CHAPTER II
REVIEW OF LITERATURE

Quantitative characters are controlled by a large number of genes which individually have small effects. Besides the environment, the modifying genes alter the expression of these genes to a great extent. Therefore, the contribution made by the individual genes can not be estimated.

The description of gene control in characters showing continuous variation was given by Fisher (1918) and he was the first to apportion hereditary variance into its three components viz., (i) additive variance resulting from average effect of genes, (ii) dominance component arising from intra-allelic interactions and (iii) epistatic part associated with non-allelic interactions. Wright (1935) defined these three components as (i) additive genetic variance, (ii) variance due to dominance deviation from additive scheme and (iii) variance due to epistasis deviation from additive scheme.

Cockerham (1954) and Kempthorne (1954) further partitioned epistatic variance into additive x additive, dominance x dominance and additive x dominance. Gardner (1963) laid emphasis on types of genetic parameters which are useful to breeders. The intensive studies in biometrical genetics started after the publication of papers by Comstock and Robinson (1948), Comstock et al. (1949) and Mather (1949). A large number of methods have been developed to estimate the genetic parameters and to understand the genetic
architecture of the character. The methods which have been used in various types of genetic analyses of the character are enumerated below.

1. Estimates based on segregating generations from the cross of two pure lines (Mather, 1949)
2. Covariance of half-sibs and full-sibs (Comstock and Robinson, 1948, 1952; Anderson and Kempthorne, 1954)
4. Inferences about gene action from combining ability (Sprague and Tatum, 1942; Rojas and Sprague, 1952; Griffing, 1956a)

Of all the above methods, diallel, partial diallel, triallel, quadriallel and line x tester analysis techniques have been applied in various crops for genetic analysis of the traits for selecting good general combiners. Each of these methods has certain limitations, though they are not common to all. As the line x tester analysis technique has the advantage of simultaneous evaluation of a large number of genotypes, it has been employed in the preliminary evaluation of germ-plasm of *Pisum* spp. The literature available on various genetic parameters and work done on peas is being reviewed hereunder.

1. Concept of combining ability

Harrington (1932) suggested that analysis of characters studied in $F_2$ population would provide a better means of predicting the value of a given crop.
Jenkins (1935) showed that combining ability worked out in early generations remains fixed in later generations as well. Sprague (1946) also reached to the same conclusion and reported that lines maintain their combining ability from $S_0$ to $S_3$ generations.

Sprague and Tatum (1942) defined general combining ability to be the average performance of a line in several hybrid combinations, while specific combining ability to the effects in certain specific combinations which may differ significantly from what could be expected on the basis of average performance of the lines involved. They also mentioned g.c.a. to be predominantly due to additive gene effects, while specific combining ability due to dominance, epistasis and environmental interactions.

Rojas and Sprague (1952) and Sprague and Federer (1952) came to the conclusion that s.c.a. involved not only dominance and epistasis but also a considerable amount of genotypic x environment interactions.

Henderson (1952) stated that g.c.a. is the average merit in respect of some traits of an indefinitely large number of progenies of an individual or line when mated with a random sample from some specific population and s.c.a. as a deviation of the average of an indefinitely large number of progenies of an individual or line from the values that would be expected on the basis of known general combining ability of these two lines or individual combining ability.

Griffing (1956a) pointed out that g.c.a. involved both
additive effects as well as additive x additive interactions. Matzinger et al. (1959) and Carnahan et al. (1960) also confirmed these findings.

Kempthorne (1957) precisely defined general and specific combining ability in terms of covariance of half-sibs and full-sibs, respectively.

Hayman (1957) observed that in the absence of epistasis g.c.a. comprises of both additive and dominance portions while s.c.a. involves only dominance. With epistasis, both these combining abilities will contain epistatic portions. He further remarked s.c.a., mainly a measure of dominance and epistasis, in unselected and selected materials, respectively.

Moll et al. (1960) pointed out that the results about the magnitude of genes based on combining ability variances are, however, not much reliable due to serious bias from genotype x environment interactions.

2. *Line x tester analysis*:

It is a modified form of top cross as suggested by Davis (1927) in maize for evaluating lines for their general combining ability. For screening a wide germ-plasm for g.c.a. and s.c.a. estimates, line x tester is the easiest technique. It has been used for testing general combining ability of inbred lines. A heterozygous tester can be used for measuring g.c.a. and a homozygous one for s.c.a.

Kempthorne (1957) suggested a method by which random
samples of $g$ sires were mated to each of $d$ dams. He then expressed the covariance of half-sibs (H.S.) and full-sibs (F.S.) in terms of variance due to general combining ($\sigma^2_{g.c.a.}$) and specific combining ability ($\sigma^2_{s.c.a.}$), respectively, where:

$$
\sigma^2_{g.c.a.} = \text{Cov half-sibs}
$$

$$
\sigma^2_{s.c.a.} = \text{Cov full-sibs} - 2\text{Cov (H.S.)}
$$

This method was used for calculating the variance due to general and specific combining ability also.

3. Degree of dominance

In polygenic inheritance the effect of individual genes is not easily distinguishable. Hence, by studying the combined effects of genes in a segregating population one can gain some insight into their behaviour and can draw inferences about the average level of dominance in the expression of a particular quantitative character.

Mather (1949) developed a formula ($\sqrt{H/D}$) for estimating the degree of dominance. If the value of degree of dominance is greater than one, there is overdominance of genes at one or more loci, but if this value is less than one, there is partial dominance. If the value is zero the dominance is absent.

Robinson et al. (1949) and Gardner (1963) recognised that estimates of degree of dominance in overdominance range for yield could be obtained as a result of repulsion phase of linkage, even though none of the genes involved was more than completely or partially dominant to its allele. Gardner and Lonnquist (1959),
Robinson and Moll (1963), Moll et al. (1964) and Williams et al. (1965) have provided experimental evidence, indicating linkage bias in the results reported earlier. The evidence concerning overdominance has provided that the problem of how important overdominance is, remains unsolved. Controversy exists whether apparent overdominance due to linkage or overdominance due to pleiotropy is to be regarded as overdominance or not. Moreover, the question of how important overdominance is, means different thing as to whether we are concerned with its frequency as a property of genes or with the amount of variation it causes.

4. Heritability

The concept of heritability is important for determining whether phenotypic differences observed among individuals are due to differences in their genetic make up or simply a result of environmental factors. Heritability is the measure of genotypic and environmental contribution to phenotypic development and is thus an index of transmissibility of characters from parents to their offsprings.

Fisher (1918) was the first to partition continuous variation into its components viz., heritable and non-heritable. Later, Lush (1940, 1943, 1949) defined heritability both in broad and narrow sense. According to him, in broad sense it is the ratio of genetic variance to phenotypic variance and in narrow sense it is only a portion of genotypic variance which is due to additivity of genes.
Robinson et al. (1949) defined it as additive genetic variance in percentage to total variance.

Heritability was also defined as the square root of correlation between genotype and phenotype in an unselected population or as the regression of genotype to phenotype (Robinson et al., 1949; Lerner, 1950; Smith, 1950).

There are several methods for estimating heritability which can be broadly classified as under.

(1) Parent offspring regression (Fisher, 1918; Lush, 1940; Robinson et al., 1949)
(2) Variance components from an analysis of variance (Fisher, 1918; Mather, 1949).
(3) Use of genetically uniform populations (Lush, 1948)
(4) Use of $F_2$ and back-cross progenies (Warner, 1952)
(5) Modified parent offspring regression method (Frey and Horner, 1957)
(6) The constant parent regression method (Griffing, 1950)

Lush (1940) made following observations regarding estimates of heritability:

(1) When heritability in narrow sense is high, reliance should be placed mainly on mass selection and as heritability becomes lower, more emphasis should be given to pedigree and sib, and progeny tests.
(2) If epistatic variance is relatively high, more reliance should be placed on selection between families and line breeding may be followed.
(3) If overdominance is prominent, the breeding plan should be oriented to development of hybrids for commercial seed production.

(4) If the variance due to interaction between heredity and environment is relatively large, the breeding plan tends more towards producing a separate variety for each ecological region.

(5) Heritability in narrow sense may be used for estimating expected improvement due to selection.

5. Genetic advance

Genetic advance is still a more useful estimate. It depends upon: (i) the amount of genetic variability, i.e., the magnitude of difference among individuals in the base population, (ii) the magnitude of masking effect of environment and interaction component of variability in genetic diversity and (iii) intensity of selection (Comstock and Robinson, 1952).

The genetic gain is a product of heritability and selection differential expressed in terms of phenotypic standard deviation of that character. Heritability value by itself does not have much significance as it fails to account for the estimate of absolute variability. It is, therefore, necessary to utilize heritability estimates in conjunction with selection differential which would indicate the expected genetic gain resulting from selection.

6. Heterosis

The increased $F_1$ vigour over the mean of the parents or
over the better parent has been observed by various workers. Kolreuter (1776) was the first to report this phenomenon. Shull (1912), put forward the idea of utilizing the vigour of $F_1$ commercially. Although, heterosis has extensively been exploited in many crops, but very little knowledge is available on the basis of its manifestation. Various theories have been expounded, but none has so far given satisfactory solution to this problem. The theories offered on this phenomenon are given below.

A. **Genetical concept**: Genetical interpretation for heterosis falls under three heads.

(i) **Theory of dominance**

(ii) **Theory of heterozygosity**

(iii) **Theory of non-allelic interactions**

(i) **Theory of dominance**: Bruce (1910) was the first to report the genes favourable for hybrid vigour and growth to be dominant and harmful ones to be recessive. The dominant genes contributed by one parent complement the dominant ones received from the other. So $F_1$ always shows favourable combination of dominant genes than either of the parents.

(ii) **Theory of heterozygosity**: Shull (1910) was the first to report heterosis to be due to some kind of physiological stimulus, resulting from union of unlike gametes. East and Hayes (1912) mentioned that the stimulus was greater when characters were in heterozygous condition than certain or possibly all the characters in homozygous condition.

(iii) **Theory of non-allelic interaction**: The role of additive x
additive, additive x dominance and dominance x dominance studied by recent geneticists who demonstrated that there exists a correlation between heterosis and presence of epistasis (Jinks, 1954, 1955; Hayman, 1954, 1963; Allard, 1956; Jinks and Jones, 1958).

B. Physiological concept: Ashby (1930) from a series of studies on growth rate of hybrids and inbreds of maize concluded that hybrid vigour is due to some process between fertilization and seed setting so it is nothing more than the maintenance of an initial advantage in embryo size which he termed as "Greater initial capital". East (1936) concluded that increase in endosperm and embryo may itself be one of the manifestations of heterosis, detectable in early stages of ontogeny, but seed size or size of any part of the seed cannot be the true cause of heterosis. As the knowledge is limited all the intricacies of heterosis can not be resolved on the basis of purely genetical or physiological ground.

Daskalov (1963) concluded that heterosis in $F_1$ is the combined effect of genetical, cytoplasmic, biochemical and physiological factors and may be attributed to estimation resulting from interaction of different heritable factors of the parents in $F_1$. Turbin (1963) introduced the concept of genetical balance which takes into account not only interactions between hereditary factors, but also the role of environmental factors.

Pal and Sikka (1952) reported heterosis breeding to be a quick, cheap and easy method of increasing yield. Considerable success has been achieved in this direction in crops which exhibit an appreciable degree of cross pollination. Comparatively, little
use of heterosis has been made in self-pollinated crops. Two factors come in the way of exploitation of hybrid vigour in self-pollinated crops; (i) firstly because of the practical difficulties involved in exploiting hybrid vigour in plants with perfect flower, especially when each act of pollination produces very few seeds and (ii) secondly as to whether hybridity by itself will have any advantage over the pure lines.

The development of methods for inducing male sterility and chemical methods of emasculation have brought economic production of hybrid seeds in self-pollinated crops into the realm of probability.

7. Correlation

The study of genotypic, phenotypic and environmental inter-relationships among various agronomic traits is of great interest to plant breeders, not only from theoretical consideration of quantitative inheritance, but also from practical standpoint, since selection is usually related with changing two or more characters simultaneously. This information may be used in the prediction of correlated responses to directional selection, in the construction of selection indices and in detection of some characters which may have no value in themselves, but are useful as indicators of the more important ones under consideration (Johnson et al., 1955; Robinson et al., 1951).

Phenotypic correlations may be of genotypic or environmental in origin and provide information about association observed between two characters. For selection, phenotypic correlation is of little
importance unless genetic and environmental correlations between two characters are in the same direction, when estimated separately genetic correlation provides a measure of genetic association between characters and is generally used in selecting one character as a means of improving another. Such correlation coefficients provide information by themselves (Miller et al., 1958) and should be helpful to breeders. Since they are based on transmissible genetic variance (Jerome et al., 1956), genotypic correlations attain practical utility when economic evaluation of crop depends upon a smaller number of traits. Information on genetic association among various character helps in formulating effective breeding programme and simplifies selection approach. The major causes for genetic correlations are pleiotropy, linkage and developmentally induced relationship (Adams, 1967; Stebbins, 1950). Pleiotropy is the property of gene affecting more than one character and results in detectable correlations as it is the net effect of all segregating genes that affect both the characters, some causing positive and others negative correlations. The development relationship occurs when two developing structures of a plant body compete for a common, possibly limited, nutrient supply. If one structure is favoured for many reasons over the other in amount of nutrient received, a negative correlation may exist between them. An event of its kind is apparently included in the broad definition of developmental correlation given by Stebbins (1950). Environmental correlation reflects influence of environmental factors on the joint variation of two characters. It is of no value in selection, but it provides
information about relationship of characters irrespective of genotypic differences in the plant material.

8. Genetic divergence

Multivariate analysis quantifies the degree of divergence among the populations. This indicates trend of evolutionary pattern, assessment of relative contribution of different components to total divergence and determines the nature of forces operating at inter- and intra-cluster levels. Thus, it permits the choice of genetically divergent parents for obtaining desirable recombinants in segregating generations as reported by Michener and Sokal (1957), Sokal (1958), Morishima and Oka (1960), Nair and Mukherjee (1960) and Murty and Qadri (1966).

Mahalanobis $D^2$ canonical analysis assesses the nature of divergence. It permits discrimination between different races and their distinct grouping, thus drawing evolutionary trends as to their geographical distribution and working out a hybridization programme on the basis of genetic divergence for maximum exploitation of heterotic effects (Mahalanobis et al., 1949; Mukherjee, 1951; Nair, 1952; Blackith, 1957-60; Nair and Mukherjee, 1960; Hughes, 1961; Murty et al., 1962; Cassie, 1965; Murty et al., 1966).

Considering the importance of this analysis various workers estimated the genetic divergence in different crop plants. Moll et al. (1962) reported genetic diversity in maize grown in different geographical regions to be due to ancestral relationship, geographical separation and adaptation, and emphasized the importance
of hybridization among widely divergent lines. Murty and Pavate (1962) classified varieties of *Nicotiana tabacum* in four tentative groups, using $D^2$ statistic, on the basis of closeness or distance and confirmed this by the use of canonical roots. Significance of groupings and discriminant function for planning future hybridization programme was, however, emphasized by them. Murty and Arunachalam (1966), working with self-incompatible types of *Brassica campestris*, linseed, wheat, *Nicotiana rustica* and sorghum, indicated that by canonical analysis of yield components the contribution of height, flowering time and tiller number to geographical diversity was confirmed. Jawahar Ram and Panwar (1970) in rice distinctly discriminated India and Japanica races; early, medium and late maturing groups; varieties of China, Japan, Taiwan and hilly and plain varieties of India, and thus established a relationship between genetic and geographical diversity. They also worked out evolutionary pattern and stressed flowering time to be major axis of differentiation. They also suggested a brief scheme of hybridization programme on the basis of genetic diversity between India and Japanica races. Singh and Singh (1976) could not establish relationship between genetic divergence and geographical distances in chillies. Similarly, Peter and Rai (1976) also could not observe any apparent parallelism between genetic and geographic divergence, however, locules per fruit and plant height were the component characters responsible for expression of genetic divergence and, therefore, could be used for heterosis breeding.
WORK DONE IN PEAS

An attempt has been made to review the available literature on pea on following aspects:

(i) Combining ability and gene action
(ii) Manifestation of hybrid vigour
(iii) Heritability and genetic advance
(iv) Correlations
(v) Genetic divergence

(i) Combining ability and gene action:

Karup et al. (1970) studied a complete six parent diallel cross including $F_2$'s and back-crosses for inheritance of basic ovule number in *Pisum sativum* L. They found this character to be controlled by simple additive genetic system. Dominance was of no relative importance, though slight indication of partial dominance for low over high ovule number was observed.

Karup and Davis (1970), while studying the inheritance of seed yield and its components, observed that seed yield ($w$) and its components viz., pods per plant ($x$), seeds per pod ($y$) and average seed weight ($z$), and also seeds per plant were all controlled by additive genetic system, some departure from additivity was indicated by deviation of $F_1$ from mid-parent for $x$, $y$ and seeds per plant, were more likely to be due to epistasis or linkage rather than dominance. Specific heterosis (s.c.a.) was important for all the components, while variety heterosis (g.c.a.) was important only for $y$ and $z$. 
Watts et al. (1970), studied six pea cultivars and their $F_1$'s and $F_2$'s under moderate epiphytotic conditions of yellow virus for flowering days, using both Griffing and Jinks' methods to assess stability of polygenic control and observed the character to be controlled by additive system with dominance for late flowering. Some gene interactions were found in both the analyses, mainly between late flowering cultivars, though test for apparent dominance was insignificant. Degree of virus infection had absolutely no effect on the expression of flowering. Slight earliness over early parent was observed in five $F_2$ progenies and slight gain in earliness by selection seemed probable.

Snoad and Arthur (1973b) compared nature of genetic control in parents and cultivars in a $6 \times 6$ diallel cross in pea for days to flower, nodes for first flower, internode length, number of flowers per node and number of ovules per pod. Earliness resulted from an accumulation of dominant alleles in primitive forms, while, in European and North-American cultivars it was due to the accumulation of recessives. Only node of first flower was under similar genetic control in two cultivars. Results of $F_2$ generation of a set of half-diallel cross, involving seven cultivars, were again discussed by these workers (1973b) regarding characters cited above. A polygenic system for four characters and the fifth, i.e., internode length, was additionally controlled by a major gene. The genetic system was mainly additive, while dominance and interactions were of minor importance. Inter-crossing among most desirable cultivars was suggested as the right procedure for bringing about
the fruitful results. Again, Snod and Arthur (1974) studied $F_2$ material of a full $6 \times 6$ diallel set, involving two each wild, primitive and European cultivars for seed weight, seedling shoot and root length (6, 7, 8 and 9 days after germination and shoot and root fresh weight, 9 days after germination). This $6 \times 6$ set had to be reduced to $4 \times 4$ as two primitive parents contained a single reciprocal translocation in relation to other four parents. Polygenic control was found for all the characters, principally additive for seed weight and dominance for seedling character. Large differences between primitive and cultivated forms for fresh weight of shoots and roots and number of lateral roots were probably due to uncontrolled selection by breeders. The differences in $F_1$ and $F_2$ over years for flowering time, flower number per node and number of ovules per pod at first and second flowering nodes were probably due to genotypic x environment interactions.

Hirdaya Kumar and Das (1974), in a diallel set of five cultivars of garden pea, studied the inheritance of primary branches, pods per plant, seeds per pod, pod length, 25-seed weight and seed yield through parents and their $F_1$ and $F_2$. Overdominance was observed for test weight and yield, and partial dominance for others in $F_2$. Significant epistasis was exhibited for number of pods per plant, seed weight and yield. Long pods were observed to be controlled by dominant genes. Additive genetic variance was significant in both $F_1$ and $F_2$ for all the traits, except yield. Non-additive component was significant for primary branches, pod length and test weight in both $F_1$ and $F_2$, and for yield in $F_1$ only.
Excess of dominant alleles was found in parents for number of primary branches in F₂ and length of pod both in F₁ and F₂. Thus, additive and non-additive genetic components were significant for number of primary branches, pod length and 25-seed weight, although former was predominant in first two traits, while non-additive component was high for 25-seed weight. Only additive genetic variance was significant for number of pods per plant and number of seeds per pod, while only dominance was significant in F₁ generation for seed yield per plant.

Hirdaya Kumar and Das (1975), while analysing the data relating to days to flower and maturity for F₁ and F₂ generations of 5 x 5 diallel cross in garden pea (P. sativum L.) by both Griffing and Haymana's methods, found that in cultivars under study both the traits were under the control of additive gene action, although substantial dominance effect was also found for maturity. They further mentioned narrow sense heritability to be high and additive gene action was preponderant. Selection of suitable parental material may result in rapid genetic advance for earliness.

(ii) Manifestation of hybrid vigour:

Heterosis breeding has been successful in cross-pollinated crops, but its exploitation has not been thoroughly explored in self-pollinated crops like pulses. Two important reasons seem to be responsible for this viz., (i) practical difficulty in every act of emasculation and pollination and (ii) lack of information regarding superiority of hybrid over pure lines.

No male sterile lines have so far been reported in pulses
which could be used in economic seed production. The use of chemicals to induce sterility has yet to be explored in these crops. However, the development of chemical methods of emasculation in future may bring economic seed production in pulses into the realm of probability, still great deal remains to be done before hybrids in pulses could be cultivated commercially.

Substantial amount of heterosis has been reported in pulses including peas from time to time. Solomon et al. (1957) reported 25 per cent heterosis for grain yield in pigeon pea, although none of the hybrids could out-yield the best variety. Bond et al. (1964) observed significantly higher yields in field bean hybrids as compared to open pollinated varieties. Ramanujam et al. (1964) reported two out of nine crosses in gram to be significantly superior in yield to the best parent. Bhatnagar and Singh (1964) and Singh and Jain (1970) reported high heterosis for yield in moong bean. Singh and Singh (1970) reported heterosis over better parent in peas of the order of 162 per cent for yield, 273 per cent for branches, 110 per cent for pods per plant, 65 per cent for pod length, 15 per cent for seeds per pod and 8 per cent for 100-seed weight. They mentioned that yield was influenced by the number of branches and pods per plant. Flowering and main branch length did not show any association with increase in yield. They have also mentioned that unless a hybrid excels from a pure line by at least 25 per cent, it can not be supposed to be economical, whereas only 26 per cent heterosis for yield over best variety was observed by them.

Karup and Davis (1970), in a 6 x 6 diallel cross in peas
reported specific heterosis (s.c.a.) to be important for all the
traits viz., yield and its components (pods per plant, seeds per
pod, test weight and seeds per plant). The variety heterosis
(g.c.a.) was important for seeds per pod and test weight alone.

Shivaji and Gritton (1975) reported substantial heterosis
and inbreeding depression for number of days to flower and for rest
of the characters, heterosis was low.

From the above findings it is clear that a great degree
of heterosis was reported to exist in pulses including peas, but
it has not so far been possible to establish the superiority of
hybrids over pure lines. Smith (1952) in tobacco and Powers (1952)
and Williams (1959) in tomato (both self-pollinated crops) have
shown that, in spite of high degree of heterosis exhibited by these
crops, the pure lines developed were either better or as good as
the hybrids. Now even in cross-pollinated crops like maize increasing
importance of additive genetic variance is being realised (Lindsey
et al., 1962; Stuber et al., 1966) for developing high yielding pure
lines.

(iii) Heritability and genetic advance:

Heritability studies in pea have not been made in detail.
Only sporadic reports are made by few workers. Karup and Davis (1970)
have reported high heritability of 38 per cent for seeds per plant
and 65 per cent for test weight. Hirdaya Kumar and Das (1974), in
a diallel analysis in peas, reported narrow sense heritability to be
quite high for almost all the characters studied viz., number of
primary branches, pods per plant, seeds per pod, pod length and
seed yield. Teehan et al. (1969) reported high heritability (broad sense) for all the above mentioned traits, except number of seeds per pod.

(iv) Correlations:

Love (1911) reported significant positive correlation between height and number of internodes, height and number of pods and height and number of seeds per plant and negative correlation between height and average weight of seed.

Grodecky (1936) found significant positive correlation between breadth and weight of seeds in pure lines of *P. sativum*, *P. arvense* and *Vicia cuspitator*.

Muhelson (1951) observed no correlation between (i) seed weight and increase in volume on swelling, (ii) protein content and increase in weight on swelling after 48 hours and (iii) cooking ability and absolute increase in volume on percentage increase in weight in such case after 48 hours of swelling. A slight negative correlation was observed to exist between seed weight and ash content, and seed weight and seed coat represented by weight.

Riempan (1961) concluded that yield of pods increased more in round seeded varieties than wrinkled seeded ones. The poor yield with early harvesting in some years, particularly in wet weathers, was attributed to failure of some pods to elongate rather than to poor setting of pods. Quality declined as yield increased. Wrinkled seeded varieties reached their maximum yield of shelled peas earlier than round seeded types.

Vandurgraff (1962) reported that weight of pods was lower
in early varieties than in mid-season and late varieties.

Rowlands (1964) observed close correlation between number of days to flowering and the node of the first flower which suggested that the rate of internode production is the same in all the seven varieties tested for diallel.

Yatindra Kumar (1965) showed that number of branches and leaves were correlated with yield per plant. Further, length of pod and weight of green seeds were also correlated. No correlation between height and yield was found to exist.

Zyl (1968), through correlation studies, found number of shoots per plant correlated with each number of pods and yield per plant. Similarly, number of pods per plant was found correlated with yield within cultivars and number of seeds per pod was correlated with yield.
Markarian (1966) found winter hardiness, indicated by rosette habit, to be independently inherited from other characters.

Mora et al. (1966), while studying 42 varieties of peas, showed that varieties attaining a height of 80 cm surpassed shorter varieties by 9.28 per cent in yield of marketable pods and by 12.88 per cent in total yield of pods. These groups did not differ in any biochemical properties, but short varieties ripen more quickly and are suited for mechanical harvest, but not valued much as taller types.

Singh and Singh (1969) studied path analysis and correlation among 40 varieties of peas. They observed that generally genotypic correlation coefficients were higher than phenotypic ones. Grain yield was found to be positively and significantly correlated with each, number of branches per plant, seeds per pod, pods per plant and 100-seed weight. Days to flowering was found associated with number of days to maturity. Pod length was found to be positively associated with each, seeds per pod and 100-seed weight, and seeds per pod with pod length. Negative correlation was found between 100-seed weight and seeds per pod and also pods per plant and 100-seed weight. It was also observed that branches per plant and length of pod were associated. Path coefficient analysis indicated that number of branches, pods per plant, seeds per pod and 1,000-seed weight seemed to be important yield contributing characters. In general, characters showing high genotypic correlations with yield showed high co-heritability.

Karup and Davis (1970) observed, yield closely related to
each pods per plant, seeds per pod and test weight in descending order. Pods per plant according to them is a good selection index for dry seed yield.

Shivaji and Gritton (1975) studied $F_1$ s of a diallel set of 8 parents of pea in a set of five different environments for eight important traits and reported that parents showed highly significant genotypic and environmental correlation; but the $F_1$ s were remarkably stable. They reported plant height to be positively correlated with each pods per plant, seeds per plant and yield, indicating, taller types to be superior yielding though indeterminate types were not suited for canning, because of excessive vine growth, uneven maturity of pods at varying nodes and harvesting was also difficult. Protein was also found to be correlated positively with yield and slight correlation between lower protein and heavier seeds was also indicated. Strong genotypic and phenotypic correlations were, however, observed between pods per plant and seeds per plant and seeds per pod and seeds per plant, and between these two traits and yield per plant. Genotypic correlation between seed weight and yield was higher than phenotypic correlation.

(v) Genetic divergence:

No information was so far available on the subject in this crop.