2. REVIEW OF LITERATURE

The relevant literature pertaining to studies in present investigation has been reviewed under the following heads:

2.1 Genetic variability
2.2 Heritability and genetic advance
2.3 Correlation
2.4 Path coefficient
2.5 Heterosis
2.6 Combining ability
2.7 Nature and magnitude of genetic variance
2.8 Genetics of resistance to disease

2.1 GENETIC VARIABILITY

The success of a breeding programme depends upon the extent and magnitude of variability in the genetic material.

Singh and Singh (1969) observed high genetic coefficient of variation (GCV) for pods per plant (82.5%), seed yield per plant (79.0%) and 100-seed weight (41.0%), while for number of branches per plant, it was comparatively low (22.7%) and the lowest value (8.6%) was observed for days to 50 per cent flowering.

Singh and Singh (1975) recorded comparatively low estimates of variability for different characters ranging from 5.89 per cent to 15.94 per cent.

Chaudhury et al. (1978) reported maximum GCV for pods per plant (28.8%) and minimum for days to maturity (5.9%).
Nandan and Pandya (1980) reported that the phenotypic coefficient of variation (PCV) was found to be greater than GCV. Maximum GCV was observed for number of pods per plant (35.37%) and the minimum for number of seeds per pod (4.32%).

Pandey et al. (1980) recorded highest PCV for number of branches per plant (62.60%) followed by number of seeds per plant (30.40%) and number of pods per plant (26.50%). However, PCV values were moderate for plant height and 100-seed weight.

Balyan and Singh (1986) reported significant genetic variability for plant height, pods per plant and seed yield per plant in 48 Indian lentil genotypes.

Sharma and Luthra (1987) studied 56 genotypes for two successive years and reported significant variations among the genotypes for all the characters but wide variability over the years was reported only for pods per plant, number of seeds per plant and seed yield per plant.

Baidya et al. (1988) reported highest estimates of phenotypic, genotypic and environmental coefficient of variability for seeds weight per plant among the six quantitative characters.

Ramgiry et al. (1989) reported variability for different characters. The PCV values for different characters were, 126.28% for pods per plant, 113.31% for harvest index, 56.68% for branches per plant, 36.21% for 100-seed weight, 34.72% for seeds per plant and 19.81% for plant height.

Thakur and Bajpai (1993) reported higher PCV for seed yield per plant (18.38%) followed by PCV for number of secondary branches per plant (14.18%), number of pods per plant (12.14%) and biological yield per plant (10.01%). Medium value of PCV was reported for 100-seed weight (7.39%).
and harvest index (7.63%), whereas for days to 50% flowering and days to maturity PCV estimate was very low (2.24%) and 1.29%, respectively.

Elwafa and Ismail (1999) reported desirable selection for yield and protein in two populations of lentil. The basic breeding material used in the study were the F7 generations of two lentil populations which were originated from a cross between lines ILL 6004 x ILL5753 and ILL 6005 x ILL 5698. Highly significant differences among the F7 families in both the populations together with satisfactory genotypic coefficient of variability were obtained for both the trait under study. After study two cycles of selection, seed yield and protein content increased in comparison with the bulk and the standard variety by 31.3 and 23.89% (population I) and 29.96 and 25.93% (population II), respectively.

Solanki et al. (1999) reported variability in physiochemical and nutritional quality traits of parents, F2 and F3 generations of lentil crosses, using ten physiochemical and nutritional quality traits (100-seed weight, seed values, seed density, bulk density, hydration capacity, hydration index, swelling capacity, protein, tryptophan and energy value). Significant variation for different traits could be observed among the genotypes. Range, means and coefficients of variation (CV%) for various traits among the parents, F2 and F3 generation revealed a wide range of variation.

Chakraborty and Haque (2000) studied the genetic variability and components of variation. A high extent of genetic variation was observed for grain yield per plant, 100-grain weight and number of pods per plant.
Singh and Singh (2001) observed wide genetic distance among genotypes in lentil. The intercluster distance was lowest between cluster II and IV and was highest between cluster III and VI.

Jeena and Singh (2002) studied the genetic divergence in wild lentils and reported that genetic diversity was not related to geographical origin and species differences. Single seed weight, leaf rachis length and percentage germination were the characters contributing most towards the genetic divergence among the accessions under investigation.

Rathi et al. (2002) reported variability, heritability and genetic advance in lentil. The GCV and PCV were low for days to flowering, days to maturity, and protein content. Contrary to this the traits number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, 100-grain weight, and grain yield per plant in both $F_1$ and $F_2$ generations and number of pods per cluster in $F_1$ expressed high GCV and PCV but moderate heritabilities. The coefficient of variability ranged from 12.6 to 26.1% while heritability was considerably low for branches per plant, clusters per plant and grain yield.

Kumar et al. (2002) analyzed genetic divergence in 44 lentil cultivars and grouped them in five clusters. Genetic distance was highest in cultivars grouped in cluster VIII and IX, indicating greater divergence between cultivars belonging to these clusters.

Hamdi et al. (2003) studied genetic variability, heritability and expected genetic advance for earliness and seed yield from selection in lentil, using 24 lentil genotypes at Giza Research Station in Egypt. The environments (season and location) showed major effects on the performance of genotypes.
High phenotypic variation was observed for number of pods and seeds per plant. Considering wide variability, heritability and genetic advance, progress could be expected from selection for number of seeds per plant and seed yield per plant. The early maturity genotypes Sina 1, FLIP87-21L, and FLIP92-54L could be recommended for planting in case the earliness in maturity is more important than seed yield. On the other hand, high yielding genotypes FLIP89-71L, FLIP95-68L, 89503, FLIP92-48L and FLIP95-50L could be recommended for planting in case high yield potential is more important than earliness in maturity.

Dixit and Katiyar (2004) observed that 22 ancestors were involved in the development of lentil cultivars which were released for cultivation. Out of these 22 ancestors, 4 ancestors contributed 37% of the genetic base while L9-12 was the most frequently used parent, followed by T8, LG-171 and JLS-2. Among them L-9-12 and T8 had a significant contribution.

Yazdi-Samadi et al. (2004) reported the genetic variation for days to 50 per cent flowering, days to 90 per cent maturity, seed yield and 100-seed weight using simple and combined analysis of variance, phenotypic and genotypic correlations and stepwise regression analysis.

Singh and Gupta (2004) reported genetic diversity for yield and related traits in lentil (Lens culinaris Medik.). $D^2$ analysis was carried-out in forty genotypes of lentil to study the genetic divergence. Analysis of variance recorded significant differences among genotypes for all the characters except days to 50% flowering, days to maturity and harvest index in both the years. The forty genotypes were grouped into six and seven clusters in the first and 2nd years, respectively. The relative composition of clusters differed in
the two years due to involvement of genotypes x environment interaction. The cluster mean values indicated a wide range of variation for number of secondary branches per plant, number of pods per plant, biological yield and seed yield per plant over two years. On the basis of inter-cluster distances and stability in the divergence, some genotypes were identified and proposed to be included in hybridization programmes.

Sultana et al. (2005) reported genetic divergence in lentil germplasm. High variability was observed for growth habit, leaf pubescence, leaflet size, seed coat colour, seed coat pattern and seed colour that could be expanded and exploited for developing breeding material and to use for marker assisted selection. Though cluster analysis grouped together accessions with great genetic similarity, the cluster did not necessarily included all the accessions from same origin. Low level of association between genetic diversity and geographical distribution is expected to be due to less representation of accessions from particular area that is needed to be studied uniformly.

Joshi et al. (2005) studied the variability in lentil. The analysis of variance revealed significant differences among the genotypes for all the traits studied. The 100-seed weight of these lines ranged between 1.1 g and 7.2 g. the seed yield, pods per plant, 100-seed weight and fruiting branches showed high PCV and GCV.

2.2 HERITABILITY AND GENETIC ADVANCE

The knowledge of heritability, which is an index of transmissibility of a character from the parents to their off-spring, is of great importance both for breeders and geneticists.
According to Dudley and Moll (1969), the estimates of genetic variance and heritability play a major role in the three stages of plant breeding viz., assembly or creation of a pool of variable germplasm, selection of superior individuals and create a superior variety.

The concept of heritability is important to determine whether the phenotypic differences observed among the various individuals are due to differences in their genetic makeup or simply a result of environmental factors. Heritability in broad sense, according to Lush (1940), as the ratio of total genetic variance to phenotypic variance. In a narrow sense, it is the ratio of additive genetic variance to phenotypic variance. There are several methods for estimating heritability which can be broadly classified as those based on:

1. Parent off-spring regression (Fisher, 1918; Lush, 1940 and Robinson et al., 1948).

2. Variance components from an analysis of variance (Fisher, 1918; Mather, 1949).


4. Use of F2 and backcross progenies as suggested by Warner (1952).

5. Modified parent off-spring regression methods (Frey and Horner, 1957).

6. The constant parent regression method (Griffing, 1950).

Lush (1940) listed that following reasons for requiring unbiased estimate of heritability:

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 sibsests and progeny test.
ii. If the epistatic variance is relatively high, more reliance should be placed on selection between families and line breeding.

iii. If over dominance is predominant, the breeding plan should be towards inbreeding with the object of producing hybrids for commercial markets.

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

v. Heritability in narrow sense may be used to estimate expected improvement due to selection.

Genetic advance is still more useful estimate. It is the improvement in the genotypic value in the new population as constructed to pat population. The genetic gain depends upon:

i. The amount of genetic variability, i.e., the magnitude of the differences among different individuals in the base population.

ii. The magnitude of masking effect of the environmental and interaction components of variability of the genetic diversity, and

iii. The intensity of selection (Comstock and Robinson, 1952).

The genetic gain in a character is a product of the heritability and selection differential expressed in terms of phenotypic standard deviation of that character. Heritability value by itself does not have much significance as it fails to account for the estimate of absolute variability. It is, therefore, necessary to utilize heritability estimates in conjunction with selection differential which would then indicate the expected gain resulting form selection.
Chakarborty and Haque (2000) estimated high heritability in conjunction with high genetic advance for grain yield per plant, 100-grain weight and number of pods per plant. Days to flowering and maturity, plant height and length of reproductive phase showed high heritability and low genetic advance.

Ali and Johnson (2000) estimated the heritability for winter hardiness in lentil under natural and controlled conditions. The estimates of narrow-sense heritability, ranged from 0.32±0.06 to 0.71±0.16 under field conditions however, under controlled conditions, the estimated heritability was maximized at 1.00±0.017 using 6-8 week old lentils. Significant transgressive sergeant were found in five of the six populations in the $F_3$ generation. This indicated that cold tolerance is under additive gene control and is environmentally sensitive in gene expressions.

Omvir and Gupta (2000) reported heritability in macrosperma x microperma derived lines in lentil. The heritability estimates across environment, regression coefficient and deviation from regression of the studied characters indicated the stability parameters in lentil appeared to be governed by different genes and gene combinations for these characters.

Singh and Singh (2004) studied heritability and genetic advance for yield and yield components in 28 $F_1$ and $F_2$ lentil progenies developed using 8 parental diallel mating system. High heritability (more than 30%) was recorded for number of days to flowering and maturity in both $F_1$ and $F_2$ generations, number of primary and secondary branches per plant and number of seeds per pod in the $F_1$ generation and 1000-seed weight in the $F_2$ generation. High heritability indicated the importance of additive and non-additive gene
components and the suitability of pedigree methods of selection for these traits. The moderate heritability (10.30%) and moderate genetic gain recorded for plant height and seed yield per plant in both generations and number of primary and secondary branches per plant showed non-additive genetic components in these traits. Low heritability estimates (less than 10%) and genetic advance were observed for number of clusters and pods per plant in both generations. Heritability estimates and genetic advance were greater in the $F_1$ than in the $F_2$ generation. The highest genetic grain was recorded for 1000-seed weight. The results suggest that for achieving the desired genetic improvement of these traits for the development of early maturing and large seeded cultivars, pedigree or mass selection may be adopted.

Joshi et al. (2005) studied the variability, association and path analysis in lentil. Days to 50% flowering, days to maturity, seed yield and pods per plant and seed weight had high genetic advance.

Singh et al. (2005) reported heritability using spatial variability models in lentil. They observed that average broad sense heritability over individual traits was found to be 0.47 for seed yield and 0.45 for biomass. Based on individual trials average heritability estimates were similar for the two seed size types. However, the presence of genotype x environment interaction reduced the estimates considerably, with an overall average of 0.21 for seed yield and 0.22 for biomass.

2.3 CORRELATION

The study of correlation is an interesting and important aspect both in pure and applied genetics and is very useful for the plant breeders. The aim of the plant breeder is to improve the genetic make up of the plants. In order to
bring about this, it is very essential to know the genetic relationships in the characters. The correlation studies are the means of detecting inter-relationship of the plant characters, which is to be considered as a reliable guide in the selection.

Investigation of genotypic and phenotypic inter-relationships between various agronomic traits are of interest to plant breeders not only from theoretical consideration of the quantitative inheritance of the characters, but also from a practical standpoint, since selection is usually concerned with changing two or more characters simultaneously.

Phenotypic correlation may be of genotypic origin and provides information about association between the two characters. For selection purpose, phenotypic correlation between pair of characters are in the same direction, when estimated separately.

Genetic correlation provides a measure of genetic association between characters and it generally used in selection for one character as a means of simultaneously improving another. Such correlation coefficient provide information by themselves (Miller et al., 1959) and should be helpful to the breeders since they are based on transmissible genetic variance.

Jerome et al. (1956) advocated that genetic correlations among various characters become of practical importance when the economic evaluation of a crop depends upon a smaller number of traits. Information on the genetic association among various characters under particular environmental conditions, besides being an important source of information to a plant breeder, may also help to formulate the most effective method of breeding in any particular case and to simplify the approach to selection.
Singh and Singh (2002) studied the correlation of seed yield and other traits in lentil. They reported that seed yield per plant was strongly and positively associated with number of seeds and number of pods per plant. Seed yield was significantly correlated with plant height and seeds per pod was correlated with plant height.

Khattab (1999) showed that pods per plant, seeds per plant, plant height and seed yield appeared to be most important characters associated positively with harvest index. Branching pattern and biological yield showed negative association with harvest index under both water regimes. Seed yield showed positive and significant association with plant height, pods per plant, seeds per plant and biological yield, whereas the latter was associated positively with branching, pods per plant, seeds per plant and seed yield in each of the two water regimes.

Naji et al. (2003) conducted the experiment on correlation between physiological parameters and yield related traits in lentil genotypes under arid conditions in Jorden. They observed that the grain yield was positively correlated with biological yield, plant height, yields per plant, seeds per pod, pods per plant, and number of primary branches. Single and combined analysis of variance showed that the lentil cultivars varied in their performance under both the environmental conditions, for all the tested traits indicating necessity of selection in the target environment. Highly significant positive correlation was found between early growth rate per month and final biomass and seed yield, whereas non-significant and negative association was found between grain yield and days to flowering with the early line producing the highest yield.
Chakraborty and Haque (2000) reported positive and significant association of grain yield with number of seeds per pod and number of pods per plant and negative significant association for 100-grain weight with number of primary branches per plant and number of pods per plant.

Bicer and Sarkar (2004) reported the genetic variability and heritability of grain yield and its components in lentil. The highest genetic variation was recorded for biological yield, grain yield and seed yield per plant. The highest heritability was recorded for seed weight and number of days to 50 per cent flowering.

Yazdi et al. (2004) conducted the experiments to evaluate genetic variation in lentil (Lens culinaris Medik.) genotypes in karaj region in Iran. They were evaluated their genetic variations for days to 50% flowering, days to 90% maturity date, seed yield and 100-seed weight using simple and combined analyses of variance, phenotypic and genotypic correlations and stepwise regression analysis.

Karde et al. (2005) reported correlation and path analysis in lentil using 25 genotypes grown under three environments. Correlation analysis revealed that seed yield per plant correlated positively with harvest index in E-1, whereas in E-2 and E-3 seed yield per plant showed positive correlation with harvest index, biological yield, 100-seed weight and seeds per pod. However, in E-1 and E-2 seed yield per plant showed negative correlation with plant height. In E-3, seed yield per plant was found to be correlated negatively with pods per plant. This type of relationship was further confirmed through path analysis, where harvest index and biological yield showed consistent relationship with seed yield in all the three environments. However, days to
maturity and pods per plant had direct contribution towards seed yield per plant in E-1 and E-2, whereas days to maturity behaved similarly in E-2 only.

Joshi et al. (2005) studied association and path analysis in lentil and reported that pods per plant, seeds per pod showed positive, whereas days to flowering, days to maturity, and 100-seed weight showed negative correlation with seed yield. The lines were grouped according to their seed weight to work out the correlation between seed size and seed yield up to the upper seeds limits of 2.5 g, 3.0 g and 3.5 g.

Yadav et al. (2005) reported character association and path coefficient analysis under two environments in lentil. The magnitude of correlation coefficients at genotypic level indicated that inspite of a strong inherent association between various characters studied, the plant height exhibited positive and significant phenotypic correlations with days to maturity. The biological yield per plant depicted significant positive association with secondary branches per plant showed highly significant positive correlation with number of pods per plant and harvest index were also observed to be highly correlated with seed yield per plant.

2.4 PATH COEFFICIENT

Yadav et al. (2005) reported that path coefficient analysis showed that biological yield per plant had the highest positive direct effect (0.648) and (0.689) on seed yield in both the environment followed by number of pod per plant (0.564) and days to maturity (0.367) in E1. The highest negative direct effects was recorded for 100-seed weight (-0.579) followed by plant height (-0.186). It was observed that the biological yield, pods per plant branches per
plant and seeds per plant were the most important as they contribute to seed yield directly as well as indirectly in both the environments.

Khattab (1999) found that pods per plant, seeds per pod and 100-seed weight were the most important characters that controlled the grain yield. On other hand, plant height, branching and pods per plant had the highest contribution on biological yield. Grain yield showed the highest positive direct effect on harvest index whereas, biological yield had a negative direct effect and positive indirect effect via seed yield.

Chakraborty and Haque (2000 in a study of path analysis indicated that pods per plant and seeds per pod with a direct positive and negative effect of days to flowering and days to maturity, respectively, were the most important traits contributing to grain yield per plant.

Joshi et al. (2005) studied association and path analysis in lentil. They grouped the lines according to their seed weight to work out the correlation between seed size and seed yield up to the upper seeds limits of 2.5 g, 3.0g and 3.5g. Pods per plant had highest direct effects on seed yield, followed by plant height and seeds per pod.

2.5 HETEROSIS

The term heterosis was coined by Shull (1914) and it is defined as the superiority of the F₁ hybrid over the mid-parental values in terms of yield and other desirable characteristics.

Singh et al. (1975) in a diallel cross analysis involving six parent observed that usually crosses showing heterosis for grain yield also exhibited heterosis for pods per plant and secondary branches per plant. F₁s showed more heterosis when the parents were from different regions than from the
same regions. Out of 15 crosses, five showed positive heterosis over mid-parent and four showed positive heterosis over better parent for yield per plant. For pods per plant, five and three crosses showed mid-parent heterosis and heterobeltiosis, respectively. For primary branches per plant, heterobeltiosis was observed in two crosses only. Positive and significant heterosis over mid-parent and better parent for secondary branches per plant was observed in three and two crosses, respectively. The mid-and better parent heterosis (%) for yield and yield components observed in the experiment ranged from -41.97 to 266.67% and 58.50 to 175.56% for grain yield, -15.80 to 200.77% and -39.99 to 126.88% for pods per plant, -26.32 to 54.72% and 27.65 to 49.61% for primary branches per plant and -28.10 to 123.10% and -32.30 to 104.23% for secondary branches per plant, respectively.

Goyal et al. (1976) studied heterosis over mid-parent based on twenty one crosses made involving seven parents. The highest mid-parent and better parent heterosis was recorded for pods per plant (45.3, 166.6%) followed by seed yield (28.6, 146.0%), days to flowering (25.9, 89.0%), secondary branches per plant (10.0, 63.5%) and primary branches per plant (7.3, 69.8%). For seeds per pod, 100-seed weight and plant height the mid-parent heterosis was in negative magnitude with moderate heterobeltiosis. There was no heterosis for plant height.

Sagar and Chandra (1980) reported heterosis for yield per plant in nine lentil crosses. All the crosses exhibited high mid-parent and better parent heterosis, which ranged from 62.08 to 163.78% mid parent heterosis for yield per plant.
Kamboj (1986) reported heterosis for eight quantitative traits in ten crosses involving five parents. The hybrids exhibited moderate to high level of standard heterosis except for 100-seed weight for which estimates were negative and high. The crosses having higher heterobeltiosis, mid-parent and standard heterosis for seed yield per plant, also revealed significant and positive heterotic effects for yield components like number of seeds per pod, pods per plant, primary branches per plant. The relative magnitude of better parent and standard heterosis ranged from 13.05 to 13.77%, -18.47 to 11.37% and -9.149 to 13.59% for plant height, -18.66 to 22.85%, -2.42 to 10.61% and -2.40 to 42.00% for primary branches per plant, -2.15 to 17.3%, -8.88 to 7.35% and 0.81 to 8.28% for pods per cluster, -25.76 to 196.00%, -4.00 to 141.82% and 48.43 to 291.46% for pods per plant, -26.19 to 22.71%, -41.95 to 17.51% and -45.69 to -10.86% for 100-seed weight -17.00 to 25.00%, -18.00 to 14.28% and 10.00 to 49.05% for biological yield per plant, -33.87 to 359.88%, -42.14 to 212.62% and -32.67 to 316.82% for seed number per plant and 50.00 to 251.00%, -62.00 to 232.00% and -62.00 to 142.00% for seed yield per plant, respectively.

Sharma (1991) studied heterosis in eight crosses involving four microsperma (Pant L639, Pant L406, L830 and L9-12) and two microsperma (Precoz and HPL 4) genotypes in a line x tester mating design under long and short days. The magnitude of heterosis was affected by the day length. Heterosis for seed yield and its components, such as harvest index, number of pods per plant and pod clusters per plant was more in cross combinations involving Precoz as one of the parents. There was no heterosis for plant height under long days while it was substantial under short days in all the
crosses. In case of flower clusters per plant, primary and secondary branches per plant, the magnitude of heterosis was higher under short days than under long days. Days to flowering revealed heterosis both under short and long days in all the crosses. As for days to maturity, the crosses Pant L406 x HPL4, PL639 x HPL4, L9-12 x HPL4 and L830 x HPL4 involving HPL4, a late macrosperma parent did not reveal any heterosis under both day lengths. However, it was observed in the crosses Pant L 406 x Precoz, Pant L 639 x Precoz, L9-12 x Precoz and L830 x Precoz, involving Precoz as one of the parents under short days. The absence of heterosis in the crosses involving Precoz under long days is due to delayed maturity in the otherwise medium flowering F₁ hybrids due to decrease in temperature towards maturity, September onwards, 100-seed weight revealed either no or negative heterosis under both the day lengths in most of the crosses. Seed yield, the most important traits revealed heterosis under both the day lengths in the crosses Pant L406 x Precoz, Pant L639 x Precoz, L9-12 x Precoz and L830 x Precoz of these, Pant L639 x Precoz exhibited the highest heterosis under long and short days (60.0 % and 56.0%, respectively), followed by L 830 x Precoz (44.4% and 44.0%). The cross involving HPL4 as one of the parents did not reveal any heterosis for seed yield per plant. In case of harvest index, practically no heterosis was recorded in crosses involving HPL4. However, substantial heterosis was observed in the crosses involving Precoz as one of the parents.

Singh and Singh (1992) studied a set of non-reciprocal diallel involving five parents and analysed heterosis over better parent for number of clusters per plant, pods per plant, seeds per pod, 100-seed weight and seed yield per
plant. They observed that heterosis over better parent was maximum for number of clusters per plant (66.66%), pods per plant (165.50%) and seed yield per plant (15.32%) in the crosses UPL-175 x RAV-101, LG-120 x RAV 101 and Pant L-406 x Pant L-639, respectively. For 100-seed weight, highest and positive better parent heterosis (19.15%) was observed in the cross Pant L-639 x UPL-175. The Pant L-639 x LG-120 and UPL-175 x RAV-101 were the only two crosses which showed a positive better parent heterosis (5.68% and 10.3%) for seeds per pod. It was also observed that all the crosses showing maximum estimates of heterosis for seed yield also had significant heterotic effects for some of the yield components.

Sharma and Chahota (2000) observed a wide range in expression of heterosis in crosses among lentil mutants.

Rathi (2004) reported variable heterosis for different characters in lentil. The maximum positive heterosis of 144.7, 68.86 and 150.5% was recorded over better, economic and mid-parents, respectively. Heterosis in grain yield was due to heterosis manifested by its components, mainly number of clusters and primary and secondary branches per plant, number of seeds per pod and test weight on the basis of 5 most out standing crosses. A hybrid B238 x P248 showing positive and significant heterosis for all the traits except all the hybrids in respect of yield heterosis (144.7%). The hybrids showing negative heterosis for either test weight or number of pods per plant showed an average decrease of ≈20% (21-24%) for both the traits jointly which resulted in a decline of 35% in yield.
2.6 COMBINING ABILITY

The concept of general and specific combining ability was given by Sprague and Tatum (1942) based on fundamental investigations in corn. They defined the term general combining ability (GCA) as the average performance of a line in a set of hybrids and the term specific combining ability (SCA) as those instances where certain hybrid combinations perform relatively better or worse than the expected value on the basis of average performance of parental lines involved.

Griffing (1956a) gave the generalized concept and methodologies for combining ability analysis. He suggested that GCA includes both additive as well as additive x additive interaction effects. Griffing (1956b) made detailed examination of the concept of general and specific combining ability variances and effects in relation to diallel mating system.

Singh et al. (1975) evaluated a half diallel involving six parents and their 15 hybrids. Their study suggested significant GCA and SCA variances for seed yield, pods per plant and number of secondary branches per plant. The genotype P887-67 was good general combiner for the characters like seed yield, pods per plant, primary branches per plant and secondary branches per plant. The SCA effects were significant in the crosses (T-36 x P887-67), (T-36 x P887-67) and (L9-12 x P887-67) for seed yield, pods per plant and primary and secondary branches per plant, respectively. Additive and non-additive components of variance were important for all the characters, under study.

Goyal and Mehrotra (1978) evaluated diallel crosses involving seven varieties. They reported significant GCA variance for yield and yield
components. The magnitude of SCA variance was also significant for all the characters except plant height, number of primary branches per plant and test weight.

Sandhu et al. (1981) analysed combining ability for harvest index and grain yield in a diallel of 15 parents. The results indicated that both GCA and SCA effects were important for these characters.

Nazeem et al. (1983) recorded observations on earliness, plant height and number of branches per plant in the parent, F₁, F₂ and F₃ generations of eight crosses involving two local lines, six exotic lines and the Egyptian variety Giza 9. In most of the crosses, degree of dominance ranged from absence to over dominance.

Singh and Singh (1990) studied combining ability in a set of materials involving 5 lentil varieties in F₁, F₂ and F₃ generations, for days to 50 per cent flowering, days to maturity, plant height and biological yield per plant. Both the GCA and SCA effects were significant for all the characters under study. The GCA effects indicated the parents like Plant L406, Pant L639 and RAU-101 to be good general combiners for days to 50% flowering, days to maturity, plant height and biological yield per plant but Pant L406 was found to be a good general combiner for days to 50% flowering and days to maturity in three generations. The crosses Pant L639 x LG120, Pant L406 x LG120, Pant L406 x RAV-101 and LG120 x RAV-101 were the best specific cross combinations for biological yield and plant height.

Chauhan and Singh (1993) studied the nature and magnitude of genetic variance determining seed yield and 100-seed weight involving six parent half diallel cross in lentil. Both additive and non-additive genetic
variances were important for 100-seed weight and seed yield per plant. However, additive genetic variance was of greater importance for 100-seed weight whereas, non-additive genetic variance was important for seed yield per plant. The GCA effects indicated that all the bold seeded parents (Precoz Selection, KL-82-2 and L4136 had significant positive GCA effect for 100-seed weight and only one parent (KL86-2) exhibited significant positive GCA effect for seed yield per plant. As far as promising crosses were concerned, three out of nine namely, Precoz x HUL-12, L4136 x PL936 and KL86-2 x HUL12 showed significant SCA effects for 100-seed weight and seed yield per plant.

Gupta and Singh (1994) reported both GCA and SCA variances to be highly significant for days to flowering, maturity, plant height, primary and secondary branches, clusters per plant, pods per plant, seeds per pod, test weight and yield per plant. The magnitude of GCA variance was higher than SCA variance indicating predominant role of additive gene action. Over dominance was indicated for number of primary branches, number of clusters per plant, number of pods per plant and number of seeds per pod in F_1 generation. The per se performance and combing ability effects indicated the superiority of parents K-80 and K-75 for yield and its components. The variety L-830 was the best general combiner for earliness.

Rathi et al. (1994) studied combining ability involving 20 diverse lentil strains 90 F_1s and 90 F_2s following partial diallel analysis. The results indicated that variances due to GCA and SCA were important for number of clusters per plant, number of pods per cluster, number of seeds per pod and grain yield per plant in both the generation and number of clusters per plant in
F₁ whereas the estimates of GCA variances were higher than SCA variances for number of pods per cluster, number of seeds per pod and grain yield per plant. None of the parents was a good general combiner for all the traits studied. However, B 238 showed high GCA for number of pods per cluster and number of seeds per pod and LG 60 for number of clusters per plant and seed yield. The mean performance of the parents was positively associated with their GCA effects.

Singh and Singh (2003) reported combining ability analysis of 8 x 8 diallel in lentil. The parents 5505-4, PL-4, DPL-62, L9-12, B-18, K-75, S-235 and L-830 and their 28 F₁s and 25 F₂s progenies were grown and observed for days to flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, 100-grain weight and grain yield per plant. The parents DPL-62 and K-75 were good general combiners for days to flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of pods per plant, 100-seed weight and grain yield per plant. DPL-62 and K-75 exhibited a higher quantity of desirable genes with fixable components for L-830 was the best general combiner for earliness. Cross combinations DPL-62 x B-18, B-18 x K-75, L-9-12 x K-75 and PL-4 x DPL-62 were promising for most of the traits.

Rathi et al. (2003) reported general combing ability (GCA) for yield and yield components in lentil. Among the parents, B-238 was a good general combiner for grain yield, early flowering and maturity, high number of secondary branches, low number of clusters per plant, high number of pods
per plant and small seed size. The parent LG-60 was a good combiners for high grain yield, but this cultivars exhibited inferior performance in terms of the other traits. The genotypes like B-256, K-75 and P-248 were also good general combiners for most of the traits. The per se performance of the parents and their general combining ability effects were generally not parallel. The associations between protein content and seed weight was negative with respect to GCA effects. The crosses B-238 x P-248, LL-19 x JL-54 and K-75 x P-237, which involved parents characterized by high x high GCA effects, recorded high grain yield (F₁) and high degree of heterosis with low inbreeding depression (F₂). The other crosses, which involved parents characterized by high x low GCA effects, exhibited high heterosis and high degree of inbreeding depression, indicating the presence of additive and dominant gene action, respectively by for grain yield per plant.

2.7 NATURE AND MAGNITUDE OF GENETIC VARIANCE

The concept that the quantitative characters are controlled by polygenes was given by Nilson-Ehle (1909), Fisher (1918) gave the idea of estimating the variance controlling the quantitative characters for the first time and partitioned it into additive, dominance and espistatic variances.

Wright (1935) defined these components of genetic variance as (i) additive genetic variance (ii) variance due to dominance and (iii) variance due to deviation from the additive scheme from the interaction of non allelic genes.

Cockerham (1954) and Kempthorne (1954), further partitioned espistatic variance into additive x additive, additive x dominance, dominance x dominance components. Robinson et al. (1949) reported that additive genetic
variance indicates extent to which the parents and progenies are related together.

According to Mather (1949) the variance observed in a character can be described due to non-heritable and heritable sources. Heritable variance was portioned into fixable and non-fixable ones.

The following methods have been commonly employed by various workers for the estimation of genetic parameters:

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


Their results confirmed that GCA was primarily due to additive effects of genes and SCA due to dominance and epistatic interactions.

Henderson (1952) considered GCA as the average merit with respect to some traits or weighted combinations of traits of an indecently large number of progenies of an individual or lines when mated with a random sample from some predicted population under a specific set of environmental circumstances. He defined SCA as the deviation of an average value of a
crop from the value which would be expected on the basis of known GCA of two lines.

Griffing (1956a) pointed out that GCA involved both additive effects as well as additive x additive interactions.

Sprague et al. (1959) and Carnaham et al. (1960) also confirmed the above findings. Kempthone (1957) precisely defined the general and specific combining ability in terms of covariances of half-sibs and full-sibs, respectively.

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

DEGREE OF DOMINANCE

The polygenic inheritance, the effect of individual gene can not ordinarily be distinguished from one another. Consequently, it is not possible to determine the mode of action of a single gene. By studying their combined effects in segregating population, however, one can gain some insight with their behaviour and can draw inferences about the average level of dominance involved in the expression of a particular quantitative character.

Mather (1949) developed a formula \( \sqrt{H/D} \) to estimate the degree of dominance. If the measure of degree of dominance is greater than zero, a certain degree of dominances in the action of genes conditioning the characters as indicated. If the value is greater than one, there is over dominance of genes at one or more loci, but if the value of degree of dominance is less than one, there is either no dominance or partial
dominance. If the value of measure of dominance equals zero, the dominance is absent (Comstock and Robinson, 1948).

Hadded et al. (1982) studied genetic variances in three lentil crosses (Cross 1 = Chilean x PL 297784; Cross 2 = Tekoa x PL 212611 and Cross 3 = Precoz x PL 212611) from the F₂ generation to F₅ generation. Additive genetic variance was the major component of variance in cross 2 for all characters except plant height and seed weight. Estimates of dominance variance appeared to be high in cross 1 and 3. Estimates of additive x additive component seemed very small in all three population. The dominance variance components estimates were consistently high for plant height in the three crosses and seed weight in crosses 2 and 3, where parental means were close, additive variance estimates were low and in many cross negative.

Emami and Sharma (2000) studied the inheritance of black testa colour in lentil using seven crosses involving parents with black, brown, tan or green tests and with orange, yellow or dark green cotyledons. Analysis of F₂ and F₃ seed harvested from F₁ and F₂ plants, respectively, revealed that although black testa is dominant over non-black testa is penetrate, its penetrate is not complete since both F₁ plants and heterozygous F₂ plants produced varying productions of the crosses between parents with brown and tan, as well as brown and green testa segregates in the ratio of 3 brown: 1 tan and 3 brown: 1 green, respectively, indicating monogenic dominance of brown testa colour over tan and green. The expression of testa colour was influenced by cotyledon colour when parents with brown or green testa are crossed with those having orange or green cotyledons. Thus F₂ seeds from the crosses with a green testa always had green cotyledons and never orange cotyledons.
Chaudhary and Kaur (2002) studied wilt disease lentil, based on soil and plant analysis of Rajasthan. The soil analysis revealed that *Fusarium oxysporum* f. *sp. lentis* was the most dominant pathogen (250-7500) followed by the other *Fusarium* species like *F. solani* F. *equisete* and *F. semitechtam* (F. *Palliodoroseum*). Root analysis showed that 77.2-97.0% of the plants were infected by *F. oxysporum* f.sp. *lentis*. The minor pathogens included *F. solani* (3.3%), *R. bataticala* (3.7%), *R. solani* (0.3%) and some unidentified pathogens (3.8%). *F. oxysporum* was the most pathogenic, paralyzing (88.9%) of the wilted plants.

Kumar and Jha (2003) reported resistant using 48 lentil cultivars in a field experiments conducted in Ranchi. They reported that resistant cultivars recorded a minimum of 5-5.4 cm main root length and 4.6-5 secondary roots, whereas, susceptible cultivars recorded longer main root length and higher number of secondary roots. The highly susceptible cultivars recorded the longest root and highest number of secondary roots.

Kumar *et al.* (2004) reported *Fusarium* wilt in lentil (*Fusarium oxysporum* f. *sp. lentis*) observed that wilt incidence was low at seedling stage and varied from 5.2 to 18.8% at different locations which was highest in Birsa. The disease incidences gradually increased and ranged from 10.4 to 37.6 at flowering and pod formation stage. There was no wilt incidence when the soil was amended with wheat straw without inorganic fertilizer unutilized soil amended with unsterilized decomposed cattle manure gave the lowest wilt incidence followed by unsterilized soil alone and unsterilized soil amended with sterilized manure.
**Rust:** *(Uromyces fabae* (Pers.) de Bary)*: Rust resistance in lentil is reported to be controlled by a single dominant gene (Sinha and Yadav, 1989). Singh, but different dominant genes for rust resistance in different varieties (Pant L 406, Pant L 639, LG 120, UPL 175) was reported by Singh and Singh (1990).

Singh and Singh (1992) reported that resistance is governed by monogenic dominant gene based on F2 and F3 analysis of 21 crosses derived from the crossing of seven resistant and three susceptible parents.

Chauhan et al. (1996) also observed a single dominant heaviour of rust resistance. Duplicate dominant genes controlling rust resistance was reported by Lal et al. (1996).

Kumar et al. (1997) have reported that resistance to rust in five genotypes (L 178, L 1534, L 2986, L 2991, HPLC 8868) is governed by a single dominant gene whereas in the genotype Precoz, it was found to be controlled by duplicate dominant genes.

Kumar et al. (2001) studied inheritance of rust resistance in 23 crosses derived from eight resistant and ten susceptible lines in different combinations. They reported that two independent dominant and one recessive genes were imparting resistance to rust in the material under study. For the first time they reported gene symbol as *Urf*1 (Precoz, L 4603), *Urf*2 (Pant L 4, L 4147) and *urf*3 (DPL 21).

Chahota et al. (2002) studied two crosses (Precoz x L 259; Precoz x Pant L 639) under green house condition and reported that the resistance was governed by the duplicate dominant genes.
Basandrai et al. (2003) reported rust resistance of 31 lentil genotypes. Results showed that genotypes L 4603 Precoz like and Precoz were free from rust. Cultivars L 4147 and PL 406 were identified as cultivars that can be directly used in infected areas. Cultivars L 4600 and Precoz like yielded consistently better than the control cultivars.

Gupta et al. (2004) have screened 250 lentil germplasm (Lens culinaris) for resistance to rust in the field under artificial epiphytotic condition. Ten cultivars, i.e. Precoz, NDL 92-1, Vipasa, LL 287, DPL 25, L 4076, LH 88-8, HUL 11, L 178 and L 1534 were consistently resistant during rabi 1993-96. These lines/cultivars may be used as a donor parents in on going rust resistant breeding programme.

Mishra et al. (2005) have reported the phenomenon of slow rusting in lentil using 305 lentil lines (255 lines from ICARDA, Syria and 50 indigenous lines) at hot spot location.

Mishra (2006) reported monogenic dominant control of rust resistance in lentil. However, the gene for resistance in the variety Precoz was different from that of PL 4 confirming partly the findings of Kumar et al. (2001).

**Blight:** (Ascochyta pisi; A. lentis; A. fabae): Ahmed et al. (1977) reported that the host resistance was controlled by two complementary dominant genes in the wild species namely, L. ervoides and L. odomensis.

Tay and Slinkard (1989) reported that each genotype Laird, ILL 5538 and ILL 5684 had single dominant genes for resistance.

Ahmed and Morall (1998) could not observed the Mendelian segregation pattern for virulence in the materials studied.
Ye et al. (2003) reported inheritance of foliar resistance to *Ascochyta* blight in lentil (*Lens culinaris*). They reported that two dominant genes, one for resistance and one for moderate resistance, are present in ILL5588. One dominant gene, which is allelic to the one for resistance in ILL5588, confers the resistance in ILL5684. One recessive gene is responsible for the resistance in Laird. The resistance in Indianhead is under the control of two recessive genes with additive effects. Two complementary genes, one on W6 3192 and one in Titore, are responsible for the resistance observed in the F2 generation of the crosses between these two susceptible cultivars.