg)

GENOTYPE MEANS

		MALES						
		1	2	3	4	5	6	7	8
F	1	223.67	277.67	274.00	227.67	297.67	253.00	271.67	261.33
E	2		297.00	223.00	216.67	294.33	276.00	240.67	320.00
M	3			196.67	196.67	257.33	234.33	215.00	245.33
A	4				0.00	235.33	0.00	0.00	0.00
L	5					301.67	302.67	232.00	337.00
E	6						531.33	0.00	508.67
S	7							0.00	0.00
	8								599.67

CHARACTER MEAN	231.89
PARENT MEAN	268.75
HYBRID MEAN	221.36

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	4723.694	2.45	(NS)
GENOTYPES	35	62733.581	32.58	****
ERROR	70	1925.799		

STANDARD ERROR	25.336
COEFFICIENT OF VARIATION	0.189

TABLE 3.1. 6: STIPULE LENGTH (mm)

GENOTYPE MEANS

	MALES							
FEMALES	1	2	3	4	5	6	7	8
1	90.33	86.33	78.33	86.33	82.00	90.00	78.00	76.67
2		82.00	72.00	81.33	71.33	78.67	73.67	68.00
3			34.33	72.67	37.33	73.00	37.33	33.00
4				77.67	73.00	74.00	71.00	66.67
5					35.00	71.67	36.00	35.33
6						68.00	64.33	58.33
7							36.00	31.00
8								28.33

CHARACTER MEAN	64.14
PARENT MEAN	56.46
HYBRID MEAN	66.33

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	163.583	12.50	****
GENOTYPES	35	1188.102	90.78	****
ERROR	70	13.088		

STANDARD ERROR	2.089
COEFFICIENT OF VARIATION	0.056

TABLE 3.1.7 : STIPULE WIDTH (mm)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	62.67	57.67	51.00	57.00	55.33	60.33	49.33	48.00
E 2		51.00	42.00	50.33	43.33	48.00	44.00	40.67
M 3			9.00	42.33	9.67	44.00	9.67	8.33
A 4				47.00	42.67	46.67	41.33	37.33
L 5					10.00	43.33	10.33	10.00
E 6						41.00	37.00	33.00
S 7							8.33	7.67
8								7.67

CHARACTER MEAN	36.31
PARENT MEAN	29.58
HYBRID MEAN	38.23

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	91.861	12.91	****
GENOTYPES	35	998.255	140.24	****
ERROR	70	7.118		

STANDARD ERROR	1.540
COEFFICIENT OF VARIATION	0.074

TABLE 3.1.8 : STIPULE AREA (cm^2)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	70.43	67.17	51.80	66.03	59.27	70.47	49.97	47.37
E 2		52.50	37.70	52.47	37.93	46.77	42.97	36.60
M 3			4.43	39.07	5.07	40.10	5.47	4.90
A 4				46.70	38.80	42.77	37.60	30.67
L 5					5.70	39.57	5.73	5.70
E 6						35.53	30.53	24.23
S 7							4.27	4.37
8								3.20

CHARACTER MEAN	34.55
PARENT MEAN	27.85
HYBRID MEAN	36.47

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	187.372	10.55	****
GENOTYPES	35	1379.736	77.67	****
ERROR	70	17.764		

STANDARD ERROR	2.433
COEFFICIENT OF VARIATION	0.1220

TABLE 3.1.9 : STIPULE WEIGHT (mg)

GENOTYPE MEANS

		MALES							
		1	2	3	4	5	6	7	8
F	1	267.33	294.00	199.33	284.33	250.00	293.00	215.67	208.00
E	2		209.33	159.00	219.00	157.33	193.00	173.00	157.00
M	3			18.67	166.33	21.33	171.67	23.33	21.00
A	4				188.33	164.67	192.33	163.00	127.67
L	5					23.33	155.67	20.67	26.67
E	6						171.67	123.00	106.00
S	7							19.00	20.33
	8								16.00

CHARACTER MEAN	145.00
PARENT MEAN	114.21
HYBRID MEAN	153.80

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	2732.111	7.38	***
GENOTYPES	35	23785.714	64.24	****
ERROR	70	370.254		

STANDARD ERROR	11.109
COEFFICIENT OF VARIATION	0.1327

TABLE 3.1.10: TENDRIL AREA (cm^2)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	1.37	1.70	1.50	1.70	1.70	2.10	1.83	2.30
E 2		0.00	1.50	2.17	0.00	0.00	2.23	0.00
M 3			1.50	1.57	1.70	2.03	1.80	1.87
A 4				8.90	2.20	14.27	11.60	16.00
L 5					0.00	0.00	1.97	0.00
E 6						0.00	14.47	0.00
S 7							8.67	14.80
8								0.00

CHARACTER MEAN	3.43
PARENT MEAN	2.55
HYBRID MEAN	3.68

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	4.237	5.83	***
GENOTYPES	35	70.155	96.56	****
ERROR	70	0.726		

STANDARD ERROR	0.492
COEFFICIENT OF VARIATION	0.2486

TABLE 3.1.11: TENDRIL WEIGHT (mg)

GENOTYPE MEANS

		MALES						
		1	2	3	4	5	6	7	8
F	1	39.67	54.67	48.00	56.00	55.00	71.33	63.00	63.00
E	2		0.00	57.33	69.00	0.00	0.00	73.00	0.00
M	3			49.00	64.33	48.67	69.33	58.00	54.67
A	4				243.00	71.33	443.33	331.33	451.00
L	5					0.00	0.00	55.33	0.00
E	6						0.00	387.00	0.00
S	7							228.00	362.67
	8								0.00

CHARACTER MEAN	99.08
PARENT MEAN	69.96
HYBRID MEAN	107.40

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	1132.583	2.28	NS
GENOTYPES	35	52823.531	106.14	****
ERROR	70	497.679		

STANDARD ERROR	12.880
COEFFICIENT OF VARIATION	0.2252

TABLE 3.1.12: NUMBER OF PODDING NODES

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	6.20	5.83	5.73	5.90	6.33	6.03	5.83	5.90
E 2		5.67	5.53	5.67	5.87	5.70	6.00	5.30
M 3			4.80	5.70	5.67	6.43	4.93	5.33
A 4				5.13	5.63	5.50	5.77	5.73
L 5					5.20	5.93	5.20	5.73
E 6						5.27	5.57	4.83
S 7							5.27	5.57
8								4.53

CHARACTER MEAN	5.59
PARENT MEAN	5.26
HYBRID MEAN	5.68

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	1.2940	6.20	***
GENOTYPES	35	0.5375	2.58	****
ERROR	70	0.2086		

STANDARD ERROR	0.2637
COEFFICIENT OF VARIATION	0.0817

TABLE 3.1.13: POD NUMBER PER NODE

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	1.82	1.88	1.86	1.82	1.85	1.84	1.82	1.88
E 2		1.84	1.87	1.85	1.85	1.75	1.83	1.88
M 3			1.78	1.79	1.79	1.84	1.79	1.84
A 4				1.88	1.93	1.87	1.76	1.84
L 5					1.77	1.88	1.80	1.75
E 6						1.85	1.83	1.92
S 7							1.60	1.70
8								1.81

CHARACTER MEAN	1.82
PARENT MEAN	1.83
HYBRID MEAN	1.79

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.0016	0.37	NS
GENOTYPES	35	0.0117	2.68	****
ERROR	70	0.0044		

STANDARD ERROR	0.0381
COEFFICIENT OF VARIATION	0.0362

TABLE 3.1.14: SEED NUMBER PER POD

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	5.90	5.78	5.55	5.09	5.12	5.01	5.26	5.15
E 2		6.02	5.51	5.87	5.23	5.44	5.80	5.95
M 3			5.48	4.94	5.05	4.98	5.79	5.73
A 4				5.93	5.99	5.98	4.85	5.39
L 5					5.17	5.79	5.08	5.48
E 6						6.67	5.30	6.15
S 7							4.11	4.55
8								5.95

CHARACTER MEAN	5.47
PARENT MEAN	5.65
HYBRID MEAN	5.42

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	1.4747	4.49	*
GENOTYPES	35	0.7673	2.34	***
ERROR	70	0.3285		

STANDARD ERROR	0.3309
COEFFICIENT OF VARIATION	0.1047

TABLE 3.1.15: GREEN PEA WEIGHT (g)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	7.41	6.95	6.06	5.19	6.38	5.40	5.55	5.23
E 2		5.42	4.92	5.40	4.95	4.62	5.63	5.41
M 3			4.30	4.72	4.56	4.78	4.79	5.20
A 4				4.95	6.11	5.14	4.05	4.51
L 5					4.05	5.66	4.29	4.50
E 6						5.56	4.10	4.90
S 7							2.53	3.34
8								3.93

CHARACTER MEAN	5.01
PARENT MEAN	4.77
HYBRID MEAN	5.08

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.5858	0.94	NS
GENOTYPES	35	2.6385	4.22	****
ERROR	70	0.6257		

STANDARD ERROR	0.4567
COEFFICIENT OF VARIATION	0.1578

TABLE 3.1.16: ADJUSTED PEA YIELD (g)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	8.83	7.22	5.74	5.15	6.92	4.87	6.12	5.67
E 2		5.49	4.41	5.44	3.98	3.96	4.64	4.67
M 3			3.83	4.19	4.27	5.13	5.31	4.64
A 4				5.56	5.91	5.12	4.14	4.57
L 5					4.01	6.32	4.30	4.75
E 6						4.91	3.77	4.69
S 7							3.93	4.14
8								3.80

CHARACTER MEAN	5.01
PARENT MEAN	5.05
HYBRID MEAN	5.00

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	1.4948	0.74	NS
GENOTYPES	35	3.5825	1.78	*
ERROR	70	2.0167		

STANDARD ERROR	0.8199
COEFFICIENT OF VARIATION	0.2834

TABLE 3.1.17: POD WEIGHT PER PLANT (g)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	15.70	13.14	11.99	10.61	12.99	11.00	10.77	11.31
E 2		11.43	10.00	10.91	10.49	9.81	11.27	10.27
M 3			8.47	9.80	9.89	9.95	9.37	10.19
A 4				9.86	11.82	10.02	8.12	9.25
L 5					10.24	11.71	9.32	10.20
E 6						11.19	8.57	10.11
S 7							5.16	6.54
8								8.36

CHARACTER MEAN	10.27
PARENT MEAN	10.05
HYBRID MEAN	10.34

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.1620	0.08	NS
GENOTYPES	35	9.9764	4.87	****
ERROR	70	2.0482		

STANDARD ERROR	0.8263
COEFFICIENT OF VARIATION	0.1393

TABLE 3.1.18: FLOWERING TIME (days from sowing)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	49.33	48.67	48.67	49.00	49.00	49.00	49.33	50.00
E 2		49.67	49.00	49.00	50.33	50.33	49.00	49.67
M 3			49.67	49.33	49.67	49.00	49.33	49.33
A 4				49.67	49.67	50.67	50.67	50.00
L 5					49.67	50.00	49.33	49.33
E 6						50.00	51.00	50.00
S 7							52.33	53.00
8								51.67

CHARACTER MEAN	49.81
PARENT MEAN	50.25
HYBRID MEAN	49.69

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	8.787	16.58	****
GENOTYPES	35	2.789	5.26	****
ERROR	70	0.530		

STANDARD ERROR	0.4203
COEFFICIENT OF VARIATION	0.0146

TABLE 3.1.19: MATURITY LEVEL (A.I.S. content)

GENOTYPE MEANS

		MALES						
	1	2	3	4	5	6	7	8
F 1	18.51	21.03	21.29	20.75	20.23	19.81	20.68	19.43
E 2		22.82	21.95	22.56	22.79	20.85	22.77	23.09
M 3			23.36	22.26	21.75	20.91	23.47	23.16
A 4				22.01	23.04	21.38	20.79	20.49
L 5					21.63	22.90	21.79	22.26
E 6						22.44	20.46	21.24
S 7							19.36	20.06
8								19.12

CHARACTER MEAN	21.46
PARENT MEAN	21.16
HYBRID MEAN	21.54

ANALYSIS OF VARIANCE TABLE

SOURCE	DF	MS	F	SIG
BLOCKS	2	8.3207	6.85	***
GENOTYPES	35	5.2042	4.29	****
ERROR	70	1.2142		

STANDARD ERROR	0.6362
COEFFICIENT OF VARIATION	0.0514

TABLE 3.2:

Relationships between array variances (Vr) and covariances (Wr)

A	Means of estimates of Wr and Vr
B	Analysis of variance (Wr-Vr)
C	Analysis of variance (Wr+Vr)
D	Regression analysis of Wr on Vr
E	Correlation between (Wr+Vr) and $\overline{P}$

TABLE 3.2.1 : LEAFLET NUMBER

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	0.1345	20.2179	20.3524	20.0834
2	17.2396	706.2731	723.5127	689.0335
3	0.2845	35.9373	36.2218	35.6527
4	7.0643	-428.8087	-421.7444	-435.8730
5	18.0297	763.8299	781.8596	745.8003
6	95845.0823	89570.0112	185415.0935	-6275.0711
7	6.7998	-421.7594	-414.9596	-428.5592
8	86414.6161	85578.4962	171993.1123	-836.1200

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	7042862	0.85	NS
TREATMENTS	7	15524969	1.87	NS
ERROR	14	8295296		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	$1.624\ 10^{9}$	2.24	NS
TREATMENTS	7	$2.054\ 10^{10}$	28.26	****
ERROR	14	$7.268\ 10^{8}$		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	37192258120	6505.44	****
RESIDUAL	22	5717097		

R^2 0.9966

bo	380.461	sebo	556.700
b1	0.9477	seb1	0.0118

$H1: \hat{b}1 = 1$ 4.451 ****

$H0: \hat{b}1 = 0$ 80.655 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = 0.99 ****

TABLE 3.2. 2 : LEAFLET LENGTH

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	9.1191	14.6667	23.7857	5.5476
2	16.4702	-6.4226	10.0476	-22.8929
3	14.0893	4.9583	19.0476	-9.1310
4	882.1548	822.0060	1704.1607	-60.1488
5	15.6071	-12.4167	3.1905	-28.0238
6	759.3929	763.4048	1522.7976	4.0199
7	1030.9881	887.9107	1918.8988	-143.0774
8	813.0297	793.8750	1606.9048	-19.1547

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	3907.6	4.51	*
TREATMENTS	7	7109.3	8.21	****
ERROR	14	865.8		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	15624	2.48	NS
TREATMENTS	7	2440029	387.29	****
ERROR	14	6300		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	4014878	1703.06	****
RESIDUAL	22	2357		

R^2 0.9873

bo	-6.450	sebo	14.118
b1	0.9375	seb1	0.0227

H1: $\hat{b}1$ = 1 2.753 *
H0: $\hat{b}1$ = 0 41.300 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.99 ****

TABLE 3.2.3 : LEAFLET WIDTH

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	4.6191	12.4524	17.0715	7.8333
2	6.9405	16.5834	23.5238	9.6429
3	8.8452	19.7381	28.5833	10.8929
4	320.3929	310.0476	630.4405	-10.3452
5	6.6548	16.7619	23.4167	10.1071
6	284.4702	292.9107	577.3809	8.4405
7	362.5179	330.7203	693.2381	-31.7976
8	297.4703	301.7083	599.1785	4.2381

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	377.3	2.48	NS
TREATMENTS	7	673.8	4.43	**
ERROR	14	152.1		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	2434.6	2.55	NS
TREATMENTS	7	313834.2	328.61	****
ERROR	14	9550.0		NS

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	515944.42	2225.96	****
RESIDUAL	2	231.79		

R^2 0.9921

bo	11.639	sebo	4.461
b1	0.9349	seb1	0.0198

$H1: \hat{b}1 = 1$ 3.285 ***

$H0: \hat{b}1 = 0$ 47.170 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.98 ****

TABLE 3.2. 4 : LEAFLET AREA

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	46.1584	69.4965	115.6550	23.3381
2	98.8802	204.1508	303.0310	105.2706
3	72.5990	130.1046	202.7035	57.5056
4	715.1551	546.1490	1261.3041	-169.0060
5	127.4732	234.4398	361.9130	106.9666
6	799.9492	785.3405	1585.2897	-14.6086
7	904.7109	607.7678	1512.4787	-296.9431
8	959.7046	887.2887	1846.9933	-72.4160

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	8638	1.98	NS
TREATMENTS	7	60055	13.76	****
ERROR	14	4364		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	135699	7.28	**
TREATMENTS	7	1551173	83.16	****
ERROR	14	18652		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	1967293.88	207.62	****
RESIDUAL	22	9475.54		

R^2 0.9042

bo	96.724	sebo	30.656
b1	0.7225	seb1	0.0501

$H1: \hat{b}1 = 1$ 5.539 ****
$H0: \hat{b}1 = 0$ 14.421 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.499 *

TABLE 3.2. 5: LEAFLET WEIGHT

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	1734.2738	1019.1131	2753.3869	-715.1607
2	1791.3690	6705.2679	8496.6369	4913.8988
3	1278.7916	3034.2143	4313.0059	1755.4226
4	14182.1726	-1611.7143	12570.4583	-15793.8869
5	2266.4524	7569.6786	9836.1310	5303.2262
6	41251.3095	43051.0833	84302.3928	1799.7738
7	17020.4167	-1831.5655	15188.8512	-18851.9821
8	48274.2500	48319.1131	96593.3631	44.8631

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	$6.919\ 10^{5}$	0.05	NS
TREATMENTS	7	$2.597\ 10^{8}$	16.71	****
ERROR	14	$1.534\ 10^{7}$		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	$2.741\ 10^{8}$	1.74	NS
TREATMENTS	7	$4.360\ 10^{9}$	27.67	****
ERROR	14	$1.576\ 10^{9}$		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	7229987580	79.92	****
RESIDUAL	22	90468471		

R^2 0.7841

bo -1507.60 sebo 2550.78

b1 0.9258 seb1 0.1036

H1: $\hat{b}1 = 1$ 0.716 NS

H0: $\hat{b}1 = 0$ 8.936 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = 0.7969 ****

TABLE 3.2.6 : STIPULE LENGTH

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	38.6072	127.1131	165.7203	88.5060
2	50.2738	165.6369	215.9107	115.3631
3	437.4881	516.0595	953.5476	78.5714
4	45.6786	141.7738	187.4524	96.0953
5	446.2321	525.9583	927.1905	79.7262
6	104.4524	184.6429	289.0952	80.1095
7	406.9762	510.8691	917.8452	103.8929
8	397.1071	503.0119	900.1191	105.9048

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	2060.0	4.09	*
TREATMENTS	7	583.4	1.16	NS
ERROR	14	504.0		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	1564	0.38	NS
TREATMENTS	7	451154	109.21	****
ERROR	14	4131		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	786845.8	1153.52	****
RESIDUAL	22	682.1		

R^2 0.9813

bo	97.771	sebo	8.772
b1	0.9824	seb1	0.0289

$H1: \hat{b}1 = 1$ 0.609 NS

$H0: \hat{b}1 = 0$ 33.993 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.9596 ****

TABLE 3.2. 7: STIPULE WIDTH

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	34.0952	108.1667	142.2619	74.0714
2	40.7083	129.1131	169.8215	88.4048
3	373.8929	438.2083	812.1012	64.3155
4	39.6786	130.4345	170.1131	90.7560
5	394.6310	453.1964	847.8274	58.5655
6	73.8214	148.0357	221.8572	74.2143
7	343.2322	426.5298	769.7619	83.2976
8	301.9167	401.7202	703.6369	99.8036

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	2099.15	23.35	****
TREATMENTS	7	582.02	6.47	***
ERROR	14	89.92		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	16589	4.99	*
TREATMENTS	7	322504	96.90	****
ERROR	14	3328		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	569743.0	1352.12	****
RESIDUAL	22	421.4		

R^2 0.9840

bo	83.376	sebo	6.781
b1	0.9790	seb1	0.0266

$H1: \hat{b}1 = 1$ 0.789 NS
$H0: \hat{b}1 = 0$ 30.803 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.9420 ****

TABLE 3.2.8 : STIPULE AREA

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	108.8526	224.2453	333.0979	115.3927
2	124.6508	272.7861	397.4369	148.1354
3	421.0757	532.0634	953.1392	110.9877
4	127.9779	273.3901	401.3680	145.4123
5	477.8560	571.8639	1049.7199	94.0079
6	204.0892	297.7287	501.8179	93.6395
7	392.9460	530.3275	923.2735	137.3814
8	312.0592	473.4979	785.5571	161.4387

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	13743.7	36.89	****
TREATMENTS	7	1997.4	5.36	***
ERROR	14	372.6		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	52774	4.51	*
TREATMENTS	7	252888	21.62	****
ERROR	14	11700		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	482515.1	229.90	****
RESIDUAL	22	2098.8		

R^2 0.9127

bo	134.347	sebo	19.685
b1	0.9685	seb1	0.0639

$H1: \hat{b}1 = 1$ 0.493 NS
$H0: \hat{b}1 = 0$ 15.156 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.8629 ****

TABLE 3.2.9 : STIPULE WEIGHT

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	2114.2798	3436.1905	5550.4702	1321.9107
2	2388.2083	4521.9405	6910.1488	2133.7322
3	6935.4881	8550.9643	15486.4524	1615.4762
4	2475.8750	4386.5298	6862.4048	1910.6548
5	8376.0416	9491.6309	17867.6726	1115.5893
6	3484.4464	5037.8512	8522.2976	1553.4048
7	6969.0833	8746.0476	15715.1309	1776.9643
8	5736.7976	7839.4464	13576.2440	2102.6488

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	1801454	7.92	***
TREATMENTS	7	391313	1.72	NS
ERROR	14	227355		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	11538930	4.80	*
TREATMENTS	7	70744333	29.45	****
ERROR	14	2402498		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	126484726	313.78	****
RESIDUAL	22	403102		

R^2 0.9345

bo	2014.62	sebo	284.52
b1	0.9328	seb1	0.0527

$H1: \hat{b}1 = 1 \quad 1.275$ NS

$H0: \hat{b}1 = 0 \quad 17.700$ ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.8947 ****

TABLE 3.2.10: TENDRIL AREA

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	0.1682	-0.1740	-0.0058	-0.3422
2	1.1270	3.4637	4.5907	2.3367
3	0.0922	-0.0546	0.0377	-0.1468
4	38.3196	5.1600	43.4796	-33.1596
5	1.0802	3.1594	4.2396	2.0792
6	41.3531	24.8542	66.2074	-16.4989
7	35.8678	5.5227	41.3905	-30.3451
8	48.2404	27.1710	75.4114	-21.0694

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	48.56	3.41	NS
TREATMENTS	7	671.44	33.25	****
ERROR	14	20.20		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	410.20	5.26	*
TREATMENTS	7	2909.67	37.34	****
ERROR	14	77.93		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	1686.555	35.98	****
RESIDUAL	22	46.875		

R^2	0.6206		
bo	0.4865	sebo	1.949
b1	0.3922	seb1	0.0654

$H1: \hat{b}1 = 1$ 9.294 ****
$H0: \hat{b}1 = 0$ 5.997 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = 0.1801 NS

TABLE 3.2.11: TENDRIL WEIGHT

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	130.1428	52.9048	183.0476	-77.2381
2	1221.3453	2940.6071	4161.9524	1719.2619
3	94.0476	304.6071	398.6548	210.5595
4	30903.6667	2795.4524	33699.1191	-28108.2143
5	1036.5179	2620.9703	3657.4881	1584.4524
6	34936.6607	19169.8095	54106.4702	-15766.8512
7	22843.4583	4238.0774	27081.5357	-18605.3810
8	33720.8691	19148.1845	52869.0536	-14572.6845

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	$1.366\ 10^{7}$	1.79	NS
TREATMENTS	7	$3.966\ 10^{8}$	51.86	****
ERROR	14	$1.373\ 10^{8}$		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	$1.380\ 10^{8}$	6.36	*
TREATMENTS	7	$1.604\ 10^{9}$	73.98	****
ERROR	14	$2.169\ 10^{7}$		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	832979728	31.39	****
RESIDUAL	2	26532589		

R^2 0.5880

bo 564.76 sebo 1481.01

b1 0.3744 seb1 0.0668

H1: $\hat{b}1 = 1$ 9.365 ****

H0: $\hat{b}1 = 0$ 5.605 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = 0.1309 NS

TABLE 3.2.12: NUMBER OF PODDING NODES

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	0.1616	0.0780	0.2396	-0.0836
2	0.1926	0.0970	0.2895	-0.0956
3	0.3514	0.1526	0.5040	-0.1988
4	0.2216	-0.0184	0.2031	-0.2401
5	0.2454	0.1029	0.3484	-0.1425
6	0.3994	0.1297	0.5287	-0.2701
7	0.2463	0.1280	0.3743	-0.1183
8	0.4432	0.2055	0.6487	-0.2377

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.002210	0.26	NS
TREATMENTS	7	0.015687	1.82	NS
ERROR	14	0.008634		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.06848	1.33	NS
TREATMENTS	7	0.07230	1.40	NS
ERROR	14	0.05157		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	0.17384	22.85	****
RESIDUAL	22	0.00761		

R^2 0.5095

bo	-0.0645	sebo	0.0405
b1	0.6152	seb1	0.1287

$H1: \hat{b}1 = 1$ 2.990 **

$H0: \hat{b}1 = 0$ 4.780 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.6163 ***

TABLE 3.2.13 : POD NUMBER PER NODE

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	0.0021	0.0015	0.0036	-0.0005
2	0.0035	-0.0002	0.0034	-0.0037
3	0.0031	0.0023	0.0055	-0.0008
4	0.0042	0.0031	0.0072	-0.0012
5	0.0086	0.0028	0.0114	-0.0058
6	0.0046	-0.0001	0.0045	-0.0046
7	0.0109	0.0069	0.0178	-0.0030
8	0.0083	0.0055	0.0137	-0.0027

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.00000650	0.60	NS
TREATMENTS	7	0.00001052	0.96	NS
ERROR	14	0.00001093		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.00004067	1.51	NS
TREATMENTS	7	0.00008379	3.10	*
ERROR	14	0.00002700		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	0.00010	14.49	****
RESIDUAL	22	0.00001		

R^2	0.3971		
bo	-0.0001	sebo	0.0009
b1	0.5026	seb1	0.1320

H1: $\hat{b}1 = 1$ 3.768 ***
H0: $\hat{b}1 = 0$ 3.808 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.7461 ****

TABLE 3.2.14: SEED NUMBER PER POD

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	0.4446	0.0722	0.5168	-0.3725
2	0.2497	0.0316	0.2813	-0.2182
3	0.3715	-0.0429	0.3286	-0.4143
4	0.4764	0.1762	0.6526	-0.3003
5	0.3440	0.1881	0.5321	-0.1558
6	0.5719	0.2710	0.8430	-0.3009
7	0.5845	0.2437	0.8282	-0.3408
8	0.5131	0.2480	0.7612	-0.2650

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.18575	5.70	*
TREATMENTS	7	0.02087	0.64	NS
ERROR	14	0.03261		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.0051	0.03	NS
TREATMENTS	7	0.1399	0.89	NS
ERROR	14	0.1573		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	0.3283	8.83	**
RESIDUAL	22	0.0372		

R^2 0.2864

bo	-0.1147	sebo	0.0969
b1	0.5922	seb1	0.1993

$H1: \hat{b}1 = 1$ 2.046 (NS)
$H0: \hat{b}1 = 0$ 2.971 **

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.0717 NS

TABLE 3.2.15: GREEN PEA WEIGHT

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	1.4640	0.7214	2.1854	-0.7426
2	1.0637	0.5655	1.6292	-0.4983
3	0.7089	0.6579	1.3668	-0.0510
4	0.5820	0.3795	0.9615	-0.2025
5	1.2144	1.0474	2.2619	-0.1671
6	0.7694	0.5346	1.3040	-0.2349
7	1.5598	1.1525	2.7123	-0.4073
8	0.8033	0.7514	1.5547	-0.0519

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.5693	6.44	*
TREATMENTS	7	0.1718	1.94	NS
ERROR	14	0.0885		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.7769	1.00	NS
TREATMENTS	7	1.0276	1.33	NS
ERROR	14	0.7748		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	3.2539	20.98	****
RESIDUAL	22	0.1551		

R^2 0.4881

bo	-0.1037	sebo	0.1982
b1	0.8131	seb1	0.1775

$H1: \hat{b}1 = 1$ 1.054 NS
$H0: \hat{b}1 = 0$ 4.580 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.0954 NS

TABLE 3.2.16: ADJUSTED PEA YIELD

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	3.5642	2.3679	5.9322	-1.1963
2	2.4156	1.4009	3.8165	-1.0147
3	0.8752	0.5492	1.4244	-0.3260
4	0.7409	0.4841	1.2250	-0.2568
5	3.9413	1.1642	5.1055	-2.7771
6	3.6847	-0.6680	3.0167	-4.3527
7	1.5875	1.2839	2.8714	-0.3037
8	0.9481	0.7112	1.6594	-0.2369

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	16.499	2.03	NS
TREATMENTS	7	6.752	0.83	NS
ERROR	14	8.134		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	30.104	3.87	*
TREATMENTS	7	9.003	1.16	NS
ERROR	14	7.781		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	0.6190	0.20	NS
RESIDUAL	22	3.0279		

R^2	0.0092		
bo	0.7671	sebo	0.4779
b1	0.0651	seb1	0.1440

$H1: \hat{b}1 = 1$ 6.488 ****
$H0: \hat{b}1 = 0$ 0.452 NS

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = 0.5602 **

TABLE 3.2.17: POD WEIGHT PER PLANT

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	5.0870	4.0548	9.1417	-1.0322
2	2.9623	2.2371	5.1994	-0.7252
3	2.3368	2.9132	5.2500	0.5764
4	1.7203	2.1936	3.9139	0.4734
5	3.0161	3.1120	6.1281	0.0959
6	3.1111	2.3393	5.4505	-0.7718
7	5.3883	5.0265	10.4148	-0.3618
8	3.2068	3.8394	7.0461	0.6326

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	3.844	3.28	(NS)
TREATMENTS	7	1.340	1.14	NS
ERROR	14	1.172		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	5.328	0.54	NS
TREATMENTS	7	14.463	1.47	NS
ERROR	14	9.854		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	44.8835	31.24	****
RESIDUAL	22	1.4366		

R^2	0.5868		
bo	0.4316	sebo	0.5547
b1	0.8298	seb1	0.1485

$H1: \hat{b}1 = 1$ 0.674 NS
$H0: \hat{b}1 = 0$ 6.051 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

$r = -0.0745$ NS

TABLE 3.2.18: FLOWERING TIME

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	0.3750	0.3453	0.7202	-0.0298
2	0.8512	0.0000	0.8512	-0.8512
3	0.3453	-0.0357	0.3095	-0.3809
4	0.8333	0.5238	1.3572	-0.3095
5	0.4226	-0.1429	0.2798	-0.5655
6	0.9048	0.4524	1.3572	-0.4524
7	2.6072	1.6310	4.2381	-0.9762
8	2.2798	1.4643	3.7440	-0.8155

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.8970	5.47	*
TREATMENTS	7	0.3040	1.85	NS
ERROR	14	0.1640		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	3.8417	4.26	*
TREATMENTS	7	7.0364	7.81	****
ERROR	14	0.9015		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	10.3751	68.06	****
RESIDUAL	22	0.1524		

R^2	0.7557		
bo	-0.1763	sebo	0.1169
b1	0.6553	seb1	0.0794

$H1: \hat{b}1 = 1$ 4.341 ****
$H0: \hat{b}1 = 0$ 8.253 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = 0.7595 ****

TABLE 3.2.19: MATURITY LEVEL

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	1.7745	1.6135	3.3879	-0.1610
2	1.3400	-0.1477	1.1923	-1.4878
3	1.8388	-0.2654	1.5735	-2.1042
4	1.5190	1.3555	2.8745	-0.1636
5	1.4391	1.2929	2.7320	-0.1462
6	2.2669	1.0804	3.3473	-1.1865
7	2.9364	2.1398	5.0762	-0.7965
8	3.3821	2.4793	5.8614	-0.9028

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.4077	0.52	NS
TREATMENTS	7	1.5155	1.93	NS
ERROR	14	0.7845		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	4.494	1.67	NS
TREATMENTS	7	7.558	2.81	*
ERROR	14	2.687		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	14.5703	15.34	****
RESIDUAL	22	0.9495		

R^2 0.4109

bo	-0.3651	sebo	0.4448
b1	0.7558	seb1	0.1930

$H1: \hat{b}1 = 1$ 1.265 NS
$H0: \hat{b}1 = 0$ 3.916 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.5801 ****

TABLE 3.2.20: LEAFLET AREA (ARRAYS 4 and 7 removed)

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	36.3224	4.4356	40.7579	-31.8868
2	87.2859	83.8159	171.1018	-3.4700
3	71.8045	44.8469	116.6518	-26.9575
5	93.5580	38.5308	132.0888	-55.0272
6	119.2154	99.1648	218.3801	-20.0505
8	160.6256	154.0988	314.7243	-6.5268

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	8965	5.55	*
TREATMENTS	5	1066	0.66	NS
ERROR	10	1616		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	14776	2.59	NS
TREATMENTS	5	26495	4.64	*
ERROR	10	5708		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	31485	14.96	****
RESIDUAL	16	2105		

R^2	0.4831		
bo	4.3693	sebo	20.3025
b1	0.7009	seb1	0.1812

$H1: \hat{b}1 = 1$ 1.651 NS
$H0: \hat{b}1 = 0$ 3.868 ***

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.1228 NS

TABLE 3.2.21: LEAFLET WEIGHT (Arrays 4 and 7 Removed)

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	1502.4222	-200.2444	1302.1778	-1702.6667
2	1450.0445	3709.1778	5159.2222	2259.1333
3	1251.6889	705.0222	1956.7111	-546.6667
5	1491.6667	3756.6333	5248.3000	2264.9667
6	20143.9111	22473.4222	42617.3333	2329.5111
8	24269.8000	26841.0333	51110.8333	2571.2333

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	13694822	1.95	NS
TREATMENTS	5	10132927	1.44	NS
ERROR	10	7021876		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	$2.494\ 10^{8}$	2.14	NS
TREATMENTS	5	$1.540\ 10^{9}$	13.20	****
ERROR	10	$1.167\ 10^{8}$		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	$2.369\ 10^{9}$	258.77	****
RESIDUAL	16	$9.155\ 10^{6}$		

R^2 0.9419

bo 960.0635 sebo 890.8711

b1 1.0282 seb1 0.0639

H1: $\hat{b}1 = 1$ 0.441 NS

H0: $\hat{b}1 = 0$ 16.091 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = 0.9504 ****

TABLE 3.2.22: TENDRIL AREA (Arrays 4 and 7 Removed)

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	0.1820	-0.1872	-0.0052	-0.3692
2	0.7171	0.6282	1.3453	-0.0889
3	0.0801	-0.1010	-0.0209	-0.1811
5	0.7785	0.6532	1.4317	-0.1252
6	1.1527	0.7946	1.9472	-0.3581
8	1.2186	0.8069	2.0254	-0.4117

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.01208	0.63	NS
TREATMENTS	5	0.05887	3.05	(NS)
ERROR	10	0.01931		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	0.2887	2.88	NS
TREATMENTS	5	2.5319	25.24	****
ERROR	10	0.1003		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	2.8689	114.30	****
RESIDUAL	16	0.0251		

R^2 0.8774

bo	-0.1428	sebo	0.0654
b1	0.8359	seb1	0.0781

$H1: \hat{b}1 = 1$ 2.101 (NS)
$H0: \hat{b}1 = 0$ 10.703 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.8896 ****

TABLE 3.2.23: TENDRIL WEIGHT (Arrays 4 and 7 Removed)

(A) MEANS OF ESTIMATES OF ARRAY VARIANCES (VR) AND COVARIANCES (WR)

ARRAY	VR	WR	(WR+VR)	(WR-VR)
1	167.2111	-189.0000	-21.7889	-356.2111
2	845.7778	668.6000	1514.3778	-177.1778
3	82.1445	-96.1778	-14.0333	-178.3222
5	737.4778	604.8667	1342.3444	-132.6111
6	1325.2222	833.2111	2158.4333	-492.0111
8	940.6334	693.2778	1633.9111	-247.3555

(B) ANALYSIS OF VARIANCE (WR-VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	21275	2.10	NS
TREATMENTS	5	55746	5.49	*
ERROR	10	10146		

(C) ANALYSIS OF VARIANCE (WR+VR)

SOURCE	DF	MS	F	SIG
BLOCKS	2	62180	1.26	***
TREATMENTS	5	2481140	50.46	
ERROR	10	49175		

(D) REGRESSION ANALYSIS WR ON VR

SOURCE	DF	MS	F	SIG
REGRESSION	1	2710326	123.38	****
RESIDUAL	16	21968		

R^2 0.8852

bo	-168.6485	sebo	63.4095
b1	0.8605	seb1	0.0775

$H1: \hat{b}1 = 1$ 1.800 (NS)
$H0: \hat{b}1 = 0$ 11.102 ****

(E) CORRELATION BETWEEN (WR+VR) AND $\bar{P}$

r = -0.9069 ****

The Wr on Vr regression analysis includes the test of significance of the slope of the regression line from zero and unity using a two tailed t-test.

Tables 3.3.1 to 3.3.19 contain the components of variation with;

(i) the second degree statistics
(ii) their perfect fit estimates, and
(iii) the derived statistics for each character analysed.
The WrVr graph and parabola, $Wr^2 = VrVp$, for each character are found in Figures 3.1 to 3.22.

3.2.1 Leaf characters

The test for the additive-dominance model for the five leaf characters showed leaflet number was the only character having (Wr-Vr) consistent over arrays. The slopes of the five regression lines were all close to unity, tests of significance however showed significant differences at the five percent level for all characters except leaflet weight. This may be attributed to the high R^2 values and low standard errors.

An examination of the WrVr graphs for leaflet length and leaflet width, figures 3.2 and 3.3, tended to indicate the presence of duplicate gene action due to the clustering of points near the origin (Mather 1967). The type of interaction was not distinguishable for leaflet area.

As the components of variation are affected by non-allelic gene interaction an accurate interpretation may be difficult (Hayman 1954a). However the results for leaflet length and width indicate the following:

(i) the high heritability, both narrow and broadsence,
(ii) additive genetic variance being greater than dominance variance and
(iii) wide, long leaflet forms being dominant to the shorter, narrower or leafless forms.

TABLE 3.3:

Second degree statistics, Vp, $\bar{V}r$, $\bar{W}r$, $V\bar{r}$ and E, and components D, H_1, H_2, F, $\sqrt{H_1/D}$, UV, $\frac{1}{2}F/\sqrt{D(H_1 - H_2)}$, h^2ns, h^2bs, KD/KR and K for each block and block means.

TABLE 3.3.1 : LEAFLET NUMBER

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	111776.7943	75646.6955	66880.1370	84767.8756
$\overline{Vr}$	31317.5683	20270.4136	16777.9872	22788.6564
$\overline{Wr}$	29493.5629	19634.5607	16805.9505	21978.0247
$V\overline{r}$	7824.2008	5102.1951	4226.2586	5717.5515
E	920.9598	920.9598	920.9598	920.9598

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	110855.8345	74725.7357	65959.1772	83846.9158
H1	114928.4968	74045.7880	62623.9647	83866.0832
H2	90750.1107	57449.5147	46983.5551	65061.0602
F	104197.8973	71373.7085	65155.0325	80242.2127
$\sqrt{H1/D}$	1.0182	0.9954	0.9744	0.9960
UV	0.1974	0.1940	0.1876	0.1930
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	1.0063	1.0134	1.0143	1.0113
h^2ns	0.3951	0.3949	0.3936	0.3945
h^2bs	0.9764	0.9635	0.9559	0.9653
KD/KR	2.714	2.844	3.056	2.872
K				1.07

TABLE 3.3. 2: LEAFLET LENGTH

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	827.3571	787.4286	721.4107	778.7321
$\overline{Vr}$	454.1875	460.3304	413.3013	442.6064
$\overline{Wr}$	435.1964	400.8571	389.4397	408.4977
$\overline{Vr}$	232.4152	205.2042	213.4573	217.0256
E	6.1696	6.1696	6.1696	6.1696

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	821.1875	781.2590	715.2411	772.5625
H1	875.5583	997.5586	789.0939	887.4036
H2	865.4956	998.9112	777.7824	880.7297
F	-95.3258	-37.8256	-124.1918	-85.7811
$\sqrt{H1/D}$	1.0326	1.1300	1.0504	1.0710
UV	0.2471	0.2503	0.2464	0.2480
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-0.5243	-0.5818	-0.6904	-0.5988
h^2ns	0.6755	0.6151	0.6795	0.6567
h^2bs	0.9910	0.9907	0.9901	0.9906
KD/KR	0.894	0.958	0.847	0.900
K				1.10

TABLE 3.3.3 : LEAFLET WIDTH

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	321.4107	308.9821	293.8393	308.0774
$\overline{Vr}$	170.4665	163.6317	150.3683	161.4888
$\overline{Wr}$	172.3638	157.5379	157.9442	162.6153
$V\overline{r}$	93.5287	80.9573	86.1091	86.8650
E	3.2902	2.2902	3.2902	3.2902

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	318.1205	305.6919	290.5491	304.7872
H1	299.0156	318.5514	248.7298	288.7656
H2	296.2355	319.1819	245.5211	286.9795
F	-51.5691	-17.1227	-49.0335	-39.2418
$\sqrt{H1/D}$	0.9695	1.0208	0.9252	0.9719
UV	0.2477	0.2505	0.2468	0.2483
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-0.8670	-0.6167	-0.8030	-0.76222
h^2ns	0.7065	0.6597	0.7260	0.6974
h^2bs	0.9875	0.9865	0.9861	0.9867
KD/KR	0.846	0.947	0.833	0.875
K				1.17

TABLE 3.3. 4: LEAFLET AREA

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	973.8712	817.3070	769.8821	853.6868
$\overline{Vr}$	512.8828	504.8459	379.0078	465.5788
$\overline{Wr}$	498.8594	435.8072	373.6100	433.0922
$V\overline{r}$	278.2067	237.7722	213.6293	243.2027
E	33.2898	33.2898	33.2898	33.2898

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	940.5814	784.0182	736.5923	820.3970
H1	916.1607	943.6577	641.6692	833.8292
H2	822.1901	951.7805	544.9997	772.9901
F	-61.6299	-158.5495	-4.6105	-74.9300
$\sqrt{H1/D}$	0.9869	1.0971	0.9333	1.0058
UV	0.2244	0.2522	0.2123	0.2296
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-0.1036	-0.9934	-0.0086	-0.3686
h^2ns	0.6965	0.6327	0.7119	0.6804
h^2bs	0.9577	0.9549	0.9434	0.9520
KD/KR	0.936	0.831	0.993	0.920
K				0.12

TABLE 3.3.5 : LEAFLET WEIGHT

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	56641.2679	50403.1429	42328.8393	49791.0834
$\overline{Vr}$	17154.5290	18132.4866	12637.6228	15974.8795
$\overline{Wr}$	14772.8013	15166.3036	9906.5915	13281.8988
$V\bar{r}$	5427.0555	6078.1998	4457.1604	5320.8052
E	1925.7992	1925.7992	1925.7992	1925.7992

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	54715.4687	48477.3437	40403.0401	47865.2842
H1	57502.0823	53601.7785	44586.8681	51896.9096
H2	40169.5968	41476.8500	25981.5524	35875.9997
F	51302.6318	37252.3726	42142.6138	43565.8727
$\sqrt{H1/D}$	1.0251	1.0515	1.0505	1.0424
UV	0.1746	0.1934	0.1457	0.1713
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	0.8330	0.7683	0.7685	0.7899
h^2ns	0.4643	0.4871	0.5003	0.4839
h^2bs	0.9138	0.9197	0.8857	0.9064
KD/KR	2.685	2.152	2.972	2.603
K				0.23

TABLE 3.3.6 : STIPULE LENGTH

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	686.2143	719.9286	571.8393	659.3274
$\overline{Vr}$	234.1875	244.7857	243.5826	240.8519
$\overline{Wr}$	339.0804	345.3125	318.7567	334.3832
$V\overline{r}$	170.1685	167.7935	181.4997	173.1539
E	13.0881	13.0881	13.0881	13.0881

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	673.1262	706.8405	558.7512	646.2393
H1	207.7462	258.9250	212.2465	226.3059
H2	210.2676	262.1605	202.5233	224.9838
F	-3.5252	38.9750	-150.9804	-38.5102
$\sqrt{H1/D}$	0.5555	0.6052	0.6163	0.5924
UV	0.2530	0.2531	0.2385	0.2482
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-0.0428	0.4075	-1.0242	-0.2198
h^2ns	0.8370	0.8087	0.8495	0.8317
h^2bs	0.9675	0.9682	0.9691	0.9682
KD/KR	0.991	1.095	0.640	0.909
K				1.71

TABLE 3.3.7 : STIPULE WIDTH

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	611.1250	559.7143	443.1250	537.9881
$\overline{Vr}$	215.2567	199.5446	185.9397	200.2470
$\overline{Wr}$	310.7879	278.4107	249.0781	279.4256
$\overline{Vr}$	159.3033	139.9018	142.0466	147.0839
E	7.1183	7.1183	7.1183	7.1183

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	604.0067	552.5960	436.0067	530.8698
H1	196.9678	212.2175	158.5391	189.2415
H2	198.8995	213.6571	150.6583	187.7383
F	-31.5791	-4.8917	-120.7398	-52.4035
$\sqrt{H1/D}$	0.5711	0.6197	0.6030	0.5979
UV	0.2525	0.2517	0.2376	0.2472
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-0.4623	-0.0867	-1.0299	-0.5263
h^2ns	0.8479	0.8212	0.8631	0.8441
h^2bs	0.9810	0.9790	0.9782	0.9794
KD/KR	0.912	0.986	0.627	0.842
K				1.56

TABLE 3.3.8 : STIPULE AREA

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	878.5364	767.1141	555.9250	733.8585
$\overline{Vr}$	289.0095	275.0122	249.5436	396.9879
$\overline{Wr}$	455.9916	401.3377	333.6343	396.9879
$V\overline{r}$	240.6323	212.7813	205.1257	219.5131
E	17.7639	17.7639	17.7639	17.7639

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	860.7725	749.3502	538.1611	716.0946
H1	130.6704	181.8746	139.6246	150.7232
H2	131.3351	186.7499	115.4979	144.5277
F	-93.5395	-97.7684	-249.3331	-146.8803
$\sqrt{H1/D}$	0.3896	0.4927	0.5094	0.4639
UV	0.2513	0.2567	0.2068	0.2383
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-1.9553	-0.8088	-1.0941	-1.2860
h^2ns	0.9041	0.8673	0.8969	0.8894
h^2bs	0.9663	0.9634	0.9607	0.9635
KD/KR	0.755	0.766	0.375	0.632
K				2.00

TABLE 3.3.9 : STIPULE WEIGHT

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	11800.1250	12207.0714	9688.7857	11231.9940
$\overline{Vr}$	5254.3147	4784.5089	4391.2589	4810.0275
$\overline{Wr}$	7021.1719	6908.0268	5574.7768	6501.3252
$\sqrt{r}$	4283.7988	3995.3560	3279.3382	3852.8310
E	370.2540	370.2540	370.2540	370.2540

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	11429.8710	11836.8174	9318.5317	10861.7400
H1	3066.5532	2046.8568	3288.5711	2800.6604
H2	2586.1746	1860.7226	3151.7938	2532.8970
F	-5039.8186	-3773.3454	-3476.9168	-4096.6936
$\sqrt{H1/D}$	0.5180	0.4158	0.5941	0.5093
UV	0.2108	0.2273	0.2396	0.2259
$\frac{1}{2}F/\sqrt{D(H_1 - H_2)}$	-1.0754	-1.2711	-1.5399	-1.2954
h^2ns	0.8929	0.9043	0.8481	0.8818
h^2bs	0.9610	0.9576	0.9514	0.9567
KD/KR	0.403	0.446	0.527	0.457
K				2.41

TABLE 3.3.10: TENDRIL AREA

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	14.3279	19.6171	12.2070	15.3840
$\overline{Vr}$	19.4800	26.1036	16.7596	20.7811
$\overline{Wr}$	7.7622	11.3116	6.8396	8.6378
$V\overline{r}$	6.2892	9.1997	5.5381	7.0090
E	0.7266	0.7266	0.7266	0.7266

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	13.6013	18.8905	11.4804	14.6574
H1	57.9294	75.5154	48.6173	60.6874
H2	50.2201	65.0725	42.3429	52.5452
F	-3.4829	-7.1021	-4.0343	-4.8731
$\sqrt{H1/D}$	2.0638	1.9994	2.0579	2.0403
UV	0.2167	0.2154	0.2177	0.2166
$\frac{1}{2}F/\sqrt{D(H_1 - H_2)}$	-0.1701	-0.2528	-0.2377	-0.2202
h^2ns	0.4828	0.5174	0.4906	0.4969
h^2bs	0.9717	0.9794	0.9673	0.9728
KD/KR	0.883	0.828	0.843	0.851
K				0.09

TABLE 3.3.11: TENDRIL WEIGHT

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	10043.6429	13811.0714	9192.2679	11015.6607
$\overline{Vr}$	13629.4509	18684.8304	14518.2344	15610.8386
$\overline{Wr}$	5661.8125	8114.4732	5450.1942	6408.8266
$V\overline{r}$	4657.7533	6585.7846	4656.4015	5299.9798
E	497.6786	497.6786	497.6786	497.6786

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	9545.9643	13313.3928	8694.5893	10517.9821
H1	39674.6428	53852.9465	43224.8750	45584.1548
H2	34144.9153	46654.3081	37705.4565	39501.5600
F	-3306.4821	-5582.2679	-4162.7589	-4350.5030
$\sqrt{H1/D}$	2.0387	2.0112	2.2297	2.0932
UV	0.2152	0.2166	0.2181	0.2166
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-0.2275	-0.2851	-0.3005	-0.2710
h^2ns	0.5043	0.5176	0.4808	0.5009
h^2bs	0.9727	0.9803	0.9740	0.9756
KD/KR	0.843	0.811	0.806	0.820
K				0.14

TABLE 3.3.12: NUMBER OF PODDING NODES

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	0.2743	0.4455	0.3484	0.3561
$\overline{Vr}$	0.2268	0.3357	0.2856	0.2827
$\overline{Wr}$	0.0693	0.1450	0.1139	0.1094
$V\overline{r}$	0.0361	0.0633	0.0439	0.0478
E	0.2086	0.2086	0.2086	0.2086

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	0.0657	0.2369	0.1398	0.1475
H1	-0.0344	0.2696	0.0965	0.1106
H2	0.0327	0.3595	0.2367	0.2096
F	-0.0415	-0.0019	-0.0717	-0.0384
$\sqrt{H1/D}$	0.7236	1.0668	0.8308	0.8737
UV	-0.2376	0.3334	0.6132	0.2363
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-0.3125	-0.0065	-0.2561	-0.1917
h^2ns	0.0847	0.1996	0.1175	0.1339
h^2bs	0.1192	0.4406	0.3125	0.2908
KD/KR	0.392	0.992	0.528	0.638
K				3.04

TABLE 3.3.13 : POD NUMBER PER NODE

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	0.0123	0.0049	0.0201	0.0124
$\overline{Vr}$	0.0050	0.0049	0.0070	0.0056
$\overline{Wr}$	0.0032	0.0013	0.0038	0.0028
$V\bar{r}$	0.0014	0.0008	0.0009	0.0010
E	0.0044	0.0044	0.0044	0.0044

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	0.0079	0.0005	0.0157	0.0080
H1	-0.0003	-0.0005	0.0131	0.0041
H2	-0.0010	0.0010	0.0090	0.0030
F	0.0052	-0.0020	0.0184	0.0072
$\sqrt{H1/D}$	0.1949	1.0000	0.9135	0.7028
UV	0.8333	-0.5000	0.1718	0.1684
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	1.1056	-1.1547	1.1467	0.3659
h^2ns	0.2906	0.0971	0.0952	0.1610
h^2bs	0.2479	0.1456	0.4014	0.2650
KD/KR	-3.903	-0.333	4.579	0.114
K				1.39

TABLE 3.3.14 : SEED NUMBER PER POD

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	0.4254	0.6281	0.9798	0.6778
$\overline{Vr}$	0.4417	0.5094	0.3823	0.4445
$\overline{Wr}$	0.1544	0.0569	0.2342	0.1485
$V\overline{r}$	0.0705	0.0270	0.0772	0.0582
E	0.3285	0.3285	0.3285	0.3285

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	0.0969	0.2996	0.6513	0.3493
H1	0.0964	0.9599	0.0939	0.3834
H2	0.3350	0.7799	0.0707	0.3952
F	-0.2595	0.5359	0.5301	0.2688
$\sqrt{H1/D}$	0.9972	1.7899	0.3798	1.0556
UV	0.8694	0.2031	0.1880	0.4202
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-0.8533	1.1537	2.1514	0.8173
h^2ns	0.1250	-0.0568	0.1727	0.0803
h^2bs	0.3028	0.3368	0.2149	0.2848
KD/KR	-0.146	2.997	-28.864	-8.671
K				0.18

TABLE 3.3.15: GREEN PEA WEIGHT

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	2.3648	1.5788	2.9601	2.3012
$\overline{Vr}$	1.0452	0.9879	1.0291	1.0207
$\overline{Wr}$	0.7540	0.4248	1.0000	0.7263
$V\overline{r}$	0.2561	0.2160	0.4050	0.2924
E	0.6257	0.6257	0.6257	0.6257

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	1.7391	0.9531	2.3344	1.6755
H1	0.7139	1.0155	0.2608	0.6634
H2	0.9664	0.8977	0.3064	0.7235
F	0.7750	0.5199	0.9816	0.7588
$\sqrt{H1/D}$	0.6407	1.0322	0.3343	0.6691
UV	0.3384	0.2210	0.2937	0.2844
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	0.5848	0.7754	1.5044	0.9549
h^2ns	0.2909	0.2448	0.4820	0.3392
h^2bs	0.4884	0.4442	0.5385	0.4904
KD/KR	2.066	1.718	4.391	2.725
K				0.17

TABLE 3.3.16: ADJUSTED PEA YIELD

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	7.7912	1.2246	4.1361	4.3840
$\overline{Vr}$	4.1004	1.0823	1.4764	2.2197
$\overline{Wr}$	1.1543	0.3697	1.2110	0.9117
$V\overline{r}$	0.4045	0.2357	0.4866	0.3756
E	2.0167	2.0167	2.0167	2.0167

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	5.7745	-0.7921	2.1194	2.3673
H1	10.5005	-5.0001	-3.8774	0.5410
H2	7.7252	-3.6721	-3.0992	0.3180
F	7.9402	-2.0546	0.4032	2.0962
$\sqrt{H1/D}$	1.3485	2.5125	1.3526	1.7379
UV	0.1839	0.1836	0.1998	0.1891
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	0.9917	-1.0016	0.1570	0.0490
h^2ns	0.0717	-0.0307	0.2741	0.1050
h^2bs	0.5258	-0.8520	-0.1787	-0.1816
KD/KR	3.080	0.319	1.151	1.517
K				0.02

TABLE 3.3.17: POD WEIGHT PER PLANT

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	10.9396	7.8099	11.5596	10.1030
$\overline{Vr}$	3.6457	3.1532	3.2618	3.3536
$\overline{Wr}$	3.2497	2.4858	3.9079	3.2145
$V\overline{r}$	1.0781	1.0108	1.5658	1.2182
E	2.0482	2.0482	2.0482	2.0482

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	8.8914	5.7617	9.5114	8.0548
H1	3.3067	1.2626	-0.2417	1.4425
H2	3.1017	1.4009	-0.3847	1.3726
F	5.8081	2.6043	4.4153	4.2759
$\sqrt{H1/D}$	0.6098	0.4681	0.1594	0.4125
UV	0.2345	0.2774	0.3979	0.3033
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	2.1510	1.4587	1.8930	1.8342
h^2ns	0.3680	0.3863	0.5730	0.4424
h^2bs	0.5416	0.4759	0.5520	0.5231
KD/KR	3.306	2.867	-5.386	0.263

TABLE 3.3.18: FLOWERING TIME

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	0.5714	1.9286	2.8571	1.7857
$\overline{Vr}$	0.7545	0.8304	1.6473	1.0774
$\overline{Wr}$	0.2857	0.5714	0.7321	0.5297
$\overline{Vr}$	0.1920	0.2411	0.3605	0.2645
E	0.5299	0.5299	0.5299	0.5299

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	0.0415	1.3987	2.3272	1.2558
H1	0.0620	0.5801	4.1333	1.5918
H2	0.3954	0.5026	3.2926	1.3968
F	-0.7949	0.7767	1.9909	0.6576
$\sqrt{H1/D}$	1.2228	0.6440	1.3327	1.0665
UV	1.5929	0.2166	0.1991	0.6695
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	-3.3792	1.1796	0.7117	-0.4960
h^2ns	0.2857	0.3479	0.3031	0.3123
h^2bs	0.3980	0.4729	0.7271	0.5327
KD/KR	-0.774	2.516	1.945	1.229
K				0.73

TABLE 3.3.19 : MATURITY LEVEL

SECOND DEGREE STATISTICS

STATISTIC	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
Vp	3.2034	2.9939	5.9530	4.0501
$\overline{Vr}$	1.9739	1.7010	2.5114	2.0621
$\overline{Wr}$	0.8993	1.0735	1.6078	1.1935
$V\overline{r}$	0.4783	0.6428	0.6465	0.5892
E	1.2142	1.2142	1.2142	1.2142

PERFECT FIT ESTIMATES

COMPONENT	BLOCK 1	BLOCK 2	BLOCK 3	MEAN
D	1.9892	1.7797	4.7388	2.8359
H1	2.0379	0.0400	4.1035	2.0605
H2	1.7327	-0.0169	3.2099	1.6419
F	0.9883	-0.1275	3.6535	1.5048
$\sqrt{H1/D}$	1.0122	0.1499	0.9306	0.6975
UV	0.2126	-0.1056	0.1956	0.1008
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	0.6342	-0.2003	0.8877	0.4405
h^2ns	0.2839	0.4480	0.3291	0.3537
h^2bs	0.4722	0.4461	0.5961	0.5048
KD/KR	1.651	0.614	2.414	1.560
K				0.041

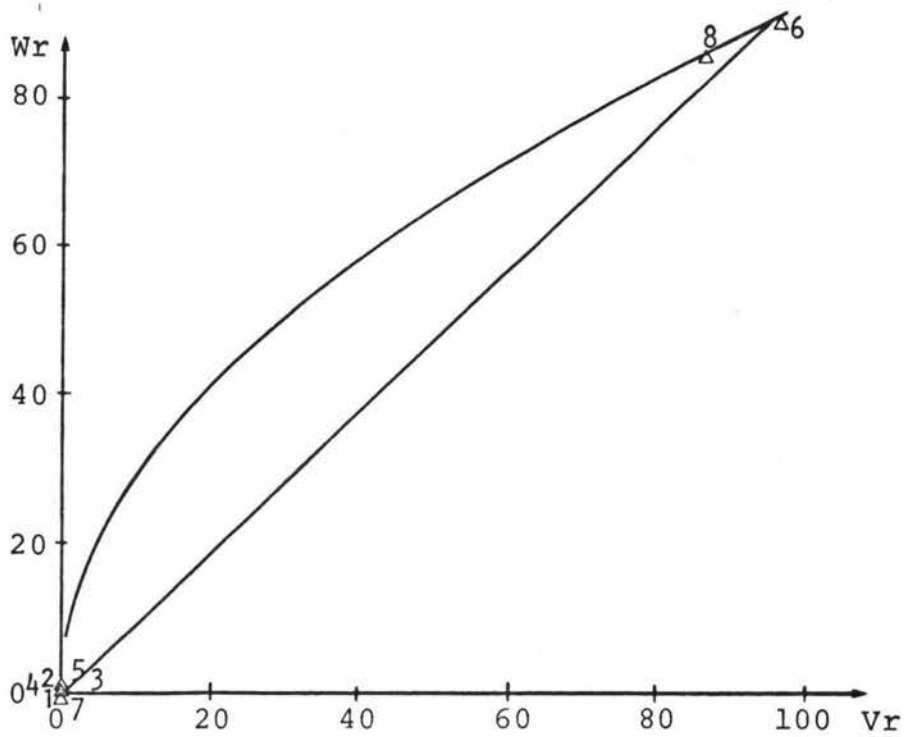

FIGURE 3.1
WrVr graph for leaflet number

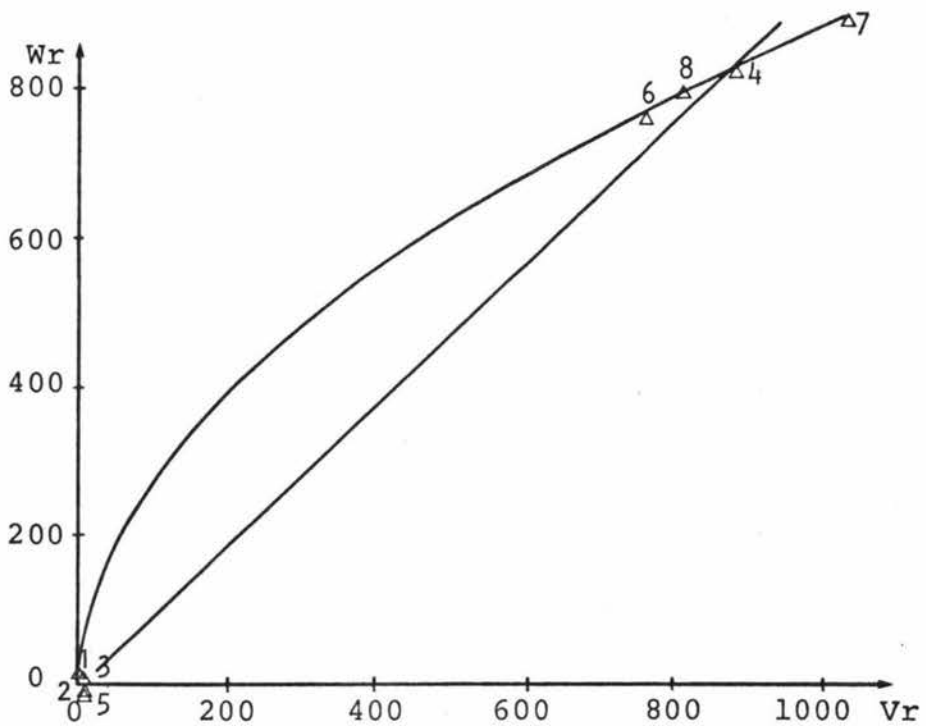

FIGURE 3.2
WrVr graph for leaflet length

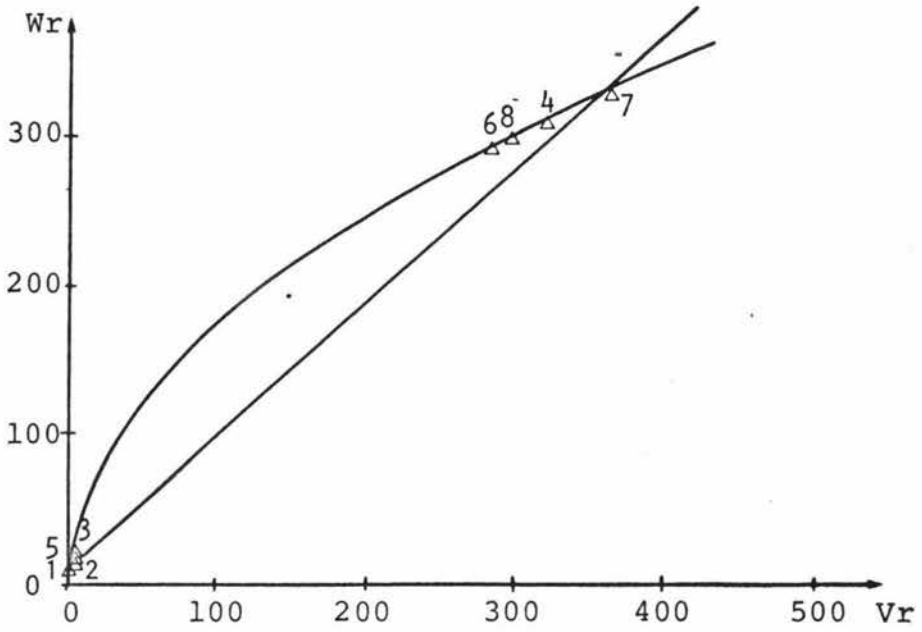

FIGURE 3.3
WrVr graph for leaflet width

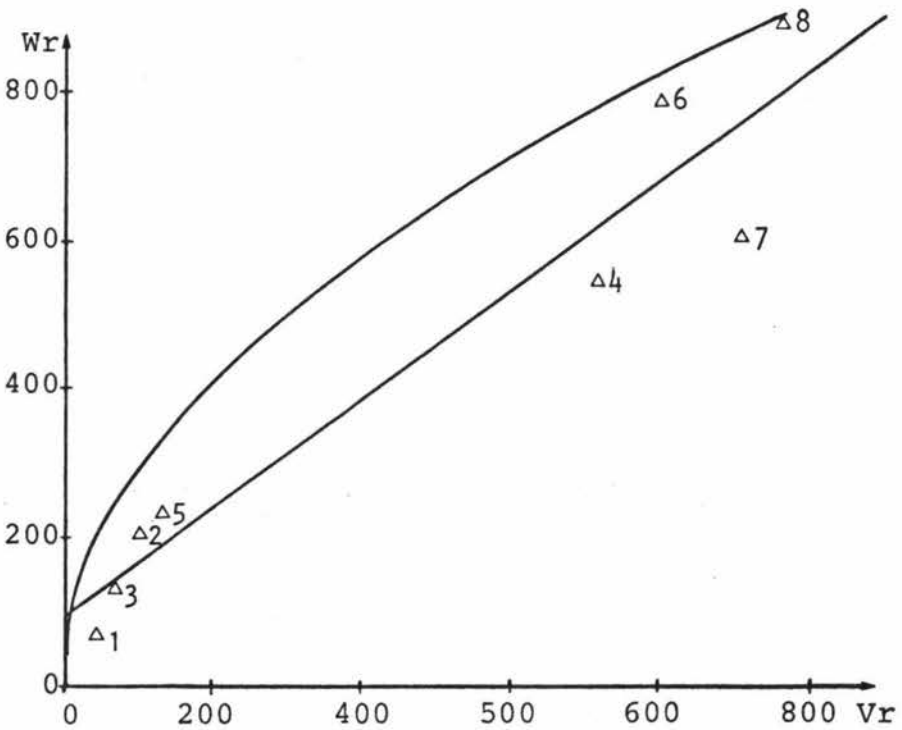

FIGURE 3.4
WrVr graph for leaflet area

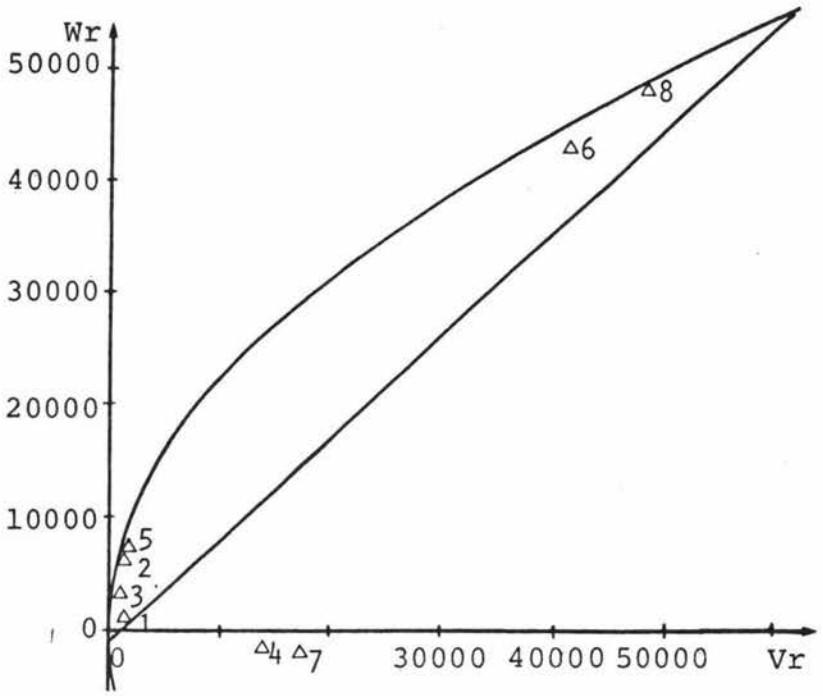

FIGURE 3.5
WrVr graph for leaf weight

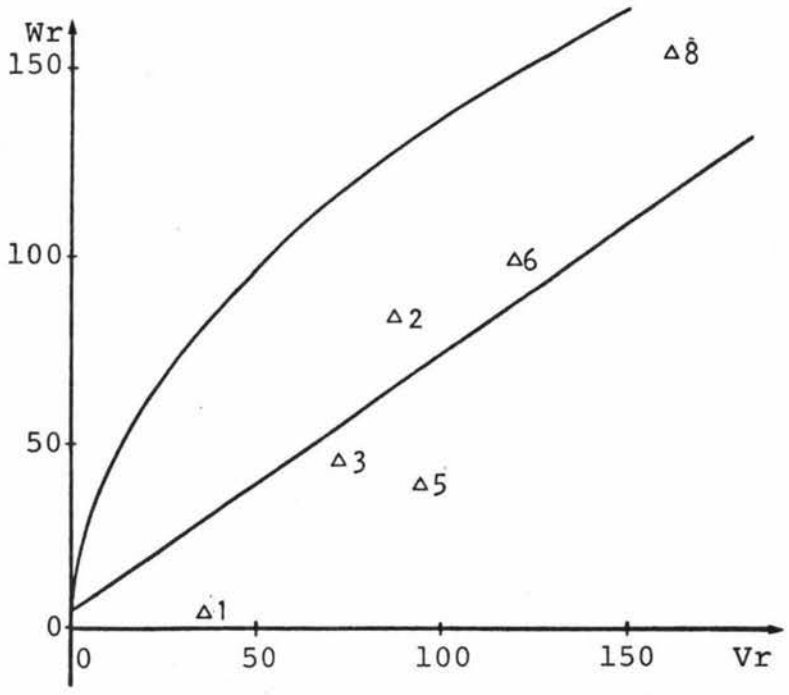

FIGURE 3.6
WrVr graph for leaflet area
(arrays 4 and 7 removed)

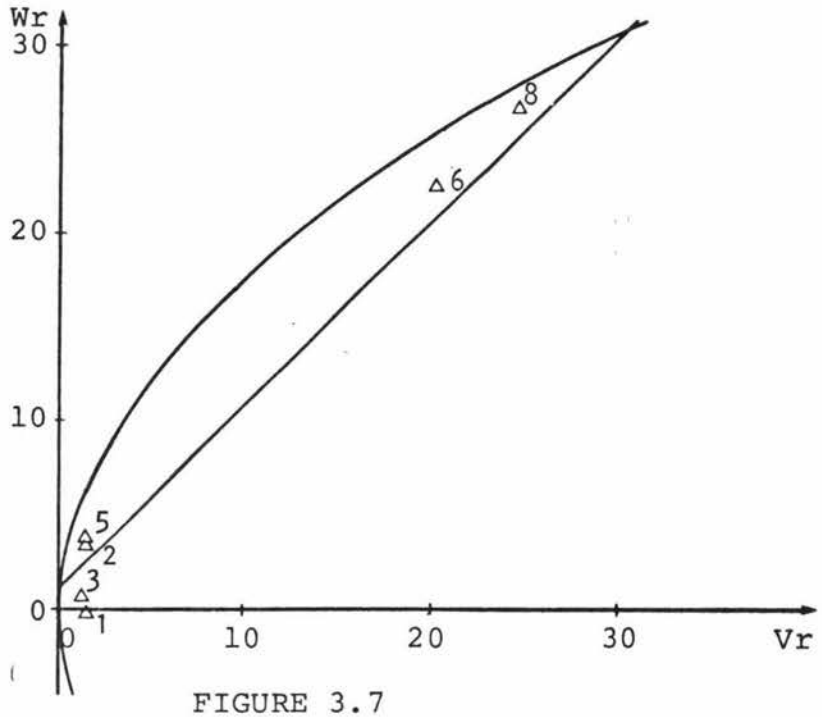

FIGURE 3.7

WrVr graph for leaf weight
(arrays 4 and 7 removed)

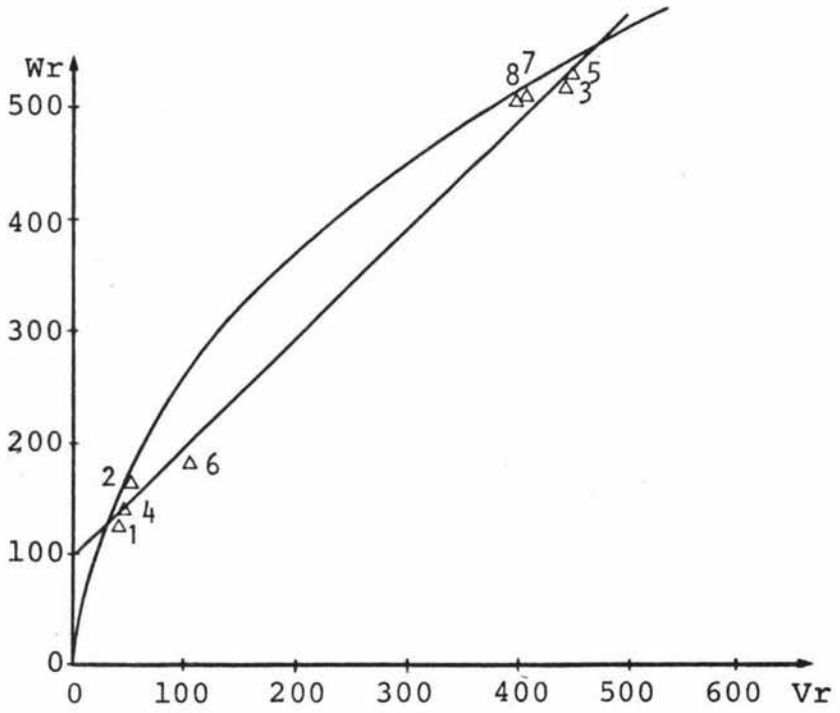

FIGURE 3.8

WrVr graph for stipule length

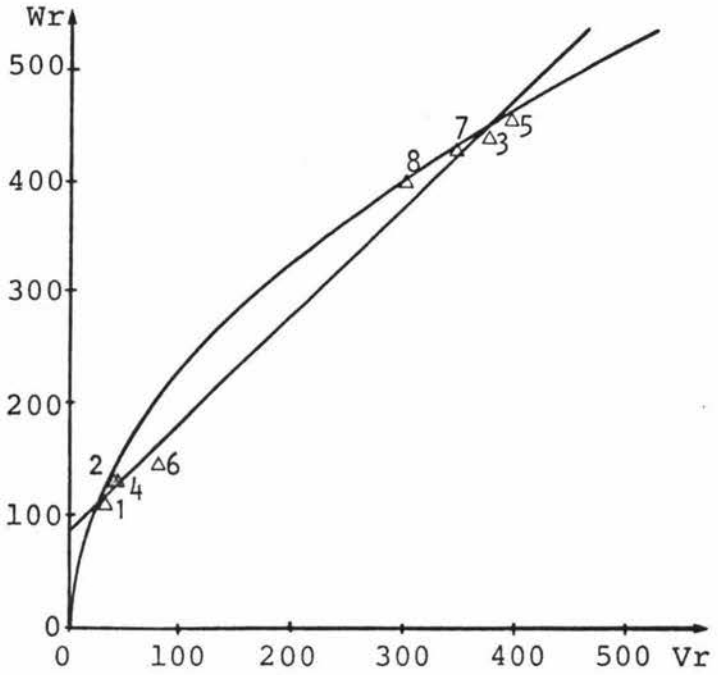

FIGURE 3.9
WrVr graph for stipule width

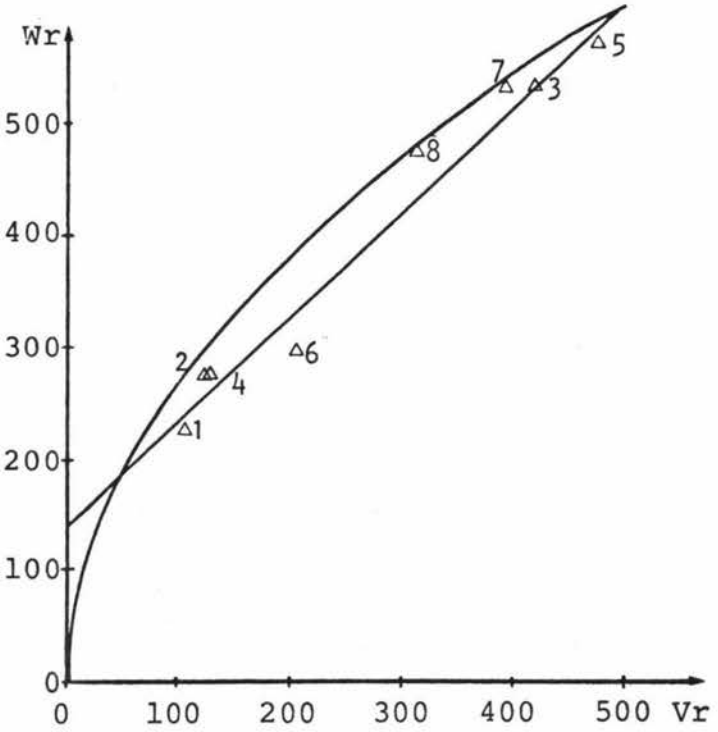

FIGURE 3.10
WrVr graph for stipule area

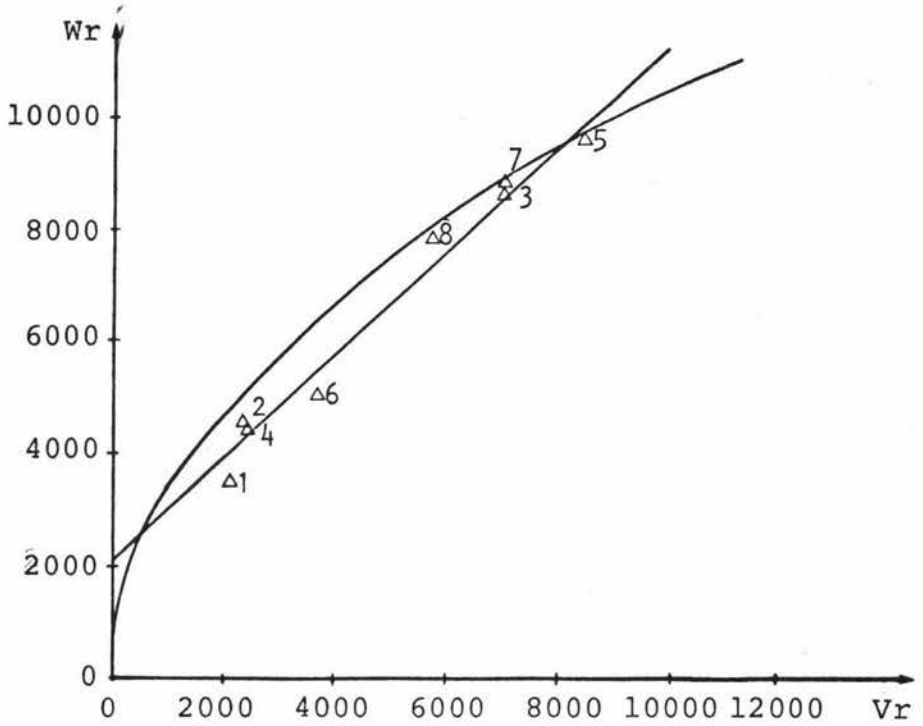

FIGURE 3.11
WrVr graph for stipule weight

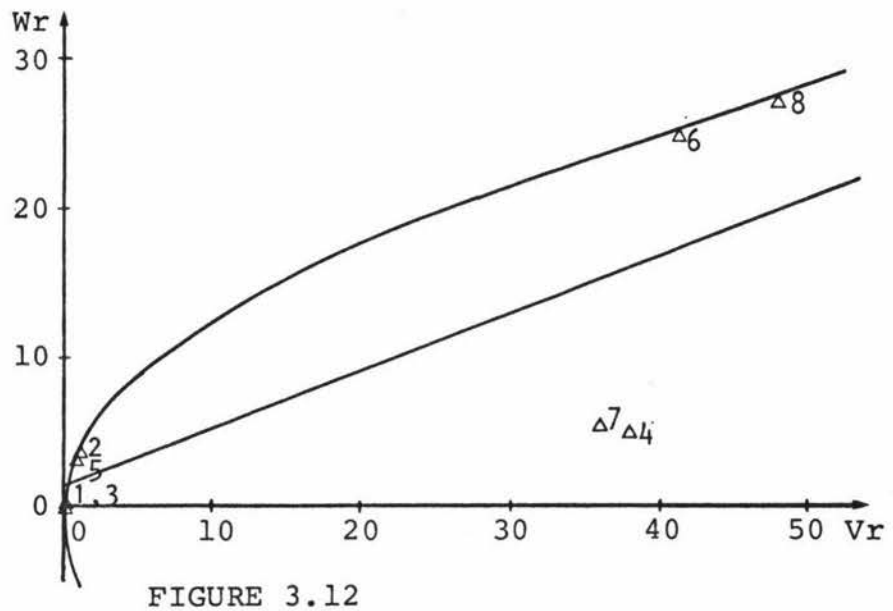

FIGURE 3.12
WrVr graph for tendril area

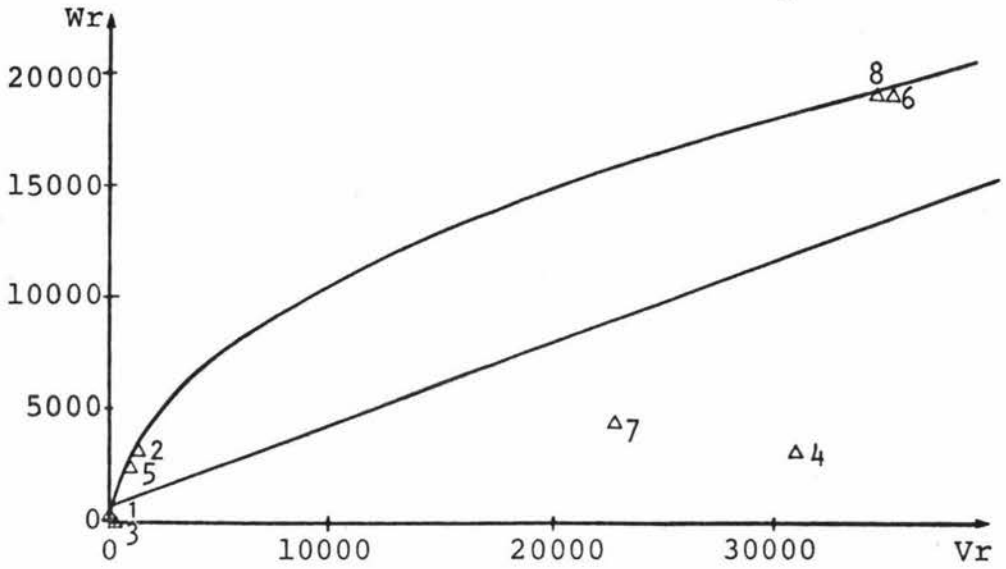

FIGURE 3.13
WrVr graph for tendril weight

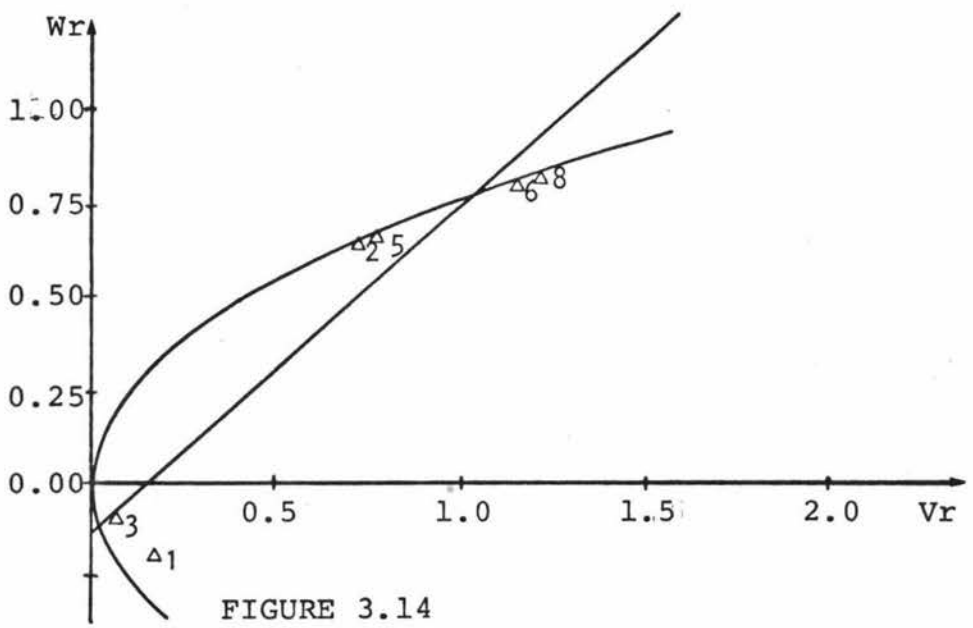

FIGURE 3.14
WrVr graph for tendril area
(arrays 4 and 7 removed)

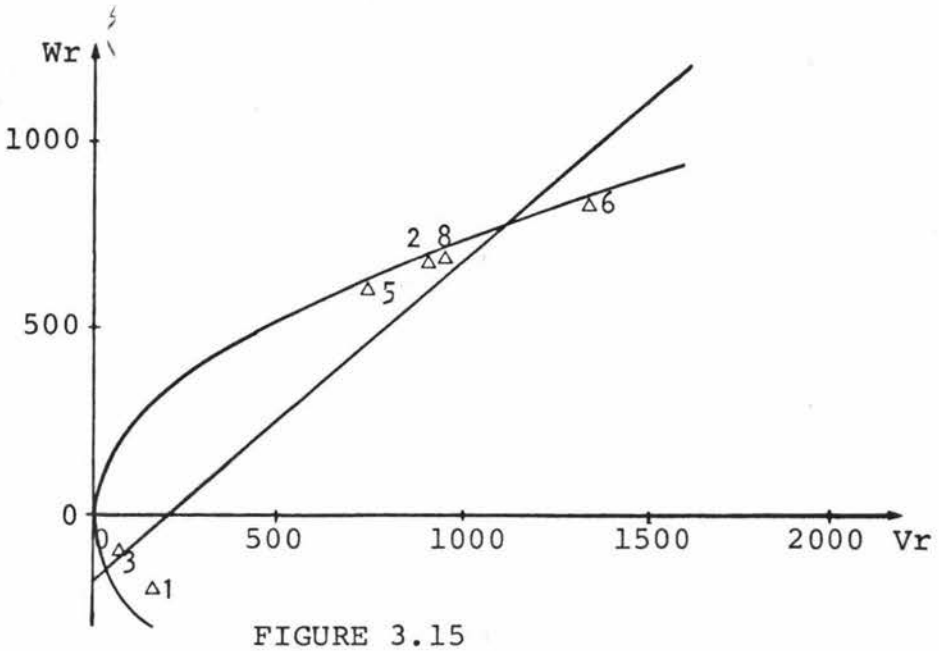

FIGURE 3.15

WrVr graph for tendril weight
(arrays 4 and 7 removed)

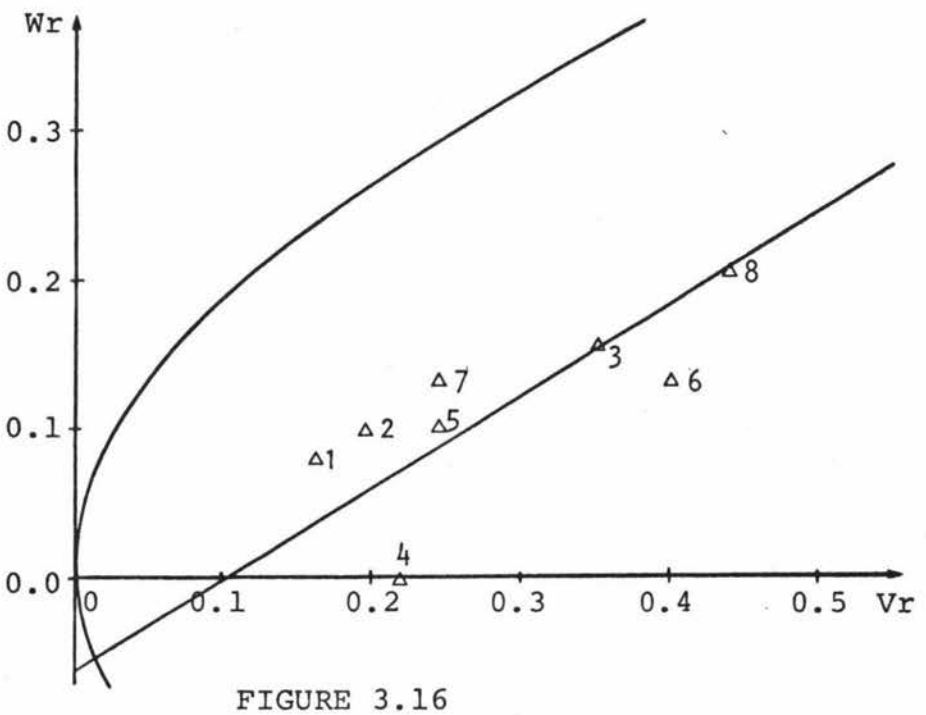

FIGURE 3.16

WrVr graph for number of podding nodes

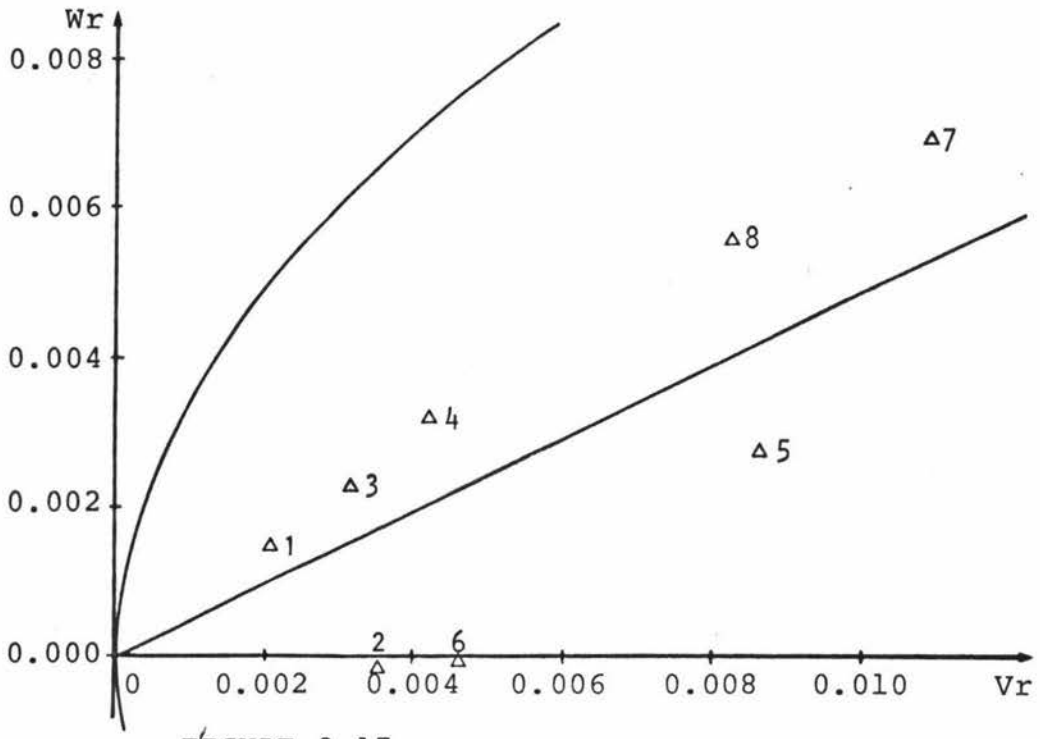

FIGURE 3.17
WrVr graph for number of pods per node

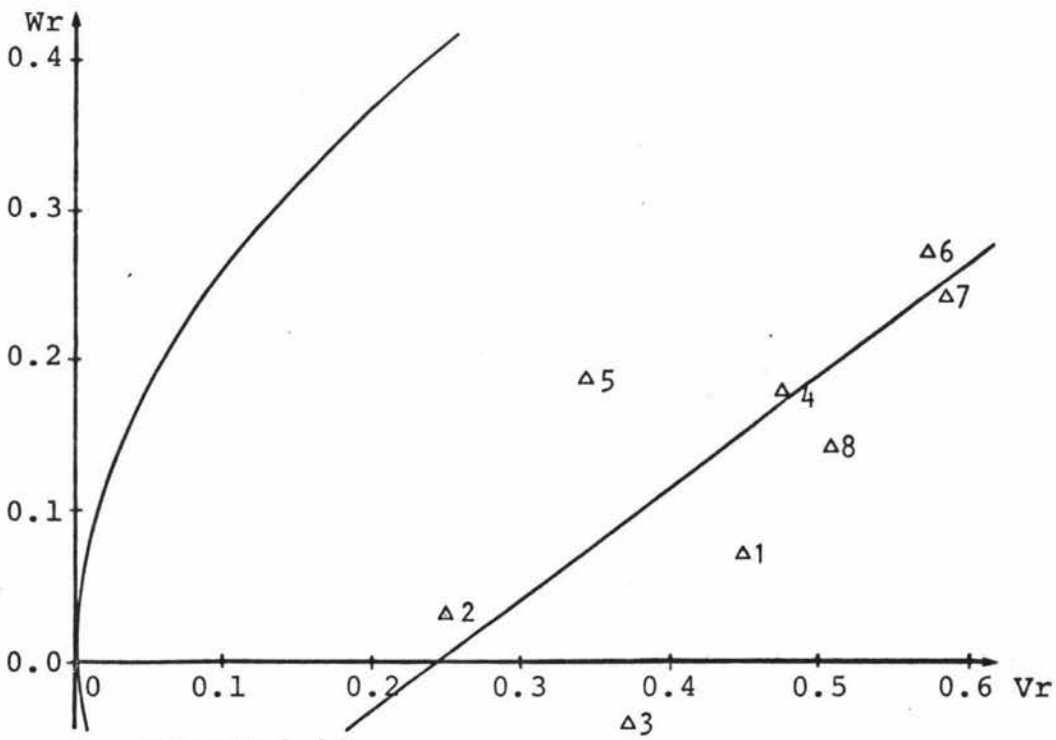

FIGURE 3.18
WrVr graph for seed number per pod

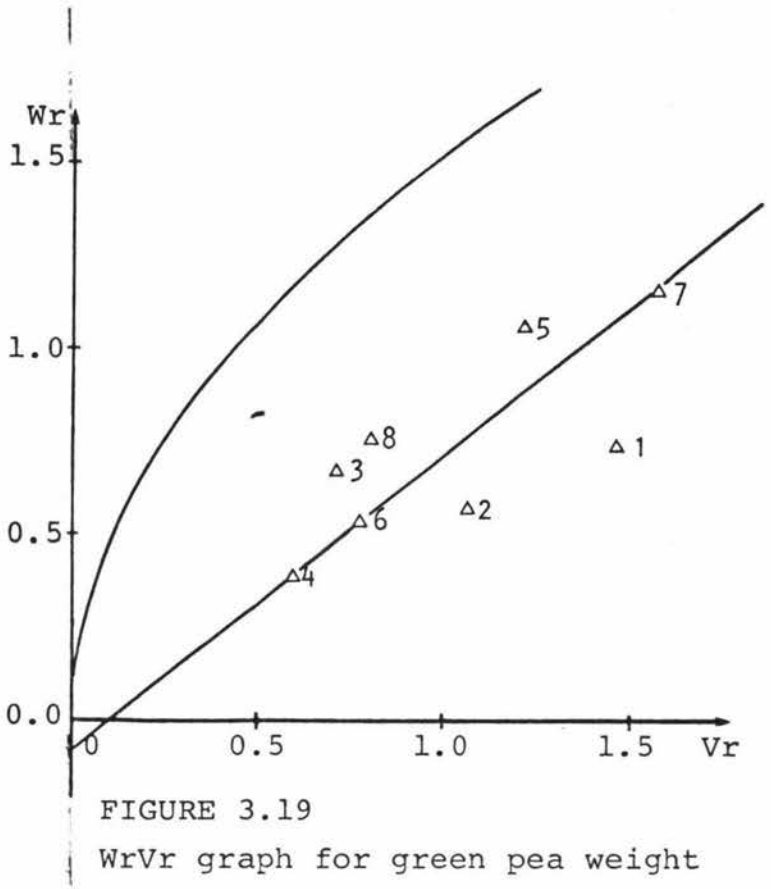

FIGURE 3.19
WrVr graph for green pea weight

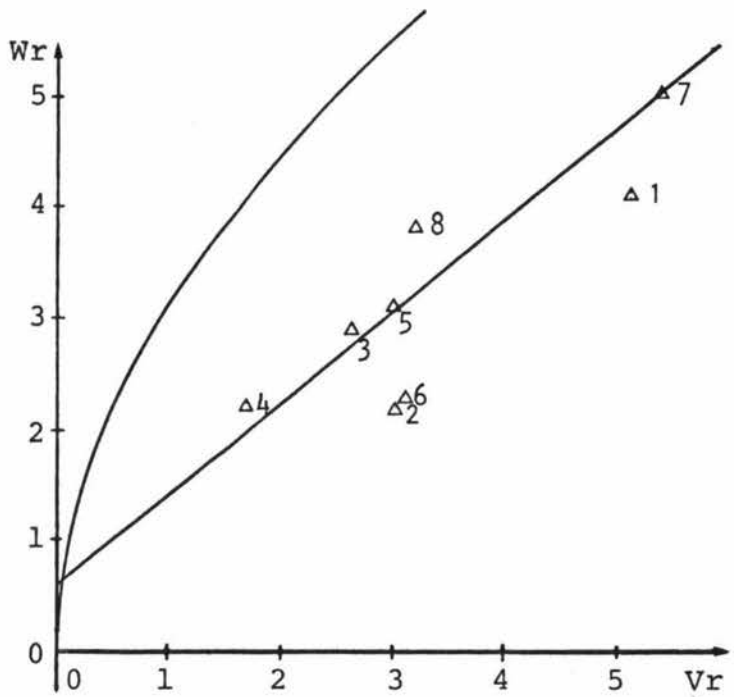

FIGURE 3.20
WrVr graph for pod weight per plant

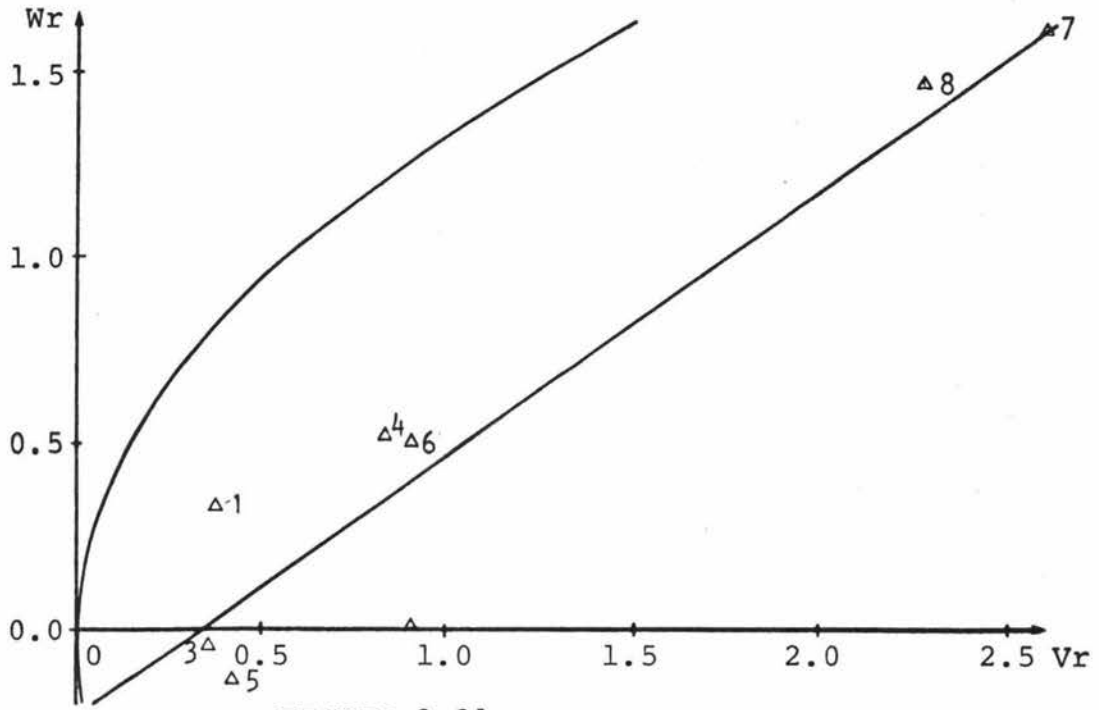

FIGURE 3.21

WrVr graph for flowering time

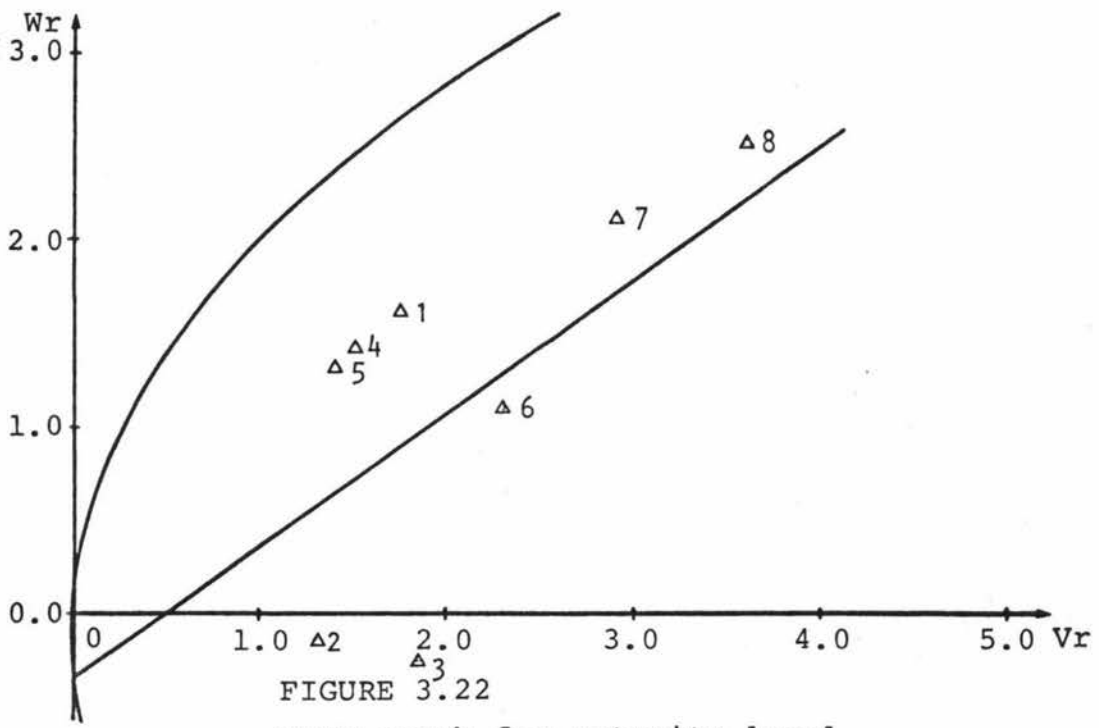

FIGURE 3.22

WrVr graph for maturity level

The result of the analyses showed that leaflet area appeared to be inherited in a similar manner to leaflet length and width. This is not unxpected as both length and width are components of area.

Leaflet number per leaf seemed to be regulated by an additive genetic system (Table 3.3.1). The higher numbered forms were dominant to the lower numbered forms. Dominance was complete with the dominance ratio, $\sqrt{H_1}/D$, of 0.996. The high F value, 80242.21, indicated that there were more dominant than recessive alleles. This was confirmed with the KD/KR ratio of 2.87 to 1. Heritability as with the other leaf characters was medium to high, 0.39 for narrow-sence and 0.97 for broadsence. Leaflet number appears to be controlled by one effective factor, however this judgement is made with the presence of epistasis.

The removal of arrays 4 and 7 from both the leaflet area and leaflet weight diallel tables, tables 3.2.20 and 3.2.21 resulted in the additive-dominance model being satisfied. Both additive and dominance variance were present. For leaflet area σ^2_A was 71.15 and σ^2_D 24.92, while for leaflet weight σ^2_A was 14173.3 and σ^2_D 3556.4. For both characters dominance seemed to be partial or almost incomplete with the $\sqrt{H_1}/\sqrt{D}$ values of 0.84 and 0.71 for area and weight respectively (See Table 3.4). Equal proportions of dominant and recessive alleles were present for leaflet area with the KD/KR ratio of 1.3 to 1 and a low value for F. Leaflet weight however was different; the ratio of dominant to recessive alleles was 3.1 to 1. The direction of dominance was ambidirectional for area, the (Wr + Vr) on $\bar{P}$ correlation being almost zero. But, for weight there was dominance for the heavier leaf types, the correlation being 0.95.

3.2.2 Stipule Characters

The testing of the additive-dominance model by the analysis of variance of (Wr-Vr) was shown to be significant over

TABLE 3.4: COMPONENTS OF VARIATION: deleted arrays (arrays 4 and 7 removed)

2° STATISTICS	CHARACTER: LEAFLET AREA	TENDRIL AREA	LEAFLET WEIGHT	TENDRIL WEIGHT
Vp	187.6367	0.5620	31147.9778	544.8667
Vr	94.8019	0.6881	8351.5889	683.0778
$\overline{Wr}$	70.8155	0.4324	9547.5074	419.1296
$V\overline{r}$	36.2497	0.3440	3285.1969	337.3018
E	45.3325	0.0479	2801.2444	25.6683
PERFECT FIT ESTIMATES				
D	142.3042	0.5141	28346.7334	519.1984
H_1	99.6925	1.3774	14225.6904	1489.4308
H_2	87.4883	1.2170	10928.1801	1297.5436
F	31.5696	-0.6695	20371.0269	-621.0010
$\sqrt{H_1/D}$	0.8370	1.6368	0.7084	1.6937
UV	0.2194	0.2209	0.1921	0.2178
$\frac{1}{2}F/\sqrt{D(H_1-H_2)}$	0.3788	-1.1657	1.0535	-0.9837
h^2ns	0.4772	0.6562	0.5046	0.6555
h^2bs	0.6477	0.9532	0.7492	0.9747
KD/KR	1.3055	0.4308	3.0586	0.4780
K	0.8119	1.2237	1.5258	1.2248

arrays for both stipule area and stipule width (Tables 3.2.7 and 3.2.8), hence the additive-dominance model was not satisfactory for these two characters. However it was acceptable for stipule length and weight (Tables 3.2.5 and 3.2.6). An examination of the WrVr graphs (Figures 3.8 to 3.11) gave no sign of non-allelic interactions for both width and area. The Wr on Vr regression analysis demonstrated that all four stipule characters had suitable regression lines, not being significantly different to unity but significantly different to zero at the 0.1 percent level.

In view of these findings the additive-dominance models were accepted and the components of variation calculated (Tables 3.3.6 to 3.3.9). The additive genetic variance, determined from the equation $D = 2\sigma^2_A$, was high, ranging from 5 to 10 times the dominance variance. However this dominance variance was significant as shown by the significance of the (Wr + Vr) analysis of variance at the 0.1 percent level. The larger, heavier stipule forms appeared to be dominant to the smaller and lighter types. Dominance was incomplete, the $\sqrt{H_1/D}$ values being 0.59, 0.60, 0.46 and 0.51 for length, width, area and weight respectively. As the $\frac{1}{2}F/\sqrt{D(H_1 - H_2)}$ terms were negative this could suggest that complete dominance and no dominanced occured together. (Mather and Jinks 1971).

Other observations which were drawn from Tables 3.3.6 to 3.3.9 were that both length and width contain an equal distribution of dominant and recessive alleles, while area and weight appear to have more recessive alleles than dominant alleles. This could imply that area is inherited independently compared with length and width. Also from these tables, both narrowsence and broadsence heritabilities were high, the environmental effects having only a minor influence. The number of effective factors was approximately two. They ranged from 1.56 for width to 2.41 for weight.

3.2.3 Tendril characters

The two tendril characters, tendril area and weight, did not satisfy the additive-dominance model. The analyses of variance of (Wr-Vr) (Tables 3.2.10 and 3.2.11) produced significant differences between arrays at the 0.1 percent level and the Wr on Vr regression slopes were signficantly different to one and zero.

An examination of both the WrVr graphs, Figures 3.12 and 3.13 showed that the points followed a curve which was concaved upwards; this suggested complimentary gene action. Removal of the arrays which contained the parents 4 and 7 together resulted in the additive-dominance model being satisfied (Tables 3.2.22 and 3.2.23). A slight possibility of some non-allelic gene interaction for the weight character still exists.

The components of variation for the deleted array model (Table 3.4) indicated that the dominance variance was greater than the additive genetic variance. Both heavy and large tendrilled forms were dominant to the lighter and smaller forms. As the dominance ratios were greater than one, 1.64 for area and 1.69 for weight, this implied over-dominance was in operation. From the KD/KR ratios, 0.43 for area and 0.48 for weight, there were more recessive than dominant alleles. Other results which could be obtained from the derived statistics were that the positive and negative alleles were present in equal proportions with positives being dominant, heritabilities both narrow-sence and broadsence, were high and one effective factor seemed to be involved for both tendril area and tendril weight.

3.2.4 Components of Yield

Four yield components: the number of podding nodes per plant, the number of pods per node, the number of seeds per pod and the weight of green peas per plant were invest-

igated in this study.

The analyses of variance of (Wr-Vr) did not result in significant (Wr-Vr) array differences for any of the four yield component characters (Tables 3.2.12 to 3.2.15). For both node number and pod number per node the Wr on Vr regression analysis produced slopes which were significantly different from zero and also from one. The WrVr graphs for node number and pod number per node (Figures 3.16 and 3.17) showed slight concave downwards curves; this may suggest duplicate gene action. These two graphs also suggest from the order of points along the respective regression lines that a high number of podding nodes and a high pod number are dominant to the lower numbered forms. For the two other yield components, the seed number per pod and green pea weight, the direction of dominance did not appear to be as well defined. From the WrVr graphs (Figures 3.18 and 3.19) and the correlations between (Wr+Vr) and the parental means which were zero, dominance was apparently ambidirectional.

For the four yield component characters, Tables 3.3.12 to 3.3.15 heritability was low to medium. Narrowsence heritability ranged from 0.08 to 0.34 and broadsence heritability ranged from 0.27 to 0.49. Genetic variation was mainly additive although there was some non-additive variation in the form of dominance and gene interaction. The type of dominance varied from partial to complete. Green pea weight and pod number per node had $\sqrt{H_1/D}$ values of 0.70. Node number was 0.87 while seed number per pod exhibited complete dominance with a value of 1.06.

3.2.5 Yield

In this study the yield of green peas per plant was adjusted to a standard maturity level to give the adjusted pea yield. The large environmental variance (Table 3.1.16) for this character does not give a very good test of the adequacy

of the additive-dominance model. The result being the Wr on Vr regresion is not significant (Table 3.2.16). The large environmental influence could imply that adjusted pea yield is an agronomic rather than a genetic character.

Yield can also be defined in terms of pod weight per plant, this includes the weight of ovules. The analysis of the pod weight data (Table 3.2.17) showed the additive-dominance model to be adequate. From the genetical components, Table 3.3.17, the additive component of variation was very much larger than the dominance component. The D component was 8.05 while H was 1.44. The value for F indicated there were more dominant than recessive alleles. The low correlation, r = -0.07, between (Wr + Vr) and the parental mean suggested that dominance was ambidirectional. Heritability was low to medium, narrowsence being 0.44 and broadsence was 0.52.

3.2.6 Flowering time

The results from the analysis of the flowering data (Table 3.2.18) showed (Wr - Vr) consistent over arrays, the analysis of variance being non-significant for arrays at the 0.1 percent level. The slope of the Wr on Vr regression line was 0.66, this was significantly different to unity. The WrVr graph (Figure 3.21) demonstrated the possible pattern of duplicate gene action with the clustering of the points towards the origin of the graph.

Although the additive-dominance model was not adequate from the values of D and H_1, (Table 3.3.18) flowering time was considered to be under control of both an additive and dominance system, with the additive genetic variance being twice the dominance variance. Broadsence heritability was only medium while narrowsence heritability was low at 0.31. It was also seen from this table that early flowering was dominant to late flowering.

3.2.7 Maturity

The maturity level was measured as the mean of the alcohol insoluble solids content between the two harvests for each plot. The additive dominance model was found to be satisfactory with the (Wr - Vr) analysis of variance having a consistent (Wr - Vr) component over arrays. The Wr on Vr regression analysis (Table 3.2.19) resulted in a slope of 0.76 which was not significantly different to 1.0.

Additivity was noted to be greater than dominance (Table 3.3.19) with the dominance variance only one-third of the additive genetic variance. A positive F component implied that there were more dominant than recessive alleles and the KD/KR ratio was approximately 2 to 1. Later maturing types seemed to be dominant to the early maturing types as shown by a negative correlation between (Wr + Vr) and the parental mean. Dominance was incomplete as the dominance ratio $\sqrt{H_1/D}$ was 0.70 which was less than 1.0. Heritability was low to medium at 0.35.

GENERAL DISCUSSION

Following this study certain aspects of pea genetics were given further consideration. Some of the more important factors include: pea crossing, handling of plant material, the evaluation of maturity and the use of the diallel cross as a statistical tool for genetic data. The present findings are also compared with results from previous workers.

4.1 Pea Inheritance Studies

4.1.1 Leaf characters

In this study the leaf characters leaflet number, area dayweight, length and width were controlled mainly by additive genetic variance although some dominance variance and non-allelic gene action were present. Previous studies by Durate and Adams (1963) on leaflet area and number for beans and by Lichter (1959) on leaflet length-width ratios for peas have drawn similar conclusions.

4.1.2 Stipule characters

The quantitative inheritance of stipule characters has not been greatly researched in the past. Most efforts have been directed towards the qualitative inheritance of the *st* gene, which is completely dominant and acts in the homozygous recessive condition. This recessive gene was present in some of the parents used in this study. As the four stipule characters (area, weight, length and width) evaluated are size related and from the resulting observations of incomplete dominance this may suggest that both a completely dominant gene and a non-dominant gene are present. However as the number of effective factors calculated includes only those factors expressing complete or partial dominance, a third partially dominant gene may also be involved.

4.1.3 Tendril characters

Overall observations from this study show that both tendril area and weight may be controlled by similar genetic systems and that like leaflet inheritance, this control could act by affecting size. There are no previous results from research on the topic of quantitative genetics of inheritance of tendril characters. Results from qualitative research have demonstrated that the presence and absence of tendrils are governed by one partially dominant gene (Vilmorin 1910, Vilmorin and Bateson 1912, White 1917, Sverdrup 1927, Nilsson 1933, Lamm 1957).

4.1.4 Yield and its Components

The results from this study of the components of yield were found to be in agreement with earlier work. The main findings being the low narrowsence heritability and the additive gene action.

Earlier researchers have investigated both the number of pods per node and the number of flowers per node. Snoad and Arthur (1973a) considered that as these two characters are correlated, they could be treated as similar. The inheritance of both these characters has been found to be controlled by a simple additive system (Snoad and Arthur 1973a, Krurup and Davis 1970b) with a low level of heritability (Ibarbia and Bienz 1970a). This present study showed high pod number per node to be dominant to low pod number. Similar results have been obtained by Snoad and Arthur (1973a) and by Ibarbia and Bienz (1970b) under controlled environmental conditions. However opposite results were reported by Ibarbia and Bienz (1970b) under field conditions and by Snoad and Arthur (1973b) using a diallel cross which included both cultivars and primitive material.

According to Krarup and Davis (1970a) and Brahmappa and Singh (1977) seed number per pod was controlled by a simple additive genetic system. This also appears to be true for the related character ovule number per pod (Krarup and Davis 1970b, Marx and Mishanec 1962, 1967, Snoad and Arthur 1973b). Singh and Singh (1979) using a generation means analysis found non-allelic interaction for seed number per pod with dominance and epistatic components being greater than additive effects.

Weight per seed, a character not examined in this study, was another parameter which has been shown to be governed by an additive genetic system (Brahmappa and Singh 1977, Dahiya *et al* 1977, Snoad and Arthur 1974). However, this component is influenced by reciprocal affects (Snoad and Arthur 1974, Davies 1975) and so does not satisfy the reciprocal assumption for the diallel analysis (Hayman 1954a).

The inheritance of seed yield has been reported by a number of authors. Results have shown that control was mainly due to an additive genetic system together with some non-additive variation (Krarup and Davis 1970, Gritton 1975, Singh *et al* 1980). Kumar and Das (1975a) considered the non-additive variation to be in the form of duplicate gene interaction while Sharma *et al* (1977) attributed it to complementary epistasis.

4.1.5 Flowering time

Results from the genetical analysis of flowering time in this study showed both additive genetic variance and dominance variation to be involved and that early flowering was dominant to late flowering. This was similar to the findings of Snoad and Arthur (1973b) and Sharma *et al* (1977) while the opposite conclusions were reached by Watts *et al* (1970), Snoad and Arthur (1973b), Gritton (1975) and Weber (1976). Snoad and Arthur (1973b) accounted for

KEARSEY, M.J. (1970); Experimental sizes for detecting dominance variation. Heredity 25: 529-542.

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these differences by the genetic variation in the parents used for their diallel cross. Most researchers have found flowering time to be under additive genetic control (Snoad and Arthur 1973b, Sharma *et al* 1977, Brahmappa and Singh 1977, Kumar and Das 1975b). Some dominance and gene interaction also appear to have a minor influence (Watts *et al* 1970, Snoad and Arthur 1973a, Gritton 1975).

4.2 Pea Crossing

Two problems which did occur during the hand pollination stage of the experiment were poor seed set and pod abscission. The causes of these were not determined as this was not the aim of the study. However attempts to overcome these problems gave rise to the following suggestions for future pea breeding studies:

1. Conditions of adequate lighting should be used. This is important especially during the winter period. Avoiding high density planting situations helps to overcome possible problems.

2. The use of a satisfactory soil nutrient level is required so as not to limit plant growth.

3. Glasshouse air temperatures, particularly winter night temperatures should be high enough so as not to limit growth. In this experiment the temperature of 20°C was acceptable.

4. Pests and diseases should be kept under control. Under glasshouse conditions where conditions of low humidity exist, powdery mildew caused by *Ephsiphe polygoni* and two-spotted spider mite (*Tetranychus urticae*) may be troublesome.

5. Flowers not required for self or cross pollination are best pinched off or removed from the plants.

6. The removal of the middle sepal from the calyx of the flower, a technique not always carried out, reduces the chance of mistaking self-pollinated flowers for cross-pollinated flowers after the elongation of the apical region of the plant.

7. Extra plants should be grown for the use of a supplementary pollen supply. Usually the pollen from one flower is only sufficient to make one cross pollination.

4.3 Post Harvest Procedures

Post harvest problems occurred in the field experiment with the handling of the green plant material. As the yield components were calculated from fresh plant material rather than the dried pea plant, this required an evaluation of the maturity level before the determination of pea yield. The disadvantage of this procedure was the limited time available for handling the material evewn though adequate low temperature storage conditions were available.

The chemical test for the maturity stage evaluation had the limitation that only a small number of samples could be handled per day. Also this method of analysis has a large requirement of alcohol, even though this can be redistilled. The time loss, however, could be partially solved by the use of the modified alcohol insoluble solids technique of Lynch and Mitchell (1950). This method eliminates both the grinding of the sample and the use of hot alcohol for extraction.

For future studies it is recommended that mature plants and seeds be used as a measure of yield and yield components. This would apply to experiments involving small plots or large numbers of treatments. Early generation selections in a breeding programme would also be in this category. The

amount of experimental material handled will not then be related to time, weightloss and degradation. The evaluation of maturity level should only be used for studies involving large sample sizes or advanced testing of breeding material. In these circumstances, under different maturity levels, comparisons of green pea yield between treatments or genotypes are more critical. This method would allow the use of the tenderometer rather than the alcohol insoluble solids technique as the sample size available is larger and also as it gives a quicker yet reasonably accurate indication of the level of maturity. A similar approach to this is used in actual pea breeding programmes (Goulden and Crampton 1976).

Plants in this experiment were grown as spaced plants in contrast to the commercial situation of a sward. This resulted in a very reduced plant density, hence extrapolation of some of the yield component results from an experimental to a commercial situation could be difficult. The lower spacing results in a higher incidence of tillering with different genotypes varying in their tillering behaviour.

4.4 Diallel Analysis

Two problems with the Hayman-Jinks diallel analysis are the choice of model used and the difficulty in meeting the assumptions underlying the analysis for the interpretation of the results.

Before using any diallel design the information to be obtained from it must be considered. Hinkelmann (1977) formulated two types of diallel experiments:

1. The comparative diallel cross
   This involves comparisons between genotypes. These may be comparisons among average performance in crosses or comparison amongst the individual crosses. This

class includes the combining ability analysis of Griffing (1956a, 1956b).

2. The exploratory diallel

This is used for determining genetic information on gene actions and includes additive effects, dominance deviations and different epistatic effects. Gene action is defined in the context of a well specified population.

A concept which should be considered is whether the parents used for the diallel cross should be regarded as the population about which inferences are made or as a random sample from some larger population. The Kempthorne approach (Kempthorne 1956) differs from that of Hayman and Jinks. Kempthorne used a random sample from a population of inbred lines, which in turn were derived from the parental population by inbreeding from an initial cross-pollinated population. The Hayman-Jinks method used a specific set of inbred lines. This implies that their analysis was based on a statistical model with fixed genotype effects, therefore the estimated components of variation could only give an approximate description of the genetic situation with a fixed set of inbred lines. As the Kempthorne analysis was based on cross pollinated crops or species these comments however do not directly affect this study. Here a random sample of inbred lines from a self-pollinated species was used.

The Hayman-Jinks diallel analysis is dependent upon six assumptions (Hayman 1954a) as described in Section 1.6.3. Gilbert (1958) claimed there were very few cases where these assumptions imposed by the diallel cross were actually met in a practical breeding situation. Some of these assumptions are critical while others may be overlooked. Independent distribution of genes in the parents was considered the most important assumption for proper interpretation of results (Baker 1978). The belief that no epistasis exists may often be false.

Independent distribution of genes implies that the presence or absence of an allele at a particular locus is statistically independent of the presence or absence of an allele at any other locus. Failure of this assumption will result in an overestimation of the average level of dominance as derived from the genetical analysis (Hayman 1954a). This may be caused by linkage of genes or from the effect of an insufficient number of parents (Baker 1978). Feyt (1976) noted that genes at n loci cannot be independent unless a minimum of 2^n parents are used. Hayman (1963) considered that a minimum of ten parents were needed before genetical interpretation could be made from estimations of population parameters. The number does not apply to this study as the population of inference was the set of pea leaf types used in the experiment.

It has been concluded that assuming a lack of epistasis cannot be justified if biochemical pathways are considered (Gilbert 1958). The Hayman-Jinks test for epistasis, based on the WrVr graphical analysis, is only reliable if there is an independent distribution of genes in the parents (Hayman 1954a). Distortion to the WrVr graph may also be caused by correlation between genes.

The Hayman-Jinks method to remove arrays from the diallel table with the occurence of epistasis until the test of the validity of the additive-dominance hypothesis is satisfied has been criticised. Gilbert (1958) considered that if a set of data contradicts the hypothesis, then it would be better to reject the hypothesis than attempt to correct the data to fit it. The idea of reanalysing the data is only an attempt to find the degree of additivity and dominance underlying the epistasis in the original set.

The problem of epistasis has not yet been overcome. The type of epistasis can be more accurately determined by a generation means analysis (Hayman 1958b, 1960c) but an accurate measurement of the additive and dominance variance cannot be determined in the presence of epistasis. This

has to be solved with the removal of arrays from the diallel table with the Hayman-Jinks analysis.

4.5 Practical Breeding Applications

Although the genetic assumptions may lack validity and despite the deficiencies of the Hayman-Jinks technique the use of diallels in plant breeding cannot be overlooked. They provide a systematic approach to experimental analysis and also give an overall genetic evaluation which makes identification of crosses with the best selection potential possible in an early generation, especially with the combining ability types.

Results directly relevant to practical breeding can be determined from estimating general and specific combining abiliites and their effects. This information is useful for evaluating the performance of hybrids or the potential of a hybrid breeding programme and also for measuring general combining abilities in the development of open-pollinated or synthetic cultivars. The combining ability diallel has the advantage that it is not subject to the restriction of the assumptions of the Hayman-Jinks diallel.

The use of the Hayman-Jinks diallel analysis means that additional information can be obtained from the progeny as well as from the parents. This includes:

1. dominance-recessive relations
2. genic interactions
3. probable linkage associations
4. number of effective factors

Other important information, including heritabilities, can be obtained from both the Hayman-Jinks and combining ability diallels.

CONCLUSIONS

1. Additive genetic variance was found to be greater than dominance variance for all vegetative characters studied with the exception of tendril area and weight.

2. Dominance variance and non-allelic interactions were also important for the vegetative characters.

3. Inheritance of yield and its components were mainly additive although some dominance was present for time to flower, maturity level and pod number per node.

4. Type of dominance varied from partial to complete for both vegetative characters and yield components. However only the two tendril characters showed any indication of over dominance.

5. Heritability was high for the leaflet, stipule and tendril characters and medium to low for yield and its components.

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APPENDIX I

HALF DIALLEL GENETICAL COMPONENTS

The second degree statistics for the full diallel design are given by Mather and Jinks (1971) as:

$$Vp = D + Ep$$

$$\bar{V}r = \tfrac{1}{4}D - \tfrac{1}{4}F + \tfrac{1}{4}H_1 + \frac{1}{n}Ep + (\tfrac{1}{2})\frac{n-1}{n}Ef$$

$$\bar{W}r = \tfrac{1}{2}D - \tfrac{1}{4}F + \frac{1}{n}Ep$$

$$V\bar{r} = \tfrac{1}{4}D - \tfrac{1}{4}F + \tfrac{1}{4}H_1 - \tfrac{1}{4}H_2 + \frac{1}{n^2}Ep + (\tfrac{1}{2})\frac{n-1}{n^2}Ef$$

Where

Vp = the variance of the parents

$\bar{V}r$ = the mean variance of arrays

$\bar{W}r$ = the mean covariance

$V\bar{r}$ = the variance of array means

Ep = environmental component (error variance) of parental family means

Ef = environmental component (error variance) of F_1 Family means

and D, H_1, H_2 and F are the genetical components.

Solving the above equations:

$$D = Vp - Ep$$

$$H_1 = Vp - 4\bar{W}r + 4\bar{V}r - Ep - \frac{2n-2}{n}Ef$$

$$H_2 = 4\bar{V}r - 4\,V\bar{r} - \frac{4(n-1)}{n^2}Ep - 2(\frac{n^2-2n+1}{n^2})Ef$$

$$F = 2Vp - 4\bar{W}r - 2(\frac{n-2}{n})Ep$$

The error variance of the F_1 family means for the full diallel model has been multiplied by a factor of $\frac{1}{2}$ (Mather and Jinks 1971) as it contains the mean of the F_1 families and their reciprocals. For the half diallel the following equations are used:

$$Vp = D + Ep$$

$$\overline{V}r = \tfrac{1}{4}D - \tfrac{1}{4}F + \tfrac{1}{4}H_1 + \frac{1}{n}Ep + \frac{n-1}{n}Ef$$

$$\overline{W}r = \tfrac{1}{2}D - \tfrac{1}{4}F + \frac{1}{n}Ep$$

$$V\bar{r} = \tfrac{1}{4}D - \tfrac{1}{4}F + \tfrac{1}{4}H_1 - \tfrac{1}{4}H_2 + \frac{1}{n^2}Ep + \frac{n-1}{n^2}Ef$$

Solving Simultaneously

$$D = Vp - Ep$$

$$F = 2Vp - 4\overline{W}r - \frac{2(n-2)}{n}Ep$$

$$H_1 = 4\overline{V}r - 4\overline{W}r + Vp - Ep - \frac{4(n-1)}{n}Ef$$

$$H_2 = 4\overline{V}r - 4\overline{V}r - \frac{4(n-1)}{n^2}Ep - \frac{4(n^2 - 2n + 1)}{n^2}Ef$$

Pooling the error components, when Ep = Ef, results with:

$$D = Vp - E$$

$$F = 2Vp - 4\overline{W}r - \frac{2(n-2)}{n}E$$

$$H_1 = 4\overline{V}r - 4\overline{W}r + Vp - \frac{5n-4}{n}E$$

$$H_2 = 4\overline{V}r - 4V\bar{r} - \frac{4(n-1)}{n}E$$

Where E is the pooled error.