Chapter – II

REVIEWS OF LITERATURE

The relevant literature on different aspects of the present investigation has been presented under following heads:

1. Diallel cross analysis
2. Variability
3. Components of variance
4. Combining ability
5. Heterosis
6. Heritability and genetic advance

Diallel Cross Analysis

Recent advances in biometrical genetics have provided a number of biometrical techniques that are used for computing actions of genes controlling quantitative traits of breeding materials. Diallel analysis is one of such approach which furnishes useful informations on the genetic mechanism of inheritance of quantitative characters, particularly in respect of gene action including additive gene effects, the order of dominance in the parents, degree of dominance, distribution of positive and negative alleles and their linkages as well as the estimation of general and specific combining ability of the parental lines and their crosses, respectively involved in the programme.

Hull (1945) was the first to consider some aspects of diallel cross method and he described the method for analyzing the data from diallel cross of homozygous lines using regression and utilized the method for estimation of dominance variance. Yates (1947) defined diallel as a set of all possible mating
among ‘n’ genotypes. According to him parents of a diallel cross could be of homozygous lines, varieties, clones and so on. Griffing (1950) suggested that parental and F₁ data have distinct advantage over the data from segregating generations in studying quantitative inheritance in diallel analysis because of the fact that they are being unaffected by genetic segregation and linkage.

Jinks and Hayman (1953) presented a method of analysis for parental and F₁ generation from a set of diallel crosses which offer a rapid evaluation of the genetic relationship among a number of parents. According to them, the method also provides identification of parents whose hybrids were more likely to respond to selection. They also presented a graphical approach using second order statistics of Wr and Vr (Wr the Covariance of the parents and their offspring in one array and Vr = Variance of one array) provided a geometric representation of degree of dominance caused by many types of non-allelic interactions.

Hayman (1958, 1960) described quite critically the various aims of diallel cross experiments and extended the analysis of fixed set of inbred lines of Jinks and Hayman (1953) to a randomly sampled inbred lines. This method provided a better estimation of components of genetic variations. He also suggested some experimental design to suit diallel analysis.

Griffing (1956) suggested that when other factors being constant the large number of the parents used in any genetic system, the estimation of parameters will be closer to population value. This also holds good for diallel analysis but the analysis of a full diallel comprising larger number of population become unmanageable.

According to Crumpacker and Allard (1962) diallel cross provides an assessment of the genetic system that appears to be useful in predicting the immediate outcome of directional selection programme. Gardener and
Eberhart (1966) proposed a model for estimation of gene effects and heterotic parameters for diallel cross related population of a fixed set of random mating varieties with arbitrary gene frequency at all loci. They criticized Griffing (1956) method II, model I which failed to provide clear picture of heterosis and gene effects.

Backer (1978) suggested from statistical point of view, that the critical issues concerned with the choice of the genotype effects. From genetic point of view, two assumptions were critical in interpreting the results of diallel analysis. The first assumption concerning the independent distribution of genes in the parents, most critical for proper interpretation but was least acceptable in actual practice. The second assumption that there was no epistasis, may frequently be incorrect.

Ferreira et al. (1993) adopted Griffing’s method IV of complete diallel cross analysis for experiments repeated in several environments using mathematical model:

\[ Y_{iik} = m + iK + g_i + S_i + (Ig)_iK + (Is)i_k + e_{iik} + iLi, \]

where \( Y_{iik} \) is the mean of the hybrids from the cross between the \( i^{th} \) and \( i'^{th} \) varieties of the group in the \( k^{th} \) environment; \( iK \) is the \( k^{th} \) environment effect; \( m, g_i, g_i, s_{ii}, e_{ii'k} \) are as described by Griffing, the remaining parameters correspond to many interactions with environment.

Chen et al. (1994) examined Hayman methods of dominance testing and concluded that some values were less constant than expected, making it likely that dominance effects were under estimated. The method was tested using data on twenty characters from several wheat diallel crosses. In 19 characters, no marked effect was found but for ear length, differences were noted and these supported the hypothesis.
Oritz et al. (2001) proved diallel mating design as informative in determining the inheritance of quantitative traits of interest to plant breeders. Apart from the well established analysis of complete diallel, the two way factorial data structure of this design lend itself to analysis by the additive main effects and multiplicative interaction model, (AMMI – model). They described the joint application of the AMMI model and Griffing method –I, model I, to gain insight into the breeding value of inbred lines in a self pollinating crop.

Sharma and Kalia (2002) made 10x10 diallel crosses in garden pea to raise 45 F₁s excluding reciprocals. The crosses were analysed by Griffing (1956) and Hayman (1954) method together informations on different components of variances and effects.

Singh and Dhillon (2003) crossed ten genetically divergent varieties by using diallel mating design to raise 45 F₁s excluding reciprocals. These crosses were analyzed through graphical analysis and various genetic parameters as suggested by Hayman (1954).

Variability

It is utmost important to study the variability in the population in order to select the desirable types. One of the major interests in genetic analysis of quantitative traits lies in estimating the magnitude of different components of genetic improvement in the breeding programme. The variability observed for any character is due to differences in genes carried by individuals of the population as well as due to differences in the environment. Therefore it is necessary to have an idea about environmental and genetic variability. The coefficient of variability is helpful to plant breeder as a mean of selection.

Narayana et al. (1999) revealed the presence of sufficient variation among generation mean of pod yield per plant, shelling percentage (%), dry
matter contents (%), total sugar (%) & protein content (%) at Dr. Y. S. Paramar University of Horticulture and Forestry, Nauni, Solan (H.P.) for all five crosses under investigation.

**Sureja and Sharma (2000)** studied genetic variability in a collection of 30 indigenous and exotic genotypes of garden pea. Considerable genetic variability for pod yield and its component characters viz. plant height, length of internodes, pod yield/plant, number of pods/plant, seed yield/plant, number of primary branches and 100 seed weight were observed.

**Ramesh et al. (2002)** studied thirty six genotypes of garden pea, including 4 field pea genotypes for genetic variation of yield and other characters. A considerable amount of phenotypic coefficient of variation and genotypic coefficient of variation was observed for most of the characters such as number of pods per plant, weight of pods per plant, internode length, plant height, mean pod weight and weight of grains per pod while the variation was low for other characters like internode length, node of the first fruit, number of pods per plant.

**Sharma and Kalia (2002)** observed significant variation for all the characters viz. pod yield per plant (g), pods per plant, pod length, seeds per pod, shelling % and total soluble solids (%) at Regional Research Station, Kukumser, Lahual and Spiti, Himachal Pradesh. It was observed that the parents and crosses used under the investigation were highly variable.

**Singh et al. (2003)** revealed higher magnitude of variability for pod length and number of pods per plant in F1 population among the 8 traits (pod length, number of pods per plant, number of seeds per pod, number of branches per plant, 100 grain weight, grain yield per plant, harvest index and protein content) The study was conducted in 10 pea cultivars, 45 F1 and 45 F2 populations.
Sharma et al. (2003) observed sixty three genotypes of pea (*Pisum sativum*) including indigenous and exotic cultivars for variability parameters. All characters viz. seed yield per plant, biological yield per plant, harvest index, plant height, 100 seed weight, seeds per pod, pods per plant, days to 50% flowering, pod length and days to maturity exhibited significant variability. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highest for seed yield per plant followed by pods per plant and biological yield per plant.

Sharma et al. (2003) observed significant differences in both F$_1$ and F$_2$ generations for days to 50% flowering and number of days to first picking indicating that the parents and crosses used in the present study were genetically diverse with respect to earliness.

Mehta et al. (2005) conducted study to evaluate 63 diverse pea genotypes including ten advanced generation. Analysis of variance for all the traits indicated significant differences among genotypes. A wide range of variability for pod yield per plant (42.99 – 100.78 g) and plant height (42.83 – 131.23 cm) along with high estimates of phenotypic and genotypic coefficient of variation indicated that these characters would respond to selection.

Kumar et al. (2007) assessed one hundred genotypes of pea in randomized block design for variability and diversity for yield and its attributes. High magnitude of variability was observed for plant height, 100-seed weight, yield per plant and fat percent.

Sharma et al. (2007) studied 20 diverse pea genotypes for genetic variability and associated studies. Phenotypic and genotypic coefficients of variation were of high magnitude for plant height and moderate for pod per plant and pod yield per plant.
**Guleria et al. (2009)** ten indigenous and exotic genotypes of garden pea (*Pisum sativum* L.) were studied for variability components and correlation of 10 different agromorphological characters among themselves. The studies indicated highly significant varietal differences for all the characters. Seeds/plant, shoot height, intermodal length, grain yield and pod number had a high degree genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

**Component of Genetic Variance and Gene Action**

The genetic variance estimated from trials using homozygous lines arrives from differences between homozygote. But the breeder is mostly concerned with segregating population eg. F₂, F₃ etc. The success in genetic improvement largely depends upon nature, magnitude and interrelationship of heritable and non heritable variations for economic characteristics. An insight into the nature of heritable variation helps in rapidly fixing the desired attributes in the crop under improvement.

**Fisher (1918)** was the first to divide genetic variance into three components, additive variance refers to that portion of genetic variance which is produced by the deviation due to the average effects of the alleles of the genes at all segregating loci. The second being dominance variance which arises due to deviations from additive scheme of gene action resulting from intrallelic interactions, that is dominance while the last being epistatic variance arises due to the deviation as a consequence of interallelic interactions. **Wright (1921,35)** divided genetic variance into additive and non additive (dominance and epistatic components), of which only additive components attributes to genetic advances under selection.

**Mather (1949)** developed a formula \( H_1/D \) for estimating the degree of dominance. According to him, if the value of dominance is higher than one,
there is over dominance of genes at one or more loci but if the value is less than one, there is partial dominance. Moreover, if the value of measure of dominance is equal to zero, indicates the absence of dominance.

**Jinks and Hayman (1953) and Hayman (1954a)** developed technique of analyzing diallel crosses between homozygous parents and they were able to estimate the genetic parameters $D$, $H_1$, $H_2$ and $F$ (following Mather’s notations) and their standard errors from second degree statistics. $D$ measured variance due to additive genetic effects, $H$ measured the dominance variance, while $F$ gave information on the preponderance of dominant and recessive alleles.

**Hayman (1954b)** pointed out that the estimate of average degree of dominance could be increased or decreased depending upon independence of genes in the parents, serious over estimation of degree of dominance may occur in such cases where dominance for all loci is in the direction of plus (favorable) alleles and where the correlation between gene frequencies at different loci is primarily due to dispersion.

**Gardener (1963)** recognized that estimates of degree of dominance, range of yield could be obtained as a result of repulsion phase linkage though none of the genes involved were more than completely and partially dominant to its alleles.

**Kaushik et al. (1986)** applied covariance techniques in diallel crosses for Griffing method I and II and modified methods for obtaining precise estimates of general and specific combining ability reciprocal effects and associated variance and sum of squares. The gain in precision obtained by using analysis of covariance rather than the standard technique was illustrated using data from diallel cross in *Brassica juncea*. 
Singh et al. (1977) observed significant additive and non-additive gene action for pod length in table pea. Singh and Singh (1977) revealed that dominance and epistatic effects were more important than additive effects for expression of seeds per pod.

Dhillon and Chanchal (1981) reported non-additive genetic variance for pod yield, pod number and seed per pod and additive genetic variance for pod length, number of days to flowering and node number of first pod formed.

Kuksal et al. (1983) reported that additive gene effects were important for pod number per plant and yield per plant while non-additive effects predominated for expression of pod number per plant, pod length and seeds per pod.

Singh et al. (1985) reported that both additive and non-additive gene effects were significant for plant height, pods per plant and yield per plant in table pea.

Srivastava et al. (1986) studied a 8 parents half diallel cross and reported partial dominance for day to flowering, node number at which first pod formed and additive effects for 8 seed yield related traits in table pea.

Saxena et al. (1987) observed that in table pea, the additive gene action was predominant for yield, number of primary branches per plant, days to maturity, seeds per pod and pod length, while non-additive for plant height.

Sarawat et al. (1994) reported that in table pea both additive and non-additive gene effects for grain yield, harvest index, branches per plant, pod per plant, seed per pod, plant height and flowering period were significant.

Kumar et al. (1996) reported that in table pea additive gene action was predominant for the inheritance of pod length and plant height while the other characters investigated were controlled mainly by non-additive gene action.
Sharma et al. (1999) reported in both additive and non-additive type of gene action in table pea. The ratio of additive variance ($\sigma^2_A$) to dominance variance ($\sigma^2_D$) indicated the predominant role of non-additive gene action for pod yield, number of pods/plant, grain weight, days to maturity and shelling percentage whereas additive gene action was found responsible for plant height.

Singh et al. (1999) reported that non-additive gene action was predominant for all the characters in table pea viz. days to initial flowering, days to maturity, plant height, 100-seed weight, biological yield/plant, seed yield/plant and harvest index. Though the additive component was also significant.

Narayan et al. (1999) studied six genetically diverse populations (P1, P2, F1, F2, B1 and B2) of five cross combinations viz. Bonneville X Lincoln, Bonneville X Solan Nirog, Bonneville X Kinauri, Lincoln X Solan Nirog and Lincoln X Kinauri together the informations on inheritance of yield and quality characters in garden pea. They revealed preponderance of non-additive gene effects for yield and quality traits and suggested that maximum gain could be attained by maintaining considerable heterozygosis through mating of selected plants in early segregating generations. They advocated, few cycle of recurrent selection followed by pedigree breeding; effective and useful for improvement of yield and quality for the genetic material under study.

Singh and Sharma (2001) reported that three crosses each for plant height, pod/plants, seeds/pod and pod length and pod yield/plant showed inadequacy of additive dominance model indicating the presence of epistasis.

Sharma and Kalia (2002) revealed validity of additive dominance model for all the characters (pods/plant, pod length, seeds/pod, shelling (%), T.
S. S %) except for pod yield / plant through $t^2$ statistics. Therefore the results obtained on the genetic components are to be viewed with caution for their validity for pod yield. They further revealed that the Hayman’s genetic component analysis indicated that the gene action for most of the traits had significant additive (D) and non-additive (H₁) genetic variance with preponderance of the latter in both F₁ and F₂ generations. However, D component was found to be non significant for pod yield / plant and pods/ plant in F₁ and for total soluble solids in both F₁ and F₂ generations.

**Singh and Dhillon (2003)** revealed that both additive and non-additive components were significantly important for all the quality traits under study viz. shelling percentage, dry matter content, crude protein and total sugar. Moreover, additive component of variance was non significant for pod yield. Based on their study they concluded that simultaneous exploitation of both additive and non-additive gene effects for improvement of the characters. They found, the F value non significant for all the traits, thereby showing the equal distribution of dominant and recessive genes in the parents. The estimates of $(H₁/D)^{1/2}$ suggested over dominance for all the traits except total sugar which revealed partial dominance. The value of $H₂/4H₁$, was less than the expected value of 0.25 for all the traits under study suggested asymmetrical distribution of favorable and unfavorable genes in the parents. The fraction $h^2/ H₂$ indicated that at least one group of genes controlled the dominance for shelling percentage and crude protein. Further two groups of genes were detected to control the dominance for pod yield, dry matter and total sugars.

**Sharma et al. (2003)** studied the nature of gene action for days to 50% flowering and number of days to first picking in the parents and their 45 F₁s and F₂s obtained through diallel mating design excluding reciprocals. The additive and non-additive components of genetic variances were significant for
both the characters for both the generations. However, the magnitude and additive genetic component was more in F₁ generation while in F₂ non additive genetic variance were more pronounced.

**Singh et al. (2006)** carried out study to investigate gene effects of yield and its components traits in 6 generations of two crosses i.e. cross I (Arkel x Matar Ageta-6) and cross II (Matar Ageta-6 x Bonneville) of pea. All types of gene actions i.e. additive, dominance and interaction components played a role in inheritance of these traits except for node at which first pod appears but degree differed with crosses. Heterosis breeding, pedigree selection and selection of desirable transgressive segregants in the early generations are suggested for improvement of yield and quality traits in pea.

**Kumar et al. (2006)** studied the nature and magnitude of genetic variance for yield and its component traits in field pea using line x tester analysis. The results revealed significant additive and non additive gene action for days to maturity, plant height, pods per plant, seeds per pod, 100 seed weight, seed yield, biological yield and harvest index. Average degree of dominance indicated over dominance for all the traits.

**Narayan (2006)** observed prevalence of additive and non additive gene action in the inheritance of yield and quality traits suggested that the suitability of recurrent selection in succeeding generations for the development of transgressive segregants.

**Combining ability**

The parental combinations have great importance to improve the qualitative and quantitative traits. These combinations help to identify desirable parents, which can be crossed either to exploit heterosis or to select desirable homozygous lines from segregating population. General combining ability
(gca) is primarily a function of additive gene action and additive x additive interaction while specific combining ability (sca) is primarily due to non-additive genetic variance as well as non-allelic interactions. The estimates of combining ability effects and their relative magnitude of genetic variance provide guidelines for selecting the best parent for hybridization. The highly significant general and specific combining ability variance indicated importance of additive and non-additive gene action governing inheritance of characters under study.

**Griffing (1956)** pointed out that the gca involve additive and additive x additive interaction. **Hayman (1957)** observed that in the absence of epistasis gca comprised the additive portion while, sca involves only dominance. Both combining abilities will contain epistatic portions while sca is mainly a measure of dominance and epistasis in unselected and selected material, respectively.

**Moll et al. (1964)** pointed out that in maize magnitude of gene action based on combining ability variance is not much reliable due to serious bias from genotypes x environmental interaction.

**Wessly (1973)** discussed the gca and sca effect in relation to means and variance of the breeding population.

The research work done on this aspect in peas for different characters under study is being illustrated hereafter.

**Singh and Singh (1990)** reported that combining ability in data derived from 8 yield related characters in 8 cultivars and their 28 F₁ hybrids. PH-1, HUVP-1, EC-33866 and VL-6 were good combiners for green pod yield, number of seeds/pod, length of pod and days to maturity of green pods. HUVP-1 x E-33866 were the best combination for total green pod yield / plant.
Singh and Mishra (1996) observed that heterosis and sca effects of the crosses were parallel.

Sharma (1999) studied 9 pea genotypes and their 18 cross which were evaluated for powdery mildew resistance. Azad P-1, Palampriya and VL-7 were the best general combiners while VL-7 x DPP-13 showed significant and positive sca effects for all 5 yield components except grain/pod.

Singh et al. (1999) reported that variances due to gca and sca showed non-additive gene action which was predominant for all the characters viz., days to initial flowering, days to maturity, plant height, 100-seed weight, biological yield/ plant, seed yield/ plant and harvest index, though the additive component was also significant. Cross Bonneville x HUDP-6 had significant desirable sca effect for seed yield and some of its components.

Roy and Das (2000) reported that genetic variability was higher for days to 50% flowering, plant stand, plant height and yield/plot which was confirming to higher gca values. Additive gene action was predominated for maturity traits, plant height and yield/plot.

Narayan et al. (2000) studied combining ability in six divergent genotypes and their $F_1$s for pod yield per plant, node at which the first flower appeared, number of pods/ plant, number of seeds / pod, pod length and girth and shelling %. Variances due to general and specific combining ability were significant for all the characters. All the characters exhibited greater importance of non-additive gene effects except for node at which first flower appeared.

Sharma et al. (2000) analyzed combining ability for yield and yield components in garden pea from parents, $F_1$ and $F_2$ generations obtained through diallel mating design except reciprocals. GCA variance was significant for all the characters except pod width for which SCA variance was higher.
Sharma et al. (2000) reported that gca variance was significant for all the characters under study except pod width for which sca variance was higher. The per se performance of parents and crosses was usually associated with the combining ability effects, Bonneville x Lincoln, Bonneville x VL-3 and Lincoln x VL-3 were the most promising hybrids.

Singh et al. (2001) studied combining ability for yield and its component in pea in 21 crosses & 7 parents. The analysis of variance for combining ability revealed that the general combining ability (gca) and specific combining ability (sca) variance were highly significant. The sca variance was predominant in comparison to gca variance for all the characters indicated that there is greater contribution of non-additive gene action for days to flowering, days to maturity, plant height, branches per plant, pod length, 100 seed weight, harvest index and yield per plant.

Singh et al. (2002) studied combining ability analysis in 10x10 diallel set for seed yield and its component characters in garden pea. The mean sum of square due to general and specific combining ability variances were highly significant for all the characters studied in both the generations except for seeds per pod in F$_1$ and F$_2$ indicates the role of additive as well as non-additive gene effects for the expression of characters under study.

Kumar et al. (2002) studied 88 crosses obtained by diallel mating design for combining ability. Mean square for general combining ability was higher than the of specific combining ability indicated preponderance of additive gene action for all the characters under study except for plant height and 10 pod weight.

Kumar and Tewatia (2003) studied combining ability for crop yield and yield components of crosses derived from line X tester set. Specific combining ability was higher than general combining ability, indicating the
preponderance of non-additive gene actions for the characters studied viz. yield, number of pods/plant, pod weight, weight of edible grains per pod, number of days to first picking, number of edible grains per pod, length of pod, internodes length, shelling percentage & number of branches per plant.

**Singh and Dhillon (2004)** assessed 10 divergent varieties along with 45 crosses obtained through diallel mating design excluding reciprocals. The relative magnitude of general and specific combining ability variances showed that additive gene effects were predominant for shelling % and total sugars. The predominance of non-additive gene effects were important in the inheritance of pod yield, dry matter, crude protein & alcohol insoluble matter. None of the parent was a good general combiner for all the characters.

**Gupta and Singh (2005)** studied combining abilities in 60 F_{1}s obtained by crossing 20 lines and 3 testers in garden pea. They revealed that the variance for general combining ability (gca) and specific combining ability (sca) were highly significant for all the characters under study namely (pod yield/plant, pods/plant, 100 pod weight, 100 green seed weight, dry seed yield/plant.

**Singh et al. (2005)** studied 6 x 6 diallel cross (excluding reciprocals) to identify the best general combiners and for the expression of seed yield and other related attributes for the improvement of field pea. They observed significant differences in parents versus F_{1}s for all the characters except for days to maturity, plant height, pod length and number of seeds per pod. Variances due to gca and sca were highly significant for days to flowering, days to maturity, plant height, number of seed per pod and grain yield. The sca variances were considerably higher than their gca variance for all the characters, indicating the predominance of non-additive variance in controlling the expression of these characters. Good general combiners were DDR-4 and HUP-2 for grain yield and harvest index, DDR-13 for days to flowering, 100
grain weight and maturity, DDR-4 for number of pods per plant, DDR-13 and KPMR-400 for plant height and DDR-4 and KPMR-400 for protein content. The best crosses mainly DDR-4 x KPMR-400, DDR-13 x DDR-4 and HUP-2 x KPMR-400 had desirable sca effects with high per se performance for seed yield.

**Pandey et al. (2006)** studied combining ability for different characters in 10 pea cultivars and their 45 diallel crosses. Significant gca and sca variances were observed for all the characters. Lincoln and NC-64086 were identified as the best general combiners for pod yield per plant.

**Narayan (2006)** studied combining ability for quality traits for 6 x 6 diallel crosses (excluding reciprocals) of garden pea genotypes. Significant differences among progenies and parents were observed for pod yield per plant, dry matter content, total sugar content and protein content. Variances due to gca and sca were significant for all the characters. Among the parents Bonneville proved to be best combiner for pod yield per plant, shelling percentage, dry matter content and protein content whereas Lincoln and VL-3 were the best combiner for all the traits except shelling percentage and protein content. Bonneville x Lincoln exhibited positive significant sca effects for all the characters except for dry matter content.

**Singh et al. (2007)** studied 10 x 10 diallel analysis (without reciprocals) in table pea which indicated that the mean squares for gca were higher than those of sca in all the characters. Sugar Bon showed highest gca for days to 50% flowering and number of branches per plant and second highest gca for plant height. Mithiphali had maximum gca effects for total and marketable green pod yield per plant. Cross combination Sugar Daddy x JP-19 recorded highest specific combining ability for total marketable green pod yield for plant followed by Early Snap x Mithiphali.
Jyothula and Guttala (2008) ten diverse cultivars of field pea were crossed in diallel mating design conducted in U.P., India. The analysis of variance for combining ability revealed that both general combining ability (Gca) and specific combining ability (Sca) variances were highly significant for all the characters studied, which indicated that both additive and non-additive gene effects were important for the inheritance of different characters studied.

Borah (2009) combining ability analysis carried out for ten characters using six diverse parents in field pea revealed that variance due to gca and sca were highly significant for days to maturity, plant height, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant indicating the importance of both the additive and non additive genetic components of variation.

Heterosis

Heterosis is defined as the superiority of F1 hybrid over it parents in terms of yield or some other characters. Negative heterosis for some of the traits like earliness and positive heterosis for most of the traits are considered desirable.

East (1908) and Shull (1909) proposed a hypothesis independently and assumed that there is a physiological stimulus to development that increases with the diversity of the uniting gametes. The term ‘heterosis’ was first coined by Shull (1914).

Jinks (1955) suggested that non-allelic interaction is more likely and frequent cause of heterosis rather than special relation between genes at the same locus.

Jinks and Jones (1958) suggested that heterosis is a complex genetical phenomenon depending upon the balance of the additive, dominance and the
interaction of homozygous / homozygous and homozygous / heterozygous components as well as on the distribution of the genes in the parental lines. It can result a wide spectrum of gene effects.

**Daskalov (1963)** proposed that heterosis in F₁ is the combine expression of genetical, cytoplasmic, biometrical and physiological factors and may be attributed to stimulation, resulting from the interaction among different heritable factors of the parents in F₁.

**Parmar and Godawat (1990)** observed heterosis from data on 10 yield related characters in 5 elite crosses involving 7 parents. Yield and pods per plant showed greatest heterosis (58.8%).

**Singh et al. (1994)** found six crosses showing significant heterosis for yield per plant in a study of 45 F₁’s obtained from 10 x 10 cross. Hybrids T-163 x 6112 and T-163 x PG-3 showed 28.73 and 26.77 percent heterosis over economic parent with 2.61 percent and 6.25 percent inbreeding depression due to additive x additive and additive x dominant type of gene action.

**Singh and Mishra (1996)** studied heterosis from data on 6 yield related component in 6 x 6 diallel. Most of the hybrids exhibited heterosis for most of the characters. The highest heterosis over mid and better parent values for yield was observed in cross VP - 7906 x VI-3 as there was high gca effects for most of the characters. The greatest heterosis estimate for earliness was recorded in UP-7906 x JP-169.

**Sharma et al. (1998)** reported highest heterosis for fertile nodes / plant followed by seeds / pod, pods / plant, pod length and seed yield / plant. The highest value of heterosis over better parent (64.50%) was recorded for seed yield / plant in the cross HFP-8909 x DPFD-69.
Abdou et al. (1999) studied heterosis from data on a number of yield related traits in the parents and F<sub>1</sub> progenies of a diallel cross involving 5 diverse pea genotypes. Heterosis expression indicated that potential gene recombination’s could occur to enhanced earliness and green pod yield.

Tyagi and Srivastava (1999) reported that six crosses exhibited significantly higher yield. The highest heterosis over better parent (89.50%) was shown by FC-1 x Pusa-10. Plant height, pods/ plant biological yield and harvest index were the major contributors to heterosis for yield increase.

Kumar et al. (2000) studied 16 parents and 48 hybrids to investigate the extent of heterosis for green pod yield and its contributing characters. Cultivars PRS-18-6, PH-10 and LMR-6585 were observed to be the top three performing parents for green pod yield per plant. Appreciable heterosis was recorded over better parent and mid parent for all the characters except total soluble solids and protein content. F<sub>1</sub> hybrids JP-83 x EC-33866, JP – 83 x Arkel and HUVP-2 x EP-3 were observed as the best hybrids for green pod yield per plant as they showed significant heterosis of 59.14, 58.41 and 73.18% respectively over the top parent PRS-18-6.

Gupta et al. (2003) reported that the greatest heterosis response for seed yield (55.37%) was recorded for KS-226 x Azad P-3, the parents of which were high x low general combiners. The numbers of days to flowering, plant length, number of branches per plant, number of pods per plant and pod width were the major contributors to heterotic yield.

Kumar and Tewatia (2005) observed that heterosis over better and top parent for all the characters except number of days to 50% flowering, number of days to first picking and node at which first pod appears, where negative heterosis is desirable.
Pandey et al. (2006) studied heterosis for different characters in 10 pea cultivars and their 45 diallel crosses (excluding reciprocals). Average heterosis was observed for plant height, pods per plant, pod length, seeds per pod, pod yield and total soluble solids. Eleven crosses exhibited significant positive heterosis over eight parents for pod yield.

Kushwaha and Sharma (2007) considering over all results on economic heterosis the crosses CHPMR-1 x PSM-34, CHPMRI x Arkel and KTP-4 x PSM-3 should be exploited to breed for stable and widely adopted varieties of vegetable pea it is expected to give early maturity and powdery mildew resistant lines of pea.

Singh et al. (2008) heterosis over parent was estimated for seed yield and related traits in 16 crosses of pea. To as certain the genetic causes responsible for the observed heterosis in pea, the estimates of genetic parameters realized from first degree (generation mean analysis) and second degree statistical (modified TTC) models have been used. The generation mean analysis revealed that the observed heterosis for seed yield per plant and pod per plant was mainly due to over dominance.

Awasthi et al. (2009) an experiment was conducted to study heterosis in garden pea for different quantitative characters. Analysis of variance for heterosis showed significant differences among all crosses for all characters, indicating that there is ample scope for selection of promising crosses from present gene pool for yield improvement in garden pea.

Karnwal and Kushwaha (2010) studies heterosis were estimated for various horticultural and soil fertility improving traits in 8 x 8 garden pea half diallel crosses involving eight genetically diverse genotypes (Arkel, VL-9, PSM-3, DARL-403, Punjab Ageta, Azad P-3, VL-316 and Pant Uphar). Analysis of variance revealed significant differences for GCA and SCA for all
the traits studied. Among the parents, DARL-403, PSM-3 and Pant Uphar emerged as a good general combiner for pods per plant, pod yield per plant and nitrogen fixing nodules per plant.

**Heritability and Genetic advance**

Heritability is an index of transmissibility of traits from one generation to another generation. The concept of heritability is important to determine whether the phenotypic differences observed among various individuals are due to differences in their genetic make up or simply as result of environmental factors. It serve as a useful guide to breeder, as the selection for traits having high heritability will be effective and improvement will be brought through selection.

According to **Lush (1940)** the heritability in broad sense is the ratio of total genetic variance to phenotypic variance. In narrow sense it is the ratio of additive genetic variance to phenotypic variance. **Lush (1940)** suggested following reasons for requiring an estimate of heritability.

(i) When heritability in narrow sense is high, emphasis should be placed mainly on mass selection and if it is low, more pressure should be on pedigree, sib-tests and progeny test.

(ii) In case of epistatic variance is relatively high, more reliance should be paid on selection between families and line breeding.

(iii) If over dominance is strong, inbreeding programme is to be emphasized with the object of production of commercial hybrids.

(iv) When the variance due to interaction between genotype and environment is relatively larger, breeding programme should be streamlined for the development of superior variety for different agro-climatic regions.
(v) Heritability in narrow sense could be utilized for estimation of expected improvement based on selection.

Robinson (1965) proposed categorization of heritability i.e. 1 to 10 percent as low; above 10 and below 30 percent as medium and above 30 percent as high. Genetic advance or genetic gain is still more useful as heritability estimate itself doesn’t have much significance as it fails to account for magnitude of absolute variability. It is improvement in the genetic value of selected plant over the base population. The genetic advance is the product of heritability and selection differential expressed in terms of phenotypic standard deviation of the characters. Heritability and genetic advance both are the estimates of component of direct selection. It is necessary to utilize the heritability estimates in connection with which would indicate the expected genetic gain.

According to Comstock and Robinson (1952) the genetic advance is an improvement in the genetic value in the new population as compared to original one and depends upon the following three factors:

(i) Heritability

(ii) Phenotypic standard deviation

(iii) The intensity of selection.

The work available with regard to heritability and genetic advance in pea is reviewed as under:

Singh et al. (1993) observed high heritability estimates for days to maturity, seed weight and plant height. Seed yield showed moderate heritability. Days to maturity and seed weight gave high values for genetic advances as percentage of the mean. Singh et al. (1993) reported high heritability estimates for seed weight and pods per plant than other traits.
Kumaran et al. (1995) reported high heritability estimates coupled with high genetic advances over percentage of mean for number of branches / plant, weight of seeds / pod, number of pods / plant and pod yield / plant. Singh (1995) reported that heritability estimates were generally high for all the characters. High genetic advances coupled with high heritability for pods per plant, pod width, seeds per pod and pod yield per plant indicated that selection for these traits should be effective for improving economic yield. Tyagi et al. (1997) reported high heritability (in broad sense) estimates for plant height, biological yield and seed yield. Gupta et al. (1998) reported high heritability estimates for days to 50% flowering, pod weight / plant, 100-seed weight and protein content. Kumar et al. (1998) reported high heritability and genetic advance estimates for plant height, biological yield, seed yield, number of pods per plant and partitioning index.

Vikas and Singh (1999) reported high estimates of genotypic and phenotypic co-efficient of variation, heritability and genetic advance for plant height, pod/ plant, seed yield/ plant and biological yield in most of the crosses.

Sureja and Sharma (2000) studied heritability and genetic advance in a collection of 30 indigenous and exotic genotypes of garden pea. High heritability in association with high genetic advance observed for plant height, length of internodes, pod yield/ plant, number of pods/ plant, seed yield/ plants, number of primary branches and 100 seed weight, indicating additive gene effects and emphasized the selection for these traits to improve economic yield.

Sinde (2000) reported significant differences which were observed for all the characters among the genotypes. The results revealed that the characters namely crude protein percentage, weight of pod yield/ ha and yield/ plant had high heritability values coupled with high percentage of genetic advance indicating additive gene effects and greater scope of selection.
Ramesh et al. (2002) studied thirty-six genotypes and revealed high estimates of broad sense heritability and genetic advance for plant height, internodal length, node of the first fruiting and number of pods per plant. High heritability with moderate genetic advance were observed for mean pod weight and reducing sugar content in the edible grain.

Singh et al. (2003) reported that high heritability and low genetic advances were recorded for harvest index, pod length, number of seed per pod, protein content and 100-grain weight in both generations. These traits were moderately influenced by non-additive gene action.

Sharma et al. (2003) studied sixty-three genotypes of pea (*Pisum sativum* L.) including indigenous and exotic cultivars and found high heritability for seed yield per plant, biological yield per plant, harvest index, plant height, 100 seed weight, seeds per pod, pod per plant, days and 50% flowering and pod length while low heritability for days to maturity. High genetic advance along with high heritability and GCV was observed for seed yield per plant, biological yield per plant and pods per plant. This indicated that selection for these characters would be effective for further improvement.

Rai et al. (2006) observed the higher genetic advance coupled with moderate estimates of heritability observed for the plant height and high heritability as compared with low genetic advance for number for seeds per pod and number of pods per plant. Genetic advance as percent of mean showed maximum value for yield per plant followed by number of pods per plant.

Mahamad et al. (2006) observed high heritability coupled with high genetic advance for plant height, number of branches per plant, number of pods per plant, green pod yield per plant, green seed yield per plant, 100 green seed weight.
**Gupta et al. (2006)** observed the range of heritability from 36.05% for total soluble solids to 96.6% for early yield per plant. Genetic advance was highest for green pod yield per plant. High heritability coupled with high genetic advance observed for days to first flowering node, plant height, number of first flowering node, dry matter weight per plant, green pod yield per plant and number of primary branches per plant.

**Gohil (2006)** revealed high heritability for green yield per plant, days to 50% flowering, days to maturity, number of pods per cluster and harvest index.

**Kumar et al. (2007)** studied one hundred genotypes of pea and reported high to moderate heritability coupled with high to moderate genetic advance for 100 seed weight, yield per plant and biological yield which indicated the dominance of additive gene action suggesting thereby selection may be effective for these traits.

**Singh et al. (2007)** studied forty advance lines for eleven quantitative characters. They reported high genetic advance coupled with high heritability estimates. High expected genetic advance coupled with high heritability estimates were recorded for seed yield per plant, number of branches per plant and number of pods per plant indicating least influence by environmental variation.

**Sharma et al. (2007)** studied 20 diverse pea genotypes. They revealed high heritability and genetic advance for plant height and moderate for pods per plant and pod yield per plant indicating the additive and non additive gene action for their expression, respectively.