CHAPTER-II

REVIEW OF LITERATURE
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Techniques involving 'diallel cross analysis' has been widely used by the breeders in different crops for understanding the nature of genetic variances involved in the expression of characters and also for the identification of suitable parents for hybridization in crop plants. A brief account of literature available on Brassica spp., on different aspects of present investigation, i.e., diallel cross analysis, components of variance, combining ability, heterosis and inbreeding depression, heritability and genetic advance and correlation coefficient analysis has been reviewed in this chapter.

1. DIALLEL CROSS TECHNIQUES:

The theory of diallel cross and its usefulness in genetic analysis of population has received increasing attention in recent years. Diallel cross study has been made in a large number of crops by several workers since 1945, when Hull (1945) applied this technique to know the properties of a group of homogeneous lines. Yates (1947) subsequently discussed this method in a series of papers. Jinks and Hayman (1953), Hayman (1954) and Jinks (1954) developed this technique based on the method of Mather (1949) and analysed diallel crosses between homozygous lines. Hayman (1954b) again analysed the diallel cross data, considering in arbitrary degree of dominance for the cause where the plants are homozygous. When only two alleles/locus were considered and the assumption of no epistasis was imposed.

Several diallel cross techniques have been proposed and applied to diverse problems relating to general and specific combining ability (Sprague and Tatum, 1942; Henderson, 1952; Griffing, 1956a
and 1956b; Matzinger et al. 1959). Another application to parental materials in breeding problems has been discussed by Jinks (1955), Allard (1956a, 1956b and 1956c); Matzinger and Kempthorne (1956); Whitehouse et al. (1958) and Matzinger et al. (1959). The theory of diallel crosses and problems for estimating certain genetic parameters in terms of gene models in varying degree of complexity have been discussed by Hull (1952), Griffing (1956a and 1956b); Hayman (1954a, 1954b, 1957, 1958 and 1960), Jinks (1954 and 1956), Durrant (1965), Kempthorne (1956); Nasser (1965) and Gardner and Eberhart (1966).

A diallel crossing system can be defined as one in which parental genotypes are chosen and intercrossed among themselves. The parental genotypes are usually inbred lines but they can also be individual clones, open pollinated varieties or other genetic entries. If all possible crosses are made among the parents, leading to the P2 matings, the system is called complete diallel cross. These P2 combinations are conveniently divided into three groups: (i) the parental combinations $P_1 \times P_1 \cdots \cdots P_n \times P_n$, (ii) one set of $1/2 P \cdot (P-1)$ F1 combinations, and (iii) the set of $1/2 P (P-1)$ reciprocal F1 combinations.

In the breeding of self-pollinated crops such as Indian mustard, the breeder usually has a multiplicity of pure lines, any one of which may be capable to produce desirable progeny in a particular hybrid combination.

Accumulated experience indicated that the best progenies are usually produced by parents which possess many desirable characteristics. Still, the breeder is likely to have so many desirable parents at his disposal that it is difficult to choose among many
crosses that seems equally likely to produced outstanding offsprings. The only guide line to determine which hybrid produce many superior offsprings and which does not, has been to grow segregating population from each hybrid. This is expensive and time consuming method that permit identification in early generations of the hybrids, promising the greatest advance, would clearly be advantageous, but progress towards such methods has been slow.

Griffing (1956b) noted that parental and F1 data have distinct advantages over the data from segregating generations in studying quantitative genetic systems because being unaffected by genetic segregation and linkage, the former data require relatively few individuals for efficient estimation of certain relevant genetic parameters. Therefore, more parents can be included and wide range of germplasm can be sampled and evaluated in a diallel cross.

A method of analysis of parental and F1 generations from a set of diallel crosses presented by Jinks and Hayman (1953) appeared to provide a rapid evaluation of genetic relationship among a number of parents. The method, thus seemed to offer promise in identifying parents whose hybrids were most likely to respond to selection. Since the parents promising to a breeder to self-pollinated crops will almost always be a selected sample, the approximate sampling assumption is that the experimental material it self constitutes the entire population about which inference are to be made. The analysis proposed by Jinks and Hayman (1953) include parents and one or both sets of F1 crosses. Hence, with respect to Griffing's classification of diallel cross technique, it is applicable to both experimental method I and II.
Kempthorne (1956) criticised Jinks and Hayman's analysis on the basis that "the diallel cross must be interpreted in terms of some population which has given to the homozygous parents in inbreedings." From another viewpoint one may question the value of estimating additive variance, dominance variance and so on unless the estimated quantities are measures of the characteristics of definite population. Since the parents of primary interest to breeder of self-pollinated crops will usually not have been derived by inbreeding from some definite population. Kempthorne evidently considers that the Jinks and Hayman's model of analysis of diallel crosses has little practical value as an aid in the improvement of self-pollinated crops.

Allard (1956a) has been given some procedure for evaluating genotypic environment interaction in diallel table. He developed the work of Jinks and Hayman (1953). Dickson and Jinks (1956) extended the method of Jinks and Hayman (1953) to include inbreeding of parental material in diallel table.

Gilbert (1958) has also criticised the assumption on which Jinks and Hayman's analysis is based, concluding that the method is not of direct relevance to plant breeding.

Hayman (1957, 1958 and 1960) has considered these criticism and has discussed some additional aspects of the theory and analysis of diallel crosses. He extended the analysis of a fixed set of inbred lines by Jinks and Hayman (1953) to a random sample inbred lines. The method provides a better estimates of the components of genetic variation. He has also suggested some experimental designs to suit diallel analysis.

Crumpacker and Allard (1962) suggested that diallel cross provides an assessment of the genetic system that appears to be
useful in predicting the immediate outcome of directional selection programme of heading date. The reciprocal analysis of Jinks (1954) and Hayman (1954a) has been extended by Durrant (1965) for recognising the mechanism and determination of reciprocal differences. He considered two more forms of inheritance which could be sub-divided into multi factor inheritance and associated group inheritance as alpha and beta.

Nasser (1965) studied the effects of correlated gene distribution due to small samples on the slopes of Wr, Vr, graph and variance of general and specific combining ability arising from differences among sample of parents.

Gardner and Eberhart (1966) have presented a model for estimation of gene effects and heterotic parameters for diallel cross and related population of fixed set of random mating varieties with arbitrary gene frequency at all loci. He criticised Griffing's (1956b) method II and model I analysis which failed to give clear picture of heterosis and gene effects.

Singh (1973a) has given an idea for diallel analysis over different environments. This method is also appreciable to analyse the data of different environments.

Baker (1978) discussed the use of diallel analysis and the range of validity of different assumptions. These methods are based on either first or second degree of statistics.

During the past few years, several reports have appeared and it was found that the diallel analysis is the quickest methods of understanding the nature of quantitatively inherited traits and to as-
2. COMPONENTS OF GENOTYPIC VARIATION:

(A) Nature of genotypic variation:

Most of the characters of economic importance are quantitatively inherited. They are governed by a large number of genes each with small effects and are characterised by continuous variation. A detailed knowledge about nature and magnitude of genetic variation is essential for efficient breeding programme.

The study of inheritance of quantitative characters in plants began with the work of Johansen (1909), Nilsson-Ehle (1909) and East (1916). Theoretical basis of quantitative genetics was established by Fisher (1918), Wright (1921) and Haldane (1932).

Wright (1921 and 1935) defined and divided the genotypic variance into (i) additive genetic variance (ii) variance due to dominance (deviation from additive scheme) and (iii) variance due to epistatic-deviation from the additive scheme, resulting from the interaction of non-allelic genes.

An interest in quantitative genetic was developed following the works of Comstock et al. (1949) and Mather (1949). Cockeraham (1954), Henderson (1954), Kempthorne (1955) and Mather and Jinks (1971) developed theoretical expectations and methodology for the estimation of various genetic parameters.

Jinks and Perkins (1969) has described a procedure for distinguishing between higher order interactions and linkage between interacting genes.
Gardner (1963) enlisted the following genetic parameters which are of interest to the plant breeders:

(i) Additive genetic variance ($\sigma^2_A$) which results from the additive effects of gene at all segregating loci.

(ii) Dominance variance ($\sigma^2_D$) which results from inter-allelic interaction of genes at segregating loci.

(iii) Epistatic variance which results from the inter-allelic interactions at genes at two or more segregating loci and which is divisible into additive x additive ($\sigma^2_{AA}$), additive x dominance ($\sigma^2_{AD}$) and dominance x dominance ($\sigma^2_{DD}$) for two locus situation, and additive x additive x additive ($\sigma^2_{AAA}$), etc. for three or more loci.

(iv) Average degree of dominance or ratio of dominance variance to additive genetic variance.

(v) Genotypic x environment interaction, which may be divided into additive gene effects x environment and non-additive gene effects x environment, and

(vi) Genotypic correlation among quantitative characters for the particular crop.

Among all these gene effects, epistasis was found to be correlated with yield (Jinks, 1955 and Gamble, 1962). Sentz et al., (1954) Bauman (1959), Johnson (1963) and Eberhart (1964) have reported the importance of epistasis in specific combining ability.

Jinks et al. (1969) who have given a new method of analysis for detecting additive, dominance and epistatic variation
which require only \( 2 \times n \) cross, out of a diallel set of \( n^2 \) crosses, described it and demonstrated its use on final height and flowering date. The conclusion drawn from this analysis showed good agreement with those from extensive diallel analysis.

(B) Methods for the Estimation of Genetic Parameters:

Following methods have commonly been used by various workers for the estimation of genetic parameters in crop plants:

(i) Estimates based on segregating generations from crosses of two pure lines (Mather, 1949).


(iv) Triallel and quadriallel analysis (Rawling and Cockerham 1962a and 1962b and Ponnuswamy; 1971).


(vi) Inferences about gene action from combining ability studies (Sprague and Tatum, 1942; Rojas and Sprague 1952; Griffing, 1956a and 1956b; Kempthorne and Curnow, 1961).

3. CONCEPT OF COMBINING ABILITY AND ITS ESTIMATION:

The concept of combining ability was first given by Sprague and Tatum (1942). They recognised the combining ability of two classes, i.e.; general combining ability (g.c.a.) and specific combining ability (s.c.a.). According to them, "general combining
ability is the average performance of a line in hybrid combination, while specific combining ability is to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of average performance of the line involved. Further they concluded that g.c.a. was primarily due to additive effects of genes, while s.c.a. was a consequence of inter-allelic interaction (dominance) and inter-allelic interactions (Epistatis).

Handerson (1952) also defined general combining ability as "the average merit with respect to some traits or weighted combinations of traits of large number of progenies of an individual or line when mated with a random sample from specified population under a specified set of environmental circumstances". The specific combining ability was defined as "the deviation of an average of an indefinitely large number of progenies of two individuals or lines from the value which would be expected on the basis of the known general combining abilities of these two lines or individuals and materials ability of these female parent".

For estimating the general and specific combining ability, five methods have been used by different workers. These are top cross, poly cross, line x tester cross, diallel cross and partial diallel cross.

Inbred x variety (top cross) cross method was first suggested by Davis (1927) and it has been extensively and widely accepted procedure for estimation of combining ability. Sprague and Tatum (1942) not only provided the concept of general and specific combining ability but outlined the formula for their estimation and also compared the relative importance of g.c.a. and s.c.a.

Griffing (1956a) gave the generalised concept and methodologies for combining ability analysis of diallel crosses and
also outlined the procedure for determining the general and specific combining ability effects and variances from diallel set of varied compositions.

Kempthorne (1957) proposed line x tester analysis, which is analogous to design II of Comstock and Robinson (1948 and 1952). In this procedure, co-variances of half-sibs and full-sibs were related to the variances due to general and specific combining ability.

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

Gardner and Eberhart (1966) developed a model for combining ability analysis by diallel cross technique involving open-pollinated and synthetics in Hardy-Weinberg equilibrium. The genotypic variances was partitioned by them into (i) due to parents, and (ii) due to heterosis. The variances due to heterosis was split into average heterosis, variety heterosis and specific heterosis.

General combining ability is associated with genes which are additive in their effects. Specific combining, on the other hand, is attributed primarily to deviation from additive scheme caused by dominance and epistasis (Sprague and Tatum 1942). This fact is also apparent from the equation derived by Griffing (1956a).

\[
2\sigma^2 \text{gca} = \sigma^2 A + Y_2\sigma^2 AA + \ldots
\]

\[
2\sigma^2 \text{sca} = \sigma^2 D + Y_2\sigma^2 AA + \sigma^2 AD + \sigma^2 DD + \ldots
\]

Where, \(\sigma^2\) gca is the variance due to general combining ability, \(\sigma^2 A\) is the additive genetic variance and \(\sigma^2 AA\) is the
additive x additive type of inter-allelic interactions. Similarly $\sigma^2$ sca is the variance due to specific combining ability, $\sigma^2$D is the dominance variance, $\sigma^2$ AD is the additive x dominance and $\sigma^2$ DD dominance x dominance interactions.

4. DEGREE OF DOMINANCE :

In polygenic inheritance, the effect of individual gene cannot ordinarily be distinguished from one another. Consequently, it is not possible to determine the mode of action of each gene. By studying their combined effect in segregating population, however, one can get some insight into their behaviour and can draw inference about the average level of dominance involved in the expression of a particular character. Fisher et al. (1932) presented a method for estimating the degree of dominance and later on it was applied to corn data. The magnitude of variance due to dominance deviation relative to that of the additive genetic variance, furnished another basis for estimating the degree of dominance (Comstock et al. 1949).

Dominance is complete, if 'a' is equal to 1.0; value over 1.0 are associated with over-dominance and value less than 1.0 with no or partial dominance and if value is equal to zero, the dominance is absent. (Comstock et al. 1949). Further they gave the formula for 'a' where it was calculated as the ratio of mean square due to females and males. They have also demonstrated that unbiased estimates were obtained in the absence of interaction of non-allelic genes. Effects of epistasis which causes bias was removed by the method suggested by Horner (1952).

Comstock and Robinson (1948 and 1952) pointed out that it was theoretically possible to obtain estimates of over-dominance due to repulsion phase linkage in the material such as they used although
the individual gene has expressed no more than partial dominance. Whether or not linkage has caused upward bias in the estimates obtained can be investigated by studying advanced generations in the manner suggested by Gardner et al. (1953) and Gardner and Lonnquets (1959). According to them if average degree of dominance decreases in later generation then linkage is confirmed.

Mather (1949) pointed out that the ratio in which deviation of F1 from the mid-parent bear half the parent differences was frequently regarded as a measure of average dominance. Later this value of each cross was pooled over all the crosses in diallel analysis by Jinks and Hayman (1953) as $\sqrt{H_1/D}$. This is the measure of dominance in Hayman's (1954a) approach.

Robinson and Comstock (1955) coined pseudo-over dominance as an upward bias due to linkage effects in the estimates of dominance variance in hybrid populations. In other words, it is the magnitude of linkage bias in estimates of dominance in hybrid population and rate at which linkage is dissipated because of recombinations. Kempthorne and Curnow (1961) calculated average degree of dominance as $\sqrt{\sigma^2_s/\sigma^2_g}$.

A brief review of recent work done on combining ability and gene action in Brassica species is given below:

Kondra and Stefansson (1965) studied the inheritance of erucic acid content of rapeseed oil (Brassica napus) and investigated that erucic acid content is controlled by two-gene pair system acting in an additive manner.

Swamy (1970) studied nine divergent varieties of brown sarson for oil content of seeds and observed that additive as well as
dominant types of gene action were concerned in the control of oil content. Dominance of both positive and negative effects of genes were apparent. He advocated that differential behaviour of dominance recessive relationship of the parents was probably related to their self-compatible or self-incompatible nature.

Tiwari and Singh (1973) reported that additive and dominance components were significant for the days to flowering and plant height. Country to the findings of Singh (1973), they found that the yield was mainly controlled by dominance component. Partial dominance was observed for days to flowering and over dominance for yield per plant.

Tiwari and Singh (1975) observed that variances due to gca were highly significant for grain yield, plant height and days to flowering and while sca variances were significant for all the traits. They suggested that maximum yield of *Brassica juncea* varieties might be attainable only with a system that can exploit both additive and non-additive genetic effects.

Yadava and Gupta (1975) studied in diallel analysis for eight characters in mustard and recorded that gca, sca and reciprocal effects were significant for oil content.

Paul *et al.* (1976b) studied the nature and magnitude of gene action involved in the inheritance of yield and some of its components in Indian mustard. They observed the importance of both additive and dominance gene effects as important in the inheritance of number of seeds per siliqua, number of siliquae per plant, and number of primary and secondary branches, but the contribution of additive gene effect was greater than those of non-additive effects. Partial dominance was observed for number of seeds per siliqua, and
number of siliquae per plant, number of primary branches and secondary branches, whereas, yield per plant and 1,000 seed-weight exhibited no-dominance.

Ram et al. (1976) observed significant gca and sca effects for all the characters in *B. juncea* studied, viz., plant height, number of primary branches, number of secondary branches, length of siliqua, number of seeds per siliqua, yield per plant and 1,000 seed-weight and predominance of non-additive gene action was reported for all the attributes. However, a substantial amount of additive genetic variance was found for all the traits.

Lutfur (1976) studied in the *F₁, F₂* and back cross population in *B. juncea* and observed that erucic acid was controlled by the same single gene pair with additive action.

Asthana and Pandey (1977) reported that seven traits were controlled by additive gene action in which days to flowering, number of secondary branches, number of siliquae on main raceme and yield were predominantly controlled by additive gene action and plant height by both additive and non-additive type of gene action in Indian mustard.

Yadav et al. (1977) in *Brassica juncea*, observed that variances due to gca, sca and reciprocal effects were highly significant. Seed yield, pods on main shoot, pod length, seeds per pod, main shoot length and secondary branch number were conditioned by both additive and non-additive genetic variances. For plant height and primary branch number, additive variances was predominant.

Grami and Stefansson (1977), while working with summer rape, concluded that oil per cent was controlled by additive gene
action, dominance was significant and epistasis was absent. Contrary to these findings, it was reported by Rao (1977) that oil content in brown sarson was conditioned by dominance gene action, while additive effects influenced plant height and siliquae set.

Labana et al. (1978a) reported the importance of gca and sca variances for all the six characters in *Brassica campestris*. The yield was found to be predominantly controlled by non-additive gene action. They suggested that for increasing yield in synthetic varieties non-additive gene effects could be utilized in breeding programmes.

Labana et al. (1978b) evaluated thirty lines of Indian mustard for general and specific combining abilities through line x tester analysis. Their results revealed that both additive and non-additive type of gene effects were equally important for the number of days to flowering, whereas for the number of primary branches, secondary branches, 1,000 seed-weight and seed yield, the non-additive type of gene effects were predominant.

Anand and Rawat (1978) studied the inheritance of seed yield and its six principal components in the F1 and F2 for combining ability. Study showed significant variances of both general and specific combining abilities for all the characters and estimated variance components revealed the predominance of non-additive gene action.

Chauhan and Singh (1979) in Indian mustard observed highly significant gca and sca variances for both F1 and F2 generations. The additive gene action was found more for days to flowering and maturity in both the generations. For primary branches, non-additive gene action in F1 and both additive and non-additive gene action in F2 was observed. The higher magnitude of \( \sigma^2_s \) and \( \sigma^2_g \) indicated over dominance for number of secondary branches, length of
main receme, yield per plant reflecting the importance of non-additive
gene action.

Duhoon et al. (1979) reported that additive gene effects
were relatively more important for number of days to flowering,
number of secondary branches and plant height, and non-additive
effects were equally distributed in the control of number of primary
branches in Brassica campestris L. var. yellow sarson.

Paul (1979) in rape seed concluded the importance of both
additive and non-additive gene action for control of primary and
secondary branches, siliquae per plant, 1000-seed weight and yield.
Dominance (mainly of higher values) varied in degree ascending to
combination, character and generation. Selection for greater
1000-seed weight and a high number of primary branches seemed to
offer the best prospects for obtaining an increase in yield.

Bunson (1980) in winter rape (Brassica napus) advocated
that gca variances were much higher than those of sca for all the
traits studied. Reciprocal effects were significant for yield and days to
flowering. Mehrotra and Chaudhary (1980) indicated that additive
gene action governed eight characters in Indian mustard, which
included number of siliquae, test weight and seed yield.

Pal and Singh (1980) reported in rapeseed that both the
gca and sca variances were significant for the expression of all yield
contributing characters. However, $\sigma^2_s/\sigma^2_g$ indicated the
preponderance of non-additive type of gene action for the characters.
Nevertheless, reports were put-forward by Govil et al. (1981) in Indian
mustard which indicated that sca was more important than gca for
seed yield, oil content and test weight.
Singh et al. (1981) carried out genetic analysis of data from cross between Brassica juncea L. varieties and found for yield, number of secondary branches and number of siliquae on main raceme, over dominance and dominance gene effects were most important. Significant effects of additive gene action was lower and predominant for days to flowering. Both additive and non-additive gene effects for number of primary branches showed equal importance. Epistatic gene effects contributed to most of the characters, particularly those showing higher magnitude of dominance effects.

Govil et al. (1983) studied genetic control of oil content in Brassica juncea L. and reported that both additive and dominance components of variation were highly significant in the F1 and F2 generations. The magnitude of dominance variance was much large than that of additive genetic variance. Average degree of dominance tended towards over-dominance.

Pal et al. (1983) observed that both additive and non-additive types of gene action were involved in the inheritance of oil content. They suggested that the dominant genes were responsible for higher oil content in Brassica campestris L. var. Toria.

Chander et al. (1985) reported high values of gca for seed yield, number of secondary branches, plant height and 1000-seed weight in Indian mustard. Parents showed highest specific combinations for seed yield, number of secondary branches, number of siliquae on main raceme. RC 1268 was a good general combiner for most of the characters.

Singh et al. (1985) reported that both additive and non-additive gene effects were important for siliquae per plant, siliqua
length, seeds per siliqua, seed weight and seeds per plant in Indian mustard. Although non-additive gene effects were predominant. The per se performance of parents was associated with their gca effects. Prakash and Laha 101 were the best general combiners for seed yield. Most of the crosses showing significant SCA effects involved both low x low or low x high general combiners. Singh et al. (1985) observed that variances due to gca and sca were highly significant for plant height, number of primary branches and secondary branches, days to maturity and seed yield. Non-additive gene effect was predominant for all the traits except plant height in Brassica juncea. Performance of parents was highly associated with their gca effects.

Singh and Srivastava (1986) in their study of half diallel cross analysis recorded that RL 18 for seed yield and P2σ/21 for oil content were best general combiners.

Jindal and Labana (1986) in Indian mustard found that additive and non-additive gene effects were equally important for all traits. Reciprocal differences were significant for all the traits except number of primary branches and days to maturity.

Kumar et al. (1986) reported that both additive and non-additive genetic components were operative for inheritance of free fatty acids and also cross combinations were isolated possessing negative sca effects and suggested that selection in early segregating generations for high yield and low free fatty acid could be appropriate for simultaneous exploitation of additive and non-additive genetic components.
Pal and Singh (1986) found that additive gene effects were important for days to maturity and day to flowering in Indian mustard.

Singh *et. al.* (1986) through combining ability variances indicated the preponderance of additive and additive x additive gene action for days to flowering, days to maturity, number of primary branches per plant, length of main shoot, whereas predominance of non-additive gene action was recorded for 1000-seed weight, secondary branches and yield per plant with small amount of additive gene effect in Indian mustard.

Kumar and Yadav (1986) worked out gca and sca effects for 7 developmental traits in a 21 F1s involving eight parent in *Brassica juncea* grown in three environments. Gca effects were more important for most of the traits, but sca effects were also significant. Gca, sca and reciprocal effects were all sensitive to environmental changes.

Chauhan (1987) studied combining ability analysis in 90 F1s involving a 20 parents in *B. juncea*. The variances due to gca and sca were highly significant for all the characters studied. The estimated components of variance revealed that additive component was pre-dominant for days to flowering, plant height, number of primary branches and non-additive component of genetic variance was important for days to maturity, secondary branches, siliqua length, seeds per siliqua, 1000-seed weight and seed yield.

Badwal and Labana (1987) revealed in Indian mustard the significant values both gca and sca variances for seed size but sca variance was significant only for oil content, and non-additive gene effects were important for all two traits. For oil content and yield, sca
variances were higher than gca variance indicating that dominance was pre-dominant for these traits.

Gupta et al. (1987) recorded additive gene effect for seed yield per plant and non-additive gene effect for number of primary branches and siliquae on main raceme in Indian mustard. The cross RLM-82 x Varuna showed desirable significant saca effects for seed yield, plant height and main shoot length, while the cross involving other females showed best gca effects for seed yield, plant height, main shoot length, primary and secondary branches and number of siliqua on main shoot.

Kumar and Sinha (1987) reported the pre-ponderance of additive gene effect for seed weight in rai.

Jain et al. (1988) determined the nature and magnitude of gene action governing the yield and yield components in Brassica juncea. Both additive and non-additive gene actions were important in controlling days to flowering, days to maturity, plant height, primary and secondary branches, number of siliquae per plant, 1000-seed weight and yield per plant. Epistatic effects on gene action were predominant over additive and dominance effect with an important role of duplicate type of epistasis for most of the traits and suggested that for exploitation of additive and non-additive gene effects recurrent crossing can give desired results.

Hu, (1988) intercrossed inbred lines of rape seed (B. napus L.) to obtain a diallel set including reciprocals, and seed oil content was examined. He found that partial dominance tended to increase oil content.
Badwal and Labana (1988) observed that both gca and sca variances were significant for seed size but sca variance was significant for oil content only, gca and sca interacted significantly for oil content. Non-additive gene effects were important for these two traits.

Prakash et al. (1988) studied 24 F2s divided form 8 parents. The study showed that gca and sca variances were significant for oil content and yield components. Sca variances were higher than gca for number of seeds per siliqua, 1000-seed weight, seed yield and oil content.

Gupta and Labana (1988) combined genetically diverse genotypes of *Brassica napus* in a diallel cross excluding reciprocals. They found that additive gene effects were involved in control of seed oil content. The parental varieties Ashai and Lores were singled out for use in future selection programme.

Malik and Singh (1988) reported that out of 15 lines and their F1 hybrids studied for 10 characters. Bra 939 x Bcr-Hc2 would be best for developing high oil yielding varieties.

Thakur et al. (1989) working on Indian mustard reported that mean squares due to genotypes, parents, crosses, lines, testers and line x testers were significant for most of the characters. The combining ability variances indicated the predominance of non-additive gene action for seed yield, primary branches, plant height and 1000-seed weight where as additive gene action for secondary branches, siliquae per plant and days to maturity.

Verma et al. (1989) studied the combining ability for yield, its components and oil content in yellow *sarson* and reported
predominance of additive gene action for yield, primary and secondary branches per plant, siliquae on main shoot, 1000-seed weight and oil content, while it was non-additive for siliquae per plant. Varieties, YST-151 and PYS-6 were good general combiners for most of characters except 1000-seed weight.

Liv and Liv (1989) in Brassica juncea revealed that erucic acid was controlled by two pairs of additive genes with low dominance effects. In additive, lower erucic acid was consistently associated with lower eicosenoic acid. Genetic behaviour of erucic acid fitted on additive dominance model with additive effect being predominant.

Podkolzina and Shpota (1989) while working on Indian mustard found that seed oil content was mainly controlled by non-additive gene action.

Gupta and Labana (1989a) studied additive dominance and epistatic components of variation for five physiological traits in F2 of GSL-1 x Nikalis and Bronowski x Topa in B. napus. The dominance component was relatively more important than the additive component. Epistasis was important in cross Bronowaski x Topa.

Gupta and Labana (1989b) further studied additive dominance and epistatic components of genetic variation for five yield related traits in Bronowski x Topa and GSL-1 x Nikalis in B. napus. Epistasis was important for seed yield and number of primary branches in Bronowski x Topa and for primary branches per plant and plant height in GSL-1 x Nikalis.

Wani and Srivastava (1989) derived information on combining ability from data on seven characters in 23 lines of Brassica juncea and their F1s and F2s. They found that parents
RK 8202, KR 5610, RK 1418, RH 30, V 10 and B 30 were good general combiners for seed yield.

Dhillon et al. (1990a) in Indian mustard worked out seven agronomic traits viz., seed yield, seed size, primary and secondary branches, plant height, main raceme length and pods on main raceme. Gca and sca variances were important for almost all the characters evaluated though former was larger in magnitude than later except for seed yield. Variety RLM 198 was found the best general combiner for all the traits except seed size.

Varshney et al. (1990) observed high genotypic coefficient of variation for grain yield in F₁ population of *toria*. Low gca was observed for this attribute in the elite stocks of *B. campestris* and *B. juncea* but it was high in *B. rugosa*. It was positively associated with grain yield. Seed yield was the major contributor to variation for HI in three *Brassica* species. Non-additive gene action was pre-ponderant for seed yield.

Yadav et al. (1990) recorded that genetic control of seed yield was mainly though dominant gene effects and epistatic effect of the additive x additive and dominance x dominance type.

Pal and Kumar (1991) studied the type of gene action involved in the inheritance of oil content in Indian mustard. Findings revealed the presence of both additive and non-additive type of gene action. Recurrent selection might be used to exploit both types of gene action for improving oil content in Indian mustard.

Singh and Yashpal (1991) crossed *B. juncea* lines (7) from India, 4 from the USSR and one from Canada and developed 66 F₁s. Non-additive genetic variance predominated for control of oil content.
RH 7859 was the best general combiner for oil yield followed by Kranti, RH 30 and Prakash.

Yadav et al. (1992) evaluated 45 experimental F1 hybrids of Indian mustard along with 10 parents and studied that all the characters (seed yield its component characters and oil content) were governed by both additive and non-additive genetic variances. Parents; Varuna, Kranti, RLC 1359 and RLC 1357 were identified as good general combiners of seed yield, earliness, silique length, seed per silique, 1000-seed weight, primary and secondary branches and oil content.

Patel et al. (1993) crosses 6 lines of mustard viz., RLC 1359, RC 1277, RH 7811, CSR 164, CSR 463 and RSK 2 with four testers, viz.; Varuna, Pusabold, Kranti and Krishna. Results indicated higher sca variance for all the characters suggesting predominance of non-additive gene action. RC 1277, CSR 164 and Kranti were good general combiners for yield, branches and silique per plant. The female parent RSK 2 and male parent Varuna had good gca effect for height and flowering. Six crosses showed significant positive sca effect for yield. Two crosses whose parents were poor in gca but exhibited high sca effects in their cross combinations for seed yield.

5. HETEROSIS AND INBREEDING DEPRESSION:

Heterosis has been defined by Allard (1960) as 'hybrid vigour' such that a F1 hybrid falls outside the range of the parents with respect to some characters or characters. Hayes et al. (1955) defined heterosis as increased vigour of F1 over the mean of the parents or over the better parent. The studies conducted by East (1908), East and Hayes (1912) and Shull (1908) on the effects of inbreeding and outbreeding in maize and Nicotiana have provided the
genetical basis to the phenomenon of heterosis. According to this concept, inbreeding tends to produce homozygosis resulting in loss of vigour, whereas, crossing between diverse parents produce heterozygosis in all characters by which the parent plant differ, there by restoring vigour in hybrids.

Diskalov (1963) concluded that the heterosis of F1 is the combined expression of genetical, cytoplasmic and physiological factors and may be attributed to stimulation resulting from the interaction of different heritable factors of the parents in the F1. Several investigators (Allard, 1960; Dickson and Jinks; 1956, Hayman; 1954b, 1963; Jinks 1954, 1955; Jinks and Jones, 1958; Kempthorne; 1956; Eberhart, 1964) observed correlation between heterosis and epistasis.

The crossing of inbred lines have played a major role in the utilization of heterosis for plant improvement in many crops. The various plant breeders have conducted studied on heterosis for nearly two centuries and have measured it with different scales, such as superiority of the F1 over the parent or better parent or over the best commercial variety prevalent in the zone.

A brief review of work done on heterosis and inbreeding depression in Brassica species is given below:

Singh (1973) observed significant heterosis values for some F1 hybrids for yield. Certain crosses showed moderately high heterosis for the number of primary and secondary branches and raceme length at an average of 49% in Brassica juncea.

Singh et al. (1975) in 16 hybrids, derived from 13 female parents and Apprsed mutant and T 59 male parents; heterosis
occurred for plant height, primary and secondary branch number, siliquae per plant and seed yield, the highest heterosis in the later compared to the better parental value being 200.45% and compared to the mid parental value being 240.97%.

Labana et al. (1975) found 76% per cent heterosis for seed yield ranging from -21.0 to 25.5% for primary branches and lower values of heterosis for plant height and siliqua length in *B. juncea*.

Yadav and Gupta (1975) observed -14.96 to 7.07% heterosis over better parent for oil content in Indian mustard.

Amrithadevarathinam et al. (1976) reported high values of heterosis for primary branches, secondary branches and siliquae on main shoot in a quantitative evaluation of inter varietal hybrids of *Brassica campestris*.

Gupta (1976) while working with Indian mustard, reported 99.0% heterosis for seed yield.

Paul et al. (1976a) estimated highly significant heterosis values for primary branches, secondary branches, seed yield per plant and 1000-seed weight in *Brassica juncea*.

Yadav et al. (1977) observed heterosis for seed yield ranged from -13.9 to 239.0% over the better parental values.

Asthana and Pandey (1977) in their study on *Brassica juncea* observed high heterosis over mid-parent for seed yield, maximum 48.0% for number of siliquae on main raceme and 19.0% for oil content.

Patnaik and Murty (1978) observed 42.5% heterosis for yield in brown sarson.
Schuster et al. (1978) studied inbreeding and heterosis phenomenon in crosses made among diverse lines in each generation of black mustard (*B. nigra*) and reported 203% heterotic values for seed yield; 123% for branching and little heterosis or no heterosis for 1000-seed weight and quality characters, though *F*₁s had high contents of oil. In case of inbreeding depression they found that mean depression relative to open pollinated sibs was 29 per cent for seed yield per plant, high for seed, siliquae and branches per plant. For test weight, it was 4% and for plant height 7% but for oil content it was showing little amount of inbreeding depression.

Chauhan and Singh (1979) observed significant negative heterosis in a large number of crosses than positive heterosis in most of yield contributing traits. They also reported inbreeding depression to be low for days to maturity, days to flower, seed per siliqua, high for plant height, secondary branches, 1000-seed weight and seed yield per plant.

Doloi and Rai (1981) studied inbreeding depression in elite rapeseed cultures for yield and its components under different forms of selling and reported that self incompatible group of culture showed inbreeding depression for days to flower, plant height, primary and secondary branches, siliquae per plant, seed per siliqua, yield per plant and 1000-seed weight either in *S*₁ and *S*₂ or in both.

Singh et al. (1983) in Indian mustard reported heterosis for yield in 27 crosses and heterosis for yield was mostly due to siliquae per plant, primary and secondary branches and siliqua length. Six crosses showed high heterosis over better parent. All the crosses involved low x low general combiners.
Anand and Rawat (1984) found significant positive heterosis for days to flower, plant height, number of primary and secondary branches, height at branches, seeds per silicia, yield per plant, and oil content.

Banga and Labana (1984) studied 139 F₁ hybrids from crosses between Indian and European lines. They found greatest heterobeltiosis for seed yield per plant, number of siliciæ on main shoot and number of secondary branches. The cross, RLM-514 x EJ-2 showed greatest superiority in seed yield to the control variety.

Singh et al. (1985) observed that the progenies of 8 crosses were superior to Indian x Indian cross progenies in number of siliciæ on main shoot, number of secondary branches and number of seeds per silicia. Highest heterosis for plant height, seed yield and number of secondary branches were recorded in RLK-78-6-1 x Pahadi rai (82.76%) and Pahadi rai x Blaze (89.66%) Indian x Exotic crosses, Varuna x Domo showed highest heterosis (84.40%) for seed yield.

Lefort-Busan et al. (1986) studied heterosis and reported a linear relationship between any of the indices. The relative efficiency of indices depended on seed yield character.

Lefort-Busan et al. (1987) reported that heterosis and F₁ performance differed among the crosses for all traits. Heterosis was greatest when parental lines were unrelated and come from different geographical pools. About 50% of seed yield variation due to mean parental heterosis were explained by variation in kinship coefficient (I-Y).

Verma et al. (1989) reported significant heterosis effects over standard variety for days to flowering, primary and secondary
branches per plant, 1000-seed weight; seed yield per plant and oil content. Hybrid PYS-3 x PSY-6 gene the highest standard heterosis of 23.6% for seed yields in yellow sarson.

Dhillon et al. (1990) reported highest heterosis (113.6%) for seed yield in the cross RLM-198 x RK-2. Heterosis in yield was mainly attributable to increased branch number.

Kumar et al. (1990) found positive heterosis of seed yield, primary branches, secondary branches, siliqua length and seeds per siliqua.

Hirve and Tiwari (1991) observed highest heterosis over better-parent for seed yield. They also observed significant (higher) heterosis for yield contributing characters. Inmost of the crosses there was no inbreeding depression, but significant positive heterosis also showed inbreeding over selfing.

Rai (1993) reported that heterosis breeding is now being recognised as a potent genetic tool for exploiting the presence of considerable amount of non-additive gene action inherent in the expression of the seed yield through the development of superior performing hybrids in Brassicas. The research work done in this direction has shown the existence of yield heterosis from 7 to 169%. The extent of inbreeding depression varied from 12.1 to 25.6 (mean = 14.0%). In the heterotic crosses made without using cytoplasmic male sterility in rapeseed to showed 4.9 to 24.6% (mean = 12%) heterosis.

Patel et al. (1993) crossed six lines of mustard with four testers and found that only three crosses RC-1277 x Kranti (41.4%),
RH-7811 x Kranti (27.9%) and RSK-2 x Kranti (25.9%) had significant heterosis for seed yield over better-parent.

Khuble et al. (1998) observed high heterosis for length of main shoot, number of primary branches, seeds per siliqua, seed yield per plant and 1000-seed weight.

5. SELECTION PARAMETERS:

a) Heritability and genetic advance:

Heritability is an index of transmissibility of traits from parents to off-springs. The concept of heritability is important to determine whether phenotypic differences observed among various individuals are due to differences in their genetic make up or simply as result of environmental factors.

According to Lush (1940, 1943, 1949) the broad-sense heritability is the ratio of total genetic variance to phenotypic variance. In narrow-sense it is the ratio of additive genetic variance to phenotypic variance.

Robinson et al. (1949) defined heritability as additive genetic variance in per cent of total variance. They considered that additive genetic variance indicate the degree of which the progenies are likely to resemble the parents.

Smith (1952) described heritability as the ratio expressed in per cent of variance component due to additive fixable gene effects ($\sigma^2 g$) to the sum $\sigma^2 G + \sigma^2 D + \sigma^2 E$ where $\sigma^2 G$, $\sigma^2 D$ and $\sigma^2 E$ are additive, dominance and environmental variances, respectively.
Several methods have been developed (Warner, 1952; Frey and Horner, 1957; Crumpacker and Allard, 1962 and Mather and Jinks, 1971) for estimation of heritability.

Genetic advance is still more useful estimate is selection programmes. Effective selection of genetically superior individuals requires the fulfillment of two conditions; (1) phenotypic variation must be adequate in the original population, and (2) heritability must be sufficiently high. In general as heritability and phenotypic variations increase, genetic advance through selection also increase. It is, therefore, necessary to utilize heritability estimates in conjunction with selection differential, which would then indicate the expected genetic gain from selection.

Lush (1940, 1943 & 1949) emphasized the following breeding programme on the basis of heritability estimation.

(i) When heritability, in narrow sense, is high reliance should be placed mainly on mass selection or as heritability becomes lower, more emphasis should be placed on pedigree, sib test and progeny test.

(ii) If over dominance is predominant, the breeding plan should be towards inbreeding with the object of producing hybrids for commercial use.

(iii) If the epistatic variance is relatively high, more reliance should be placed on selection between families and line breeding.

(iv) If the variance due to interaction between heredity and environment is relatively larger, the breeding plan tends more towards producing a separate variety for each ecological region.
(v) Heritability, in narrow sense, may be used to estimate expected improvement due to selection.

According to Comstock and Robinson (1952) the genetic advance depends upon :-

(i) The amount of genetic variability in base population.

(ii) The magnitude of masking effect of environment and interaction components of variability on the genetic variability and.

(iii) Intensity of selection.

The work done on the heritability and genetic advance in *Brassica* species by various workers in reported as under :-

Singh *et al.* (1970b) observed high estimate of heritability for plant height in *B. campestris*.

Singh *et al.* (1970b) in *Brassica campestris* estimated high heritability for days to flower, and primary branches and lower for plant height, secondary branches and seed yield.

Singh *et al.* (1971) in yellow sarson found high heritability for days to flower, moderate for plant height and low for primary branches and seed yield per plant.

Singh (1972) observed high heritability for plant, height; low for siliquae on main raceme and seed yield per plant in Indian mustard.

Singh and Singh (1972) estimated high heritability for days to flower and plant height whereas low heritability was reported for primary branches and secondary branches, length of raceme and yield per plant in Indian mustard.
Chauhan and Singh (1973) recorded high heritability for the days to flower, number of siliquea on main branch and plant height and moderate heritability for the number of primary branches and moderate genetic advance only for siliquea on main raceme and low for the plant height, days to flower and primary branches in Indian mustard.

High heritability for days to flower, low for plant height, moderate for primary branch number and yield. Raceme length and secondary branch number was reported by Singh (1973) in Indian mustard.

Zuberi and Ahmad (1973) estimated relatively high value of heritability for seed yield; number of siliquea per plant and other yield components in *B. campestris* L. var. *toria*.

Katiyar et al. (1974) observed in *Brassica juncea* broad sense heritability as well as genetic advance high for plant height and yield per plant.

Thurling (1974) found low expression of heritability for seed yield and 1000-seed weight in rapeseed.

Rao (1977) observed high heritability values in brown sarson for type of branching; days to flower and seed size. The expected genetic gain was highest (60% and 75%) for type of branching and days to flower.

Grami and Steffansson (1977) observed that in broad-sense, the heritability was 33% for oil content and 25% for protein content in summer rape.
Wahhab and Bechyne (1977) estimated high heritability for 1000-seed weight and low for oil and protein content in Indian mustard.

Asthana et al. (1979) reported high heritability for oil content and the expected genetic advance was 3.14% in *B. campestris* L. var. yellow *sarson* and 1.94% in *Brassica juncea*. Eight mustard and four *sarson* varieties showed significant improvement in oil content after three years of selection compared to unselected stock as revealed by analysis based on single plant or plot bulk sampling or both.

Govil et al. (1980) however, advocated that in Indian mustard substantial improvement may be achieved by increasing oil content, seed yield or both through pedigree selection or biparental mating in advanced generations.

Labana et al. (1980) estimated the high values of heritability for seed yield in Indian mustard.

Pal et al. (1981) observed that narrow sense heritability, was high for number of primary branches, moderate for number of days to flower and low for 1000-seed weight along with high genetic advance for plant height in Indian mustard.

Yadav et al. (1981b) found higher heritability estimate for 1000-seed weight than for yield and earliness in Indian mustard.

Chaudhary and Sharma (1982) reported high heritability for number of primary branches per plant in Indian mustard.

Pal et al. (1983) studied the inheritance of oil content in rapeseed and reported low heritability for this character.
However, they suggested that recurrent selection could be conducted for improving oil content.

Wan and Hu (1983) observed high heritability values for flowering data and position of effective branches. The highest expected genetic advance was reported for the number of days to flowering.

Yadav (1983) reported high heritability with high genetic advance for days to flowering in Indian mustard.

Jindal and Labana (1985) recorded highest heritability (58.15%) for oil content in Indian mustard.

Singh (1986) concluded from his experiment in Brassica species in four environments and reported higher heritability estimates for secondary branches, seed weight and number of seeds per silique.

Bang et al. (1986) elucidated in study of nine characters and varieties of Brassica species that broad sense heritability, estimates were high for flowering time, seed yield and plant height. For raceme length and total number of branches, it was moderately high.

Kumar and Sinha (1987) examined inheritance of seed weight in Indian mustard and recorded 83% of heritability estimates.

Badwal and Labana (1988) found heritability value of 20% in the narrow sense, for seed yield in Indian mustard.

Kumar et al. (1988) taken 7 characters from 16 genotypes and revealed that all the traits had high heritability (64.3-93.7%) except yield (20.2%). Heritability and expected genetic advance data
were taken to indicate a predominance of non-additive gene action for yield.

Hu (1988), while working on rape seed (*Brassica napus*), found that narrow sense heritability for oil content and glucosinolate content was estimated to be 56.4 and 87.4%, respectively. Narrow sense heritability of protein content was found to be 42.4%.

Podkolzina and Shopta (1989), while working on *B. juncea*, found that heritability for seed oil and erucic acid was low. To obtain forms with a high oil content free of erucic acid recurrent selection in reciprocal inter specific hybrids was recommended.

Wang and Qiu (1990) reported both broad sense (74.8%) and narrow sense (57.2%) heritability for seed protein content in *Brassica napus*.

Chaudhary and Goswami (1991) recorded high heritability (broad-sense) and genetic advance for number of siliqua per plant together with plant height.

b) Correlation coefficient:

The knowledge of genetic correlations among economic characters and other traits helps to improve the efficiency of selection by use of favourable combination of characters and to minimise the retarding effect of characters that are negatively correlated.

Burton (1952) stated the usefulness of correlation studies in plant improvement and emphasized that estimates of correlation between various characters are of great value in planning and evaluating of the breeding programme of a crop.
Very often, it is observed that certain characters, which can be noted during the period of growth of a plant, can be taken as a safe index for the yielding ability of that plant. Keeping it into consideration, knowledge of nature of association between yield and its components and between various components characters would be of great promise.

The elaborated elucidation of correlation was presented by Fisher (1918 & 1936). Lush (1940) and Hazel (1943) have applied genetic correlation to animal breeding. Several workers such as Waber and Moorty (1952) (Johnson et al. (1955a) in soyabean; Miller et al. (1958) in cotton; Smith (1955) in wheat; Abraham et al. (1954) in rice and Lerner (1950) in poultry have reported genotypic; phenotypic and environmental correlation between different pairs of economic characters.

Joshi and Dhawan (1966) advocated that a knowledge of genetic correlations between different characters that are economically important, is very essential for a plant breeder, if correlated response in unselected characters are to erode or nullify the gain achieved by pains taking selection.

Genotypic correlation is the net effect of segregating genes that effect the characters, some causing the positive and other negative correlations. The major cause underlying such genetic correlations are pleiotropy, linkage and developmentally induced relationships (Stebbins, 1950; Adams; 1967).

Muhammed et al. (1931) reported that yield per plant in Brassica campestris var. toria was positively correlated with the number of primary branches and 1000-seed weight.
Rai (1963) observed significant correlation of yield with days to flowering, number of primary branches, number of secondary branches, number of siliquae per plant and 1000-seed weight.

Quadri et al. (1966) observed positive and significant correlation between primary branches and secondary branches and negative phenotypic correlation was found between number of primary branches and days to flower.

Seed yield was positively and significantly correlated with number of primary and secondary branches, and number of siliqua per plant as reported by Chaudhary (1967) in *Brassica juncea* and Banerjee et al. (1968) in *B. campestris* var. yellow sarson.

Singh et al. (1969) in Indian mustard observed seed yield to be closely associated with number of primary and secondary branches and days to flower. They also observed strong associations between days to flower and number of primary and secondary branches, and concluded that these characters could easily be taken as criteria for selecting high yielding strains in Indian mustard.

Asthana and Singh (1973) in *rai* recorded significant correlation of seed yield with the plant height, number of primary and secondary branches and number of siliquae on main raceme.

Agrawal and Rai (1973) reported that seed yield, number of siliquae per plant and oil content showed positive and significant association with oil yield.

Zuberi and Ahmad (1973) also reported total seed yield to be correlated with number of siliquae per plant.
Rao (1977) in Indian mustard observed a strong positive correlation of seed size with number of primary branches.

Rawat and Anand (1977) in *Brassica juncea* observed that at phenotypic level, yield and oil content were correlated with number of primary branches and days to 50 per cent flowering. They further reported that yield was correlated with number of secondary branches, 1000 seed-weight and oil content.

Paul *et al.* (1978) in Indian mustard concluded from his study that seed yield per plant was significantly correlated with siliquae number per plant and with primary and secondary branch number.

Yadav *et al.* (1978) reported number of days to flowering to be correlated with 1000 seed weight.

Shpota *et al.* (1979) found existence of high correlation between content of erucic acid and that of both oleic and linoleic acids. It indicates that it is possible to select for low erucic acid content while increasing oleic and linoleic acid content.

Labana *et al.* (1979) in *B. campestris* var. yellow *sarson* reported highly significant and correlation of seed yield with number of siliquae per plant.

Sudhaker *et al.* (1979) reported in *B. campestris* that grain yield was significantly correlated with number of primary branches and secondary branches, number of siliquae per plant and 1000 seed-weight.

Brar (1980) in brown and black mustard observed that protein content and oil content were negatively correlated.
Jonsson (1980) found positive correlation between content of erucic acid and eicosencaic acid in rapeseed.

Boiko (1980) reported that selection for high oil content to a fall in seed size owing to negative correlation between these characters. Selection for both the characters was less successful than selection for one of them.

Yadav (1982) observed that seed yield showed significant positive correlation with primary and secondary branch number, total siliquae number and days to flowering in rapeseed.

Varshney and Singh (1983) worked out the correlation of harvest index with other characters and reported that harvest index was positively correlated with primary branch number, siliquae per plant and 1000 seed weight.

Wan and Hu (1983) reported association of seed weight per plant with siliquae number per plant in rape.

Yadav et al. (1983) reported that 1000 seed - weight and oil content were positively correlated with seed yield. However, he also reported association of seed yield with number of primary branches, siliquae per plant and 1000 seed weight.

Singh et al. (1983) suggested from his studies that number of secondary branches and seed size should be considered in breeding for increased yield.

Kumar et al. (1987) in yellow sarson reported that yield was highly correlated with number of secondary branches followed by primary branches, days to 50% flowering, plant height number of seeds per siliquae showed high direct effect on yield.
Chaudhary et al. (1988) observed that yield per plant showed positive and significant genotypic correlation with days to maturity, plant height, number of primary branches, number of siliqua on the main raceme, number of siliquae on lateral branches, siliquae length and 1000 seed weight. Number of primary branches has the highest positive correlation with yield in *Brassica juncea*.

Kumar et al. (1988) found the yield was positively and significantly correlated with number of primary branches, secondary branches and siliquae per plant in Indian mustard.

Ahuja et al. (1989) reported oil content was positive correlated with that of erucic acid and observed negative correlation between linoleic and erucic acid content \((r = -0.71)\). Thus it is possible to evolve nutritionally improved *toria* cultivars with high linoleic and low erucic content.

Yadav et al. (1990) in Indian mustard computed correlation among the traits, harvest index, biological yield and seed yield at, both phenotypic and genotypic levels and biomass production showed positive and significant relationship with seed yield but had no correlation with each other.

Wang and Qui (1990) found that seed protein content was negatively correlated with oil content in *Brassica napus*.

Dhillon et al. (1990b) in Indian mustard worked out a high correlation with the length of main raceme, oil content and yield per plant, number of primary branches was associated with number of secondary branches. The length of main raceme had a high correlation with number of pods and oil content.
Behl et al. (1992) reported phenotypic correlation coefficients of oil yield with siliqua per plant, seed yield and turgor potential were positive and significant in *Brassica juncea*.

Mandel et al. (1993) analysis the variation of the oil and protein level with in different germplasm lines as well as amongst five species of protein content values were negatively correlated. Maximum correlation coefficient (0.9259) was found in *Brassica carinata* followed by *B. juncea* (0.9211), *yellow season* (0.9177) *B. napus* (0.8978) and minimum in *toria* (0.8569).

Singh et al. (1996) reported high magnitude of variance for *sca* for days to flowering number of secondary branches and seed per siliqua, seed yield and oil content. However estimates of *gca* variance was high for plant height. Varshney and Rao (1997) reported that plant height was governed by two dominant gene in complementary pattern in *Brassica campestris*.

Kumar et al. (1997) reported genotype × environment interaction in relation to combining ability. They observed the environment of both *gca* and *sca* variances for number of siliqua on main fruiting branch and seed yield per plant. Non additive variances was of greater importance that additive variance. Difference among the environment was significant for both *gca* × environment and *sca* × environment interaction variances were significant for these two characters, while further partioning revealed higher magnitude of non-additive × environment interaction then additive × environment for these two characters.

Choudhary and Sinha (1999) reported the importance of mutation breeding in *Brassica juncea* for obtaining variability in primary branch in main shoot and flowering. They observed reduction
in the number of primary branches and earliness. Chauhan et al. (2000) reported significant differences, days to maturity and oil content and for all the characters in females except for secondary branches per plant and seed yield per plant.

Rai and Singh (1994) reported heterosis over the better parent and commercial check for seed yield, oil content and some yield components in 28 inter varietal crosses of Brassica campestris. The average heterosis over better parent for seed yield and oil content was 21.3% and 32.0% respectively. Highest being 78.8% for seed yield and 11.4% for oil content while number of primary branches per plant exhibited 36.2%.

Singh et al. (1996) recorded heterosis over better parents in the tune of 77.6% for seed yield and 13.1% for oil content.

Varshney and Rao (1997) reported the predominance of non-additive genetic variance for 6 character, (i) days to flowering, (ii) days to maturity (iii) plant height (iv) number of primary branches, (v) number of siliquae on fruiting branches and (vi) seed yield per plant in F1 and F2 generations.

Varshney and Rao (1997) observed highest heterosis over better parent for seed yield per plant (129.4%) and primary branch per plant (88.1%).

Chauhan et al. (2000) reported heterotic responses in single and three way crosses in Indian mustard from 25 single crosses and 12 three ways crosses. They observed highest heterotic response for seed yield followed by number of primary branches and secondary branches over better parent. When compared to standard check highest being 78.7% for seed yield.
Singh *et al.* (1996) observed positive association between oil content and seed yield indicating the possibility of simultaneous improvement of these characters.

Kumar *et al.* (1997) reported positive association between number of siliquae on main fruiting branch with seed yield per plant.

Sikarwar *et al.* (2000) observed positive and significant correlation between number of secondary branches per plant and siliqua length. Siliqua length emerged as the single most important trait to influence 1000-grain weight directly as well as indirectly.