Chapter - II
Review of Literature
REVIEW OF LITERATURE

Maize (Zea mays L.) is one of the most important economic crop plant and is almost an ideal cereal forage crop because of quick growing with high yielding potential and nutritious with high palatability. It is a widely distributed cereal crop throughout the world with many uses. It is much exploited cereal crop in the world mainly as food crop but it is also very important forage crop. The selection of maize hybrid for forage production in many countries, including major maize growing region in India has generally been based on their grain production potential. The mode of utilization of maize as fodder may vary from its use as green fodder, hay or silage. The main objective of any forage production programme is to provide high nutritious fodder in accordance with the feed requirement of animals. The maize plant forms excellent forage for cattle with above average dry matter yield and digestible nutrients per hectare (Perry, 1988).

Very little attention has been given to the improvement of maize as a fodder crop. Some research results are available that could be useful in improving maize as forage crop. However, limited work has been done on this aspect. Keeping this in view, efforts have been made to review the information available on this species pertaining to different aspect like genetic variation, genetic divergence, association and stability aspect vis-à-vis genotype x environment interaction of the accessions for yield and yield contributing characters as well as quality characters. The information available on these aspects on maize is reviewed under the following sections:

2.1 Genetic variability
2.2 Genetic divergence
2.3 Character association and path- coefficient analysis
2.4 Gene x Environment interaction and phenotypic stability
2.1 Studies on genetic variability

Genetic diversity is an essential requirement for any crop improvement programme, because genetically diverse parents when crossed can bring together gene combinations, which can be exploited to obtain superior recombinants. Genetic improvement mainly depends upon the amount of genetic variability present in a population. In any crop, germplasm serves as valuable source of base population and provides scope for wide variability. Information on the nature and degree of genetic divergence would help the plant breeder in selecting the right type of parents for breeding programme. Vavilov (1951) was first to indicate the importance of greater range of variation in material for rapid improvement.

Availability of genetic variability for the component characters is a major asset for initiating a fruitful crop improvement programme. Plant breeding has amply been defined as a purposeful management of variability. Since whole breeding pursuit relates to the creation and management of genetic variability, the proper information on this aspect is a pre-requisite before embarking on any breeding method. Finlay (1971) has stressed the importance of continuous infusion of new genetic variability in active plant breeding programmes.

Singh and Sharma (1970) reported that the genetic variability estimates were high for yield per plant, number of days to 75% silking, plant height and position of cob in maize.

Gouesnard et al. (1989) found genetic variance in intra and inter population hybrids was the same, dominance variance was significant for yield and cob leaf length, whereas additive variance explained most of the genetic variability in earliness of flowering, plant and cob height, cob width and dry matter content. Additive variance was similar for highly heritable traits but that for yield was markedly different.

Alika (1994) studied genetic variability among S$_1$ families for ogi yield in maize and found ogi yield ranged from 33.9 to 56.5% with mean of 49%. The 100 grain weight ranged from 19.1 to 35.5 g with a mean of 26.7 g.

Bertoia et al. (1995) subjected commercial maize hybrids normally grown for grain to principal component analysis for forage traits over three years. Plant height,
stover digestibility were the traits with the greatest discriminatory values in the first component, which explains 46.25% of total variation.

The inheritance of grain yield, cob diameter, cob length, number of grain rows and 100 grain weight was studied by Turgut et al. (1995). Both dominance and additive effects appeared significant for all the traits, but the dominance component of genetic variance was more important for all traits except 100- grain weight. Dominance effects in the direction of high grain yield, but was not unidirectional for components of yield. Dominance was complete for all traits except number of grain rows.

Betran and Hallouer (1996) found additive genetic variance component was the most important component of genetic variability for all traits. Except for grain yield, additive by environment interpopulation variance estimates were smaller than their corresponding additive variance. For grain yield, the additive variance component increased with selection; however, the original population cross-showed greater additive by environment interaction variance than the improved population crosses. The estimates of additive genetic variance increased for plant and cob height with recurrent selection for yield. Except for grain yield all traits exhibited a decrease in estimates of the dominance variance component after selection.

Chen Ling et al. (1996) found that additive gene effects were more important for cob thickness and kernel rows/cob. Inheritance of cob length, 100 grain weight and dominant effects controlled grain yield/plant. For cob thickness, recessive genes had positive effects and dominant genes had negative effects.

Mani and Bisht (1996) studied genetic variability in local maize of U. P. hills and found that genotypic coefficient of variation was having moderate to high genetic variability for the majority of characters, except cob girth, number of rows/cob and shelling percentage, that showed low variability. The genetic variability in the local germplasm for the desired traits, viz, grain yield, maturity, cob length and 100 grain weight will be of greatest value, for breeding highly adapted early maturing composites and hybrids of maize for the UP hills.

Katiyar et al. (2001) studied variability pattern in collected genetic material of maize for various cob and kernel attributes. Wide variation occurred in cob length.
(6.4- 24.0 cm). About 5% accessions had cob length between 22- 25 cm whereas the highest number of accessions (84) was observed in class interval 14.0- 17.90 cm. The cob diameter ranged from 2.20 to 4.90 cm although majority of accessions had cob diameter varied from 3.48 to 4.12 cm. Kernel number per row also depicted unimodal asymmetrical distribution. Extreme high as well as low classes of kernel number/row was observed in about 8 and 6% accessions respectively. So far as kernel colour is concerned it showed wide variability as: 118 accessions (53%) had yellow kernel, 69 accessions (31.22%) white, 11 accessions (4.98) purple, 9 accessions (4.07%) variegated and 14 accessions (6.34%) had brown colour.

2.1.1 Heritability and genetic advance

With the help of genotypic coefficient of variation alone, it is not possible to determine the amount of heritable variation. Heritability estimate (in broad sense) is a reliable parameter for evaluating the genetic potential of a given population. Wright (1923) put forth the concept of heritability in pure lines as additive genetic variance expressed as percentage of the total variance. Lush (1949) defined heritability in broad sense, as the ratio of total heritable variance to the total phenotypic variance. He further suggested that heritability in narrow sense includes only average effects of a gene transmitted from parents to the progeny or the ratio of the additive variance to the total variance.

Heritable variation can be found out with greater degree of accuracy when heritability in conjunction with genetic advance is studied (Dudley and Moll, 1969). Hence, both heritability and genetic advance were determined to get a clear picture of the scope of improvement in various characters through selection.

Sviridov (1979) calculated the coefficients of heritability for plant height, number of grain rows per cob and cob length taking into account the close correlation between number of grains/ cob and cob length and also between number of leaves/ plant and plant height. Heritability estimates were greater for number of grain rows per cob (60) and plant height (59.9) in which the latter character showed over dominance. Cob length gave the lowest heritability estimates (31.1).
Kumar (1982) reported high coefficient of variation and estimates of heritability and genetic advance were found for leaf weight, cob weight and forage yield/plant.

Gallais et al. (1983) studied heritability in maize and reported heritability estimates were high for morphological characters and earliness and low for dry matter yield.

Claudio et al. (1988) found high narrow sense heritability estimates for plant height and cob length and low for leaves/plant and grain yield/plant whereas, cobs/plant had the lowest heritability.

El-Harary (1989) reported moderate to high heritability estimates for all components, ranging from 23.5 (rows/cob) to 67.1 (grain/row) in a synthetic variety of maize.

High heritability estimates and substantial expected genetic advance were found for leaf area and 1000-grain weight. Singh et al. (1989)

Arha et al. (1990) in their studies on heritability and expected genetic advance in maize observed heritability was highest for days to silking; moderate values were recorded for plant and cob height, number of leaves above the cob and cob length.

Progenies from S1 families derived from a maize population introgressed by Zea diploperennis were evaluated in 1988-89 (Pischedd and Magaga, 1990). Heritability estimates ranged from 27% for plant height to 63% for 50 grain weight. Heritability of prolificacy was high (61%) but that of yield (cob weight/plant) was low (33%).

Alik a (1994) found broad sense heritability estimates to be 55.4 and 52% for yield and 100 grain weight respectively. The value for predicted genetic advance from 30% selection for ogt yield and 100 grain weight averaged 6.1 and 7.2% respectively, while the actual genetic advance averaged 9.6 and 13.6% respectively.

Satyanarayana and Saikumar (1995) observed wide and significant phenotypic variation for grain yield and other characters in maize. Grain yield recorded low genotypic coefficient of variation estimates combined with low to medium heritability and low genetic advance. This indicated the probable predominant role of non-additive gene action governing the inheritance of grain yield.
Betran and Hallouer (1996) found that heritability estimates for grain yield increased with recurrent selection. Heritability estimates of the original and selected cross population were similar for the other traits.

Chen Ling et al. (1996) estimated heritability for cob length, cob thickness and kernel rows/cob, which ranged from 50.8 to 87.9% and was higher than those for 100 grain weight and grain yield/plant.

Mani and Bisht (1996) made a study on genetic variability in maize germplasm of Uttar Pradesh and observed high heritability (Broad sense) along with high genetic advance for days to 50% silking, grain yield, total number of leaves, cob height and moisture percentage in grain at harvest. For plant height these values were moderate, while they were low for the rest of the characters.

Satyanarayana and Saikumar (1996) found differences between the genotypes with respect to grain yield and number of days to 50% tessaling. Heritability and phenotypic and genotypic variance estimates were high for yield, suggesting this character may be improved by recurrent selection. Whereas, Ortiz and Sevilla (1997) reported highest heritability and coefficient of variation for cob length, rows of kernels, cob diameter and kernel width.

Tusuz and Balabanli (1997) studied heritability of main characters affecting yield and determination of relationships among these characters. Over two years of the experiment, heritability in the broad sense was highest for 50% silking (0.93) and low for plant height (0.12), cob length (0.31) and for yield (0.06). Yield was significantly correlated with 50% silking days ($r = 0.67$), plant height ($r = 0.50$) and cob length ($r = 0.42$). The yield potential of all varieties changed from year to year and a significant environmental effect was observed.

### 2.1.2 Studies on quality parameters

Maize is grown over a wide range of environments and geographical areas than any other cereal crop, with its multifold use for human, livestock feeding and industry. The residual stover after removal of cobs is important roughage for ruminants in tropical countries. Nutritionally, maize stover has higher crude protein and lower cell wall content and silica than sorghum and pearl millet stover (Sen and
Roy, 1971). Cell wall constituents of a plant are very important factor, which affect the forage intake and digestibility (Von Soest, 1965). Sugar contents, leaf–stem ratio and their proportionate thickness have a significant effect on forage yield and its nutritional quality.

Crude protein content, cell wall constituent's concentration and dry matter degradability are the potential criteria for screening the diverse genetic material at initial stage of forage breeding programme from the livestock feeding point of view. The main objective of any forage production programme is to provide nutritious fodder in accordance with the feed requirement of animal (Hulton, 1975).

Roth et al. (1970) studied the genetic variation of quality traits in maize and found that genetic variability was apparent for in vitro digestible dry matter constituents and crude protein. All the characters except crude protein content were found inter co-related.

Laredo and Minson (1973) reported higher crude protein and lower NDF (Neutral detergent fiber), ADF (Acid detergent fiber) and lignin contents in leaf and stem fractions of grasses.

Fairey (1980) evaluated 97 hybrids differing in maturity and genetic constitution in three dissimilar environments and reported that forage yield was linearly related to grain yield at each site and the relationship was distinct for each site. However, grain yield was not a good indicator of forage productivity. At each site, forage dry matter content depended on the dry matter of the Stover and the proportion of total dry matter as grain or in the cob.

Singh and Katiyar (1999) studied fodder yield and nutritional variability in leaf and stem of seven maize genotypes and found crude protein value ranged from 10.32 to 12.92 in leaves and 3.49 to 6.69% in stem fraction, respectively.

Information is needed on the factors that maximize yield and quality of recently developed maize forage hybrids. A study was conducted by Widdicombe and Thelen (2002) to determine the effect of row width and plant density on forage yield and quality of forage maize hybrids and dual-purpose hybrids. They found that when row width was reduced, forage dry matter increased. As plant density
increases from the lowest level to the highest, forage dry matter increased by 1.6 t/ha\textsuperscript{-1} and crude protein decreased from 76 to 72 g/kg\textsuperscript{-1}.

Sananta et al. (2003) studied silage quality of different forages reported dry matter of the forage ranged from 28.60 to 31.52%. Water-soluble carbohydrate content was highest (6.12%) in fodder sorghum while it was lower in natural grasses (1.51%). Similarly, the CP content was also lowest (3.68%) in natural grasses and relatively more in maize and fodder sorghum (6.58%).

2.2 Genetic divergence

The importance of genetic divergence for improving yield potential, per se through hybridization has been emphasized by several authors and reviewed by Frey (1971). Although, breeders have long appreciated it, the basic difficulty has always been one of recognizing such diversity and its reliable estimation without making actual crosses (Bhatt, 1970). Since most of the quantitative characters are highly influenced by environments, it becomes difficult to separate non-heritable components from heritable components of variability based on phenotype.

In the past, geographical distance of species and varieties has often been considered as a criterion for the measures of genetic diversity (Dhawan and Singh, 1961; Moll et al., 1962; Singh and Joshi, 1966) but the criterion was overruled by Somayajula et al. (1970), Jayaprakash et al. (1974) and Chandra (1977). Therefore, a technique, which can provide direct and reliable estimates of diversity at genetic level, will obviously be more useful. Hutchinson’s polygraph (Hutchinson, 1936) and metroglyph and index score analysis (Anderson, 1957) broadly classified the germplasm but they did not provide numerical estimates for precise comparison.

To discriminate the function, Fisher (1936) suggested the useful criterion to select the best individuals from populations based on single parameter. However, the situation becomes difficult when the number of variables to be considered is increased. Pearson (1926) suggested the coefficient of racial likeness (CRL) as a single numerical measure, which would express the degree of resemblance or divergence of two races when several characters were measured on relatively few
individuals from either or both the races. Rao (1948) pointed out that CRL was an imperfect tool because it neglects correlations between characters under study.

Mahalanobis (1925) gave the concept of generalized distance based on second-degree statistics and it is self-weighing on the basis of genetic variability. Mahalanobis (1928) suggested that CRL was a ‘test’ of divergence between two samples rather than an actual measure of magnitude of genetic divergence and it would be logical to use measure and not the test of divergence for quantitative comparisons between the populations. Mahalanobis (1930) for the first time applied his $D^2$ statistics on the extensive measurement of Swedish (human) population. In anthropological survey of united province this technique was further applied (Mahalanobis, 1949).

Genetic improvement mainly depends upon the amount of genetic variability present in a population. In any crop, germplasm serves as a valuable source of base population and provides scope for wide variability. Information on the nature and degree of divergence would help the plant breeder in choosing the right type of parents for breeding programme (Vivekanandan and Subramanian, 1993). Hence estimation of genetic diversity for fodder and grain yield as well as other traits among accessions is important for planning the future crossing programmes. Characterization of genetic divergence for selection of suitable and diverse accessions should be based on sound statistical procedures, such as $D^2$ statistic (Mahalanobis, 1936) and non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973). These potent tools for estimation of divergence have been emphasized by many workers (Murty and Arunachalam, 1966; Anand and Murty, 1968 and Arunachalam, 1981).

In maize it is well known that genetic diversity is necessary in breeding programme for development of high yielding varieties. Multivariate analysis is a useful tool for quantifying the degree of divergence between biological population at genotypical level and assessing relative contribution of different components to the total divergence at both intra and inter cluster level (Ram and Panwar, 1970 and Sachan and Sharma, 1971).
Endang et al. (1971) stated that clustering pattern could be utilized in choosing parents for cross combination, which likely to be generate the highest possible variability for the effective selection of various economic traits.

Little attempt has been made to classify genetic diversity in maize however, some efforts have been initiated and 1571 maize accessions collected from the important maize growing areas of India (Singh, 1969). This study leads to the recognition of 15 distinct races and 3 sub-races. These races were further grouped into primitive, advanced or derived, recent introduction and hybrid races, all of which could be easily assigned to three of the six lineages postulated by Mangelsdorf (1974).

Cruz et al. (1994) quantified genetic divergence among five maize varieties for eight yield-related traits and values obtained were used to evaluate the efficiency of predicting the performance of corresponding hybrids.

Cruz et al. (1994a) again estimated genetic divergence among five maize varieties for seven yield related traits by four different methods. Mahalanobis generalized distance and the average Euclidean distance based on standardized variables, on the scores of the first two canonical variables and on first two principal components representing more than 94% of the total variance). Coefficient of correlation estimated at higher than 0.93 between the measures of divergence showed a high degree of agreement between the methods.

Katiyar et al. (2000) used non-hierarchical Euclidean cluster analysis to compare the maize genotypes. Accessions were classified into 12 broad groups. Group E was the largest, consisting of 35 accessions, while minimum number (18 accessions) were observed in cluster J. There was no correlation between genetic and geographical diversity.

Lakshmi Kant et al. (2001) used non-hierarchical Euclidean cluster analysis for different traits of wheat germplasm. The accessions were grouped into eight clusters. Cluster V was most divergent as well as early flowering. Cluster I was the best for yield while, cluster VII for test weight. Cluster II and VII were highly diverse from each other while, cluster VI and VIII were closely related. Geographical diversity did not relate to genetic diversity.
Genetic variability among 25 genotypes of maize was estimated by Alom et al. (2003) for eight traits. The genotypes were grouped into seven clusters. The inter cluster distances was larger than the intra cluster distance suggesting wider genetic diversity among the genotypes of different groups. The cluster III contained the highest number of genotypes with highest yield and 1000- grain weight. The inter cluster distance was highest between cluster III and II and of lowest between cluster IV and V. Intra cluster distance was highest in cluster IV and lowest for cluster VI.

2.2.1 Isozyme studies

Isozyme analysis has been used widely to estimate genetic diversity of populations. This method has been useful in addressing question on genetic structure of population and their conservation. Knowledge of the genetic diversity of species is particularly important. Since advance breeding practices involving selections for high biomass have narrowed the genetic diversity of cultivated crops. This reduction in genetic diversity could severely limit future breeding programmes for adaptive traits such as resistance to stress and stability.

Biochemical methods have been widely used for rapid identification of cultivars and detection of inheritance of multiple forms of single protein. Since their discovery isozymes have played a key role in many branches of biology and have become the most widely recognized links between the organisms and molecular approach. The advantage of using isozyme markers make them ideal for use in linkage studies for construction of genetic maps of plant chromosomes. The detection of isozyme of a specific enzyme depends upon plant age cell or tissue origin, growth environment and enzyme stability as well as method of extraction, separation and visualization (Sheen, 1983).

Isozyme polymorphisms have provided population geneticists and systematists with the simple genetic markers necessary to analyze gene flow, differential selection pressure and genetic relationships among populations and taxa. It has been repeatedly demonstrated that genetic diversity is correlated with genetic distance as measured by allozyme variation. (Brown and Weir, 1983). Many genera, including important crops, have been subjected to evolutionary and taxonomic
analysis involving isozymes surveys, such as Zea (Doebley et al. 1986; Kohler et al. 1986 and Smith et al. 1985)

Detection of isozyme using electrophoresis techniques has been extensively used for the characterization and identification of species, inbred lines, isogenic lines and crosses in plant breeding studies. In maize, enzyme diversity has mainly been studied to know the genetic variability in relation to geographical distribution and evolution.

Liu et al. (1981) reported P x 7 is the largest of the maize peroxidase isozymes, with a molecular weight of about 75000. The R₁ heterozygotes in crosses between P x 7R and P x 7S lines had only two bands which migrated together with each of the parental allelic bands, suggesting that P x 7, despite its high molecular weight behaved as a monomer. Hulton E. M. 1975. *Forage Res.*, 1: 87.

Khavkin (1991) noted variable bands of anodic esterase and peroxidase in zymograms of leaf extracts from 8 second generation (SC₂) maize somaclones. The extent of variation within several sibs from the same SC, cob was sometimes greater than the deviation from the standard (line A188). Some of the bands active in the somaclones but absent from the leaves of the stand and were previously described as characteristics of other, not leaf tissue. Some loci appeared to be more susceptible to somaclonal variation than others.

Based on several studies (isozyme pattern) in Maydeae, least genetic distance was observed between *maize teosinte*. The hierarchical order of *Maydeae* is *maize > teosinte > coix > triolobanche > chionachne* (Sachan and Singh, 2001).

### 2.3 Character association and Path-Coefficient analysis

Knowledge of interrelationships serve two main purposes, firstly these are useful in selection of characters, which are not easily observed or genotypic values which are modified by the environmental effects. There is ample evidence to show that selection directly for yield is not easy. Thus, any morphological character that is associated with yield would be useful in the improvement of yield. Secondly, inter-
relationship between characters serves as a source of information to determine the nature, extent and direction of selection pressure to be applied on a character. Therefore, the character associations among yield traits and path co-efficient analysis for various yields and quality character of fodder and seed in maize are reviewed.

Simple correlation hardly takes into account the extremely complex inter-relationships. Path co-efficient analysis suggested by Wright (1960) and discussed by Li (1954 and 1956), Tukey (1954), Kemphorne (1957), Turner and Stewens (1959) and Neihour and Pickett (1966) involves partitioning of direct and indirect contribution of various factors towards building up of a complex correlation.

Chopra (1964) in his studies on genetic correlation between yield and number of cobs, days to flower, plant and cob length in maize, reported medium to high positive correlation between plant height and cob length.

Nanda (1964) studied general and specific combining ability of maize and obtained poor correlation for yield and shelling % but they were of sufficiently high magnitude for maturity characters, plant and cob length to have predictive value.

Chase and Nanda (1965) found positive and significant correlation between the average number of leaves per plant and average number of days to 50% anthesis.

Laszlo et al. (1969) in their studies on correlation among grain yield, 1000 grain weight, cob per plant and plant height observed significant correlations between 1000-grain weight and yield and dry matter content and yield. Other correlations were significant only under certain conditions.

Singh (1970) reported that seed yield was positively associated with cob length, cob girth and seed size in maize germplasm. From the path co-efficient analysis, it was shown that the cob girth was the most important component of yield.

Cross and Zuber (1973) evaluated ten strains of maize for interrelationship among plant height, number of leaves and flowering days and found significant correlation between plant height and number of leaves in majority of strains. The degree of relationship among the three characteristics varied among strains.
Sviridov (1979) reported close correlation between number of grains per cob and cob length ($r=0.62$) and also between number of leaves per plant and height ($r=0.48$).

Fairey (1980) made a study for the assessment of forage potential of maize and reported that forage yield was linearly related to grain yield at each site and this relationship was distinct for each site. However, grain yield was a good indicator for forage productivity. Forage dry matter content depended on the dry matter content of the stover and the preparation of total dry matter as grain or in the cob.

Regazzi et al. (1980) analyzed covariance and correlations in maize, which showed that genotypic correlations were greater than phenotypic in 17 out of 21 pairs of characters. From several of these correlations, it was concluded that in absence of lodging, yield was closely associated with plant height, height of cob insertion and number of cobs per plot.

Kumar (1982) studied genetic variability of quantitative characters contributing to forage yield in maize and reported that forage yield was highly correlated with leaf length, leaf number, leaf breath and plant height. Leaf length and cob weight were the main contributors to forage yield per plant.

Gallais et al. (1983) reported positive correlation of dry matter yield with cob length and plant height and negative correlation between dry matter yield and protein contents.

Dubas and Waligora (1984) made a three year investigation for assessment of the suitability of maize varieties for the production of grain and whole plant dry fodder. Correlations based on actual yield showed that when judged as a dual-purpose crop, some varieties failed to justify the promise of their high ranking.

Patel and Shelke (1984) observed that percent N content in the plant had significant correlation with forage yield, both directly and indirectly.

Paramathma and Balasubramanian (1986) observed that stem girth and plant height and leaf breath and stem girth were the most important traits for improving fodder yield in forage maize.

Forage yield may be increased by improving such characters like plant height, leaf area, N percentage, stem girth and number of internodes per plant. However,
Patel and Shelke (1988) reported positive and significant association among all the traits measured except leaf-stem ratio, leaves per plant, internodes per plant and dry matter yield per plant. Leaf area per plant exhibited positive and highly significant relationship with stem girth; internodes number and dry matter yield per plant.

Gupta and Singh (1990) studied genotypic and phenotypic association of leaf number, leaf area and dry leaf weight and found that all the characters were significantly and positively associated with sink size (grains/ kernel row) and ultimately with grain yield.

Correlation between grain yield and certain morphological characteristics were studied by Angelow (1992) who observed highly significant correlation between yield and plant height, number of leaves and length of the first cob. Correlation between yield and cob length and number of grains per cob were also significant. Yield was not correlated with number of grain rows per cob.

Partial and multiple correlations were carried out on yield and its components by Altinbas and Algan (1993). Partial correlations between earliness and other traits were non-significant, except for days to silking and grain row number. Multiple correlations of earliness with grain yield per plant, cob diameter and 100 grain weight were significant. Cob diameter was the major component of grain yield and grain yield per plant was positively affected by 100-grain weight.

Singh and Major (1993) reported that grain yield was associated with cob girth, rows per cob and grains per row. Path analysis indicated high direct effects of these three traits on grain yield.

Dost Mohammad et al. (1995) made a study on fodder yield and quality potential of forage maize and evaluated number of leaves per plant, green fodder yield and dry matter yield. Plant height and leaf area were positively correlated with green fodder yield and dry matter yield.

Rahman et al. (1995) found that grain yield was significantly and positively correlated with plant height, cob length, number of grains/cob and 1000 grain weight. Path analysis revealed that cob length, plant height and 1000 grain weight were main contributors to grain yield.
Choukan (1996) found that leaf- stem weight and stem weight showed the highest correlation with fodder yield \((r = 0.97 \text{ and } 0.96, \text{ respectively})\). Stem weight and plant weight had the highest correlation with forage yield/plant \((r = 0.81 \text{ and } 0.66, \text{ respectively})\).

Wang et al. (1997) derived information on yield correlation from data on 7 yield- related characters. Results showed that 100 seed weight, rows per cob, cob diameter and kernel/ row had the height correlation with grain yield.

Katiyar and Choudhary (1999) indicated that green fodder yield had positive correlation with plant height, number of leaves, leaf length, leaf width and dry fodder yield but it was negatively associated with crude protein content. Path coefficient analysis revealed the highest and positive contribution of plant height towards green fodder yield followed by leaf length, internode length, leaf/stem ratio and leaf width, respectively. Gurrath et al. (1989) and Geiger et al. (1992) also reported that green fodder yield was significantly and positively associated at phenotypic level with plant height, number of leaves, leaf length and leaf width.

Mani et al. (1999) made a study on variability and path coefficient analysis in indigenous maize. Results revealed that grain yield per plant had highly significant positive correlation with all the attributes and the highest was with cob weight per plant. Path analysis also suggested that cob weight per plant followed by grains per row were the major direct contributor to grain yield per plant. Hence, maize, breeders may concentrate much on cob weight/plant and grains per row as selection criteria for yield improvement.

Rana et al. (2000) studied the inter-relationships and path coefficient analysis in maize and computed phenotypic coefficient of correlation for grain yield and its component traits. Grain yield showed positive association with 1000 grain weight, kernels per row, cob length and plant height at the phenotypic level. Path coefficient analysis indicated that plant height and kernels per row were the main characters through which the indirect correlation of most of the traits was positive and higher. Similar results regarding to correlation coefficient for plant height with cob length (Krishnan and Natarajan, 1995) have been observed. Direct positive contribution of kernels per row and kernel rows per cob towards grain yield have been reported by
Gyanendra et al. (1993), whereas plant height was positively associated with kernels per row and 1000-grain weight reported by Debnath and Khan (1991).

2.4 Gene x Environment interaction and phenotypic stability

The study of genotype x environment interaction leads to successful evaluation of the stable genotypes, which could be used in future breeding programmes. Earlier Finlay and Wilkinson (1963) considered linear regression slopes as a measure of stability. Eberhart and Russell (1966) modified the techniques and considered both the linear (bi) and nonlinear ($S^2_{di}$) components of genotype x environment interaction for judging the phenotypic stability of the variety. They used corn hybrids which were a highly selected material developed from improved inbreds and suggested that an ideal variety should have high mean, linear regression and a ($S^2_{di}$) as small as possible. Later on Breese (1969), Samuel et al. (1970), and Paroda and Hays (1971) advocated that the linear regressions could simply be regarded as a measure of response of a particular genotype, which in fact is dependent largely on the number of genotypes included in a particular study. Whereas, the deviations from regression line ($S^2_{ai}$) were considered as a better measure of stability. The genotypes with lowest squared deviations being the most stable and vice versa. Using the above definition of the term stability it could be possible to judge the phenotypic stability with due consideration to mean performance and linear response of the individual genotypes. Looking into different opinions for evaluating genetic materials for stability, a scale of stability was later on adapted in forage crops by Shukla et al. (1993) in lablab bean, and Singh et al., (2000) in Clitoria ternatea. The scale spells out the parameters to be considered for evaluating stability of the genotypes as under:
\[ X_i > \text{GM: Grand mean of the populations (invariably for all the genotypes selected).} \]

\[ b_i = 1: \text{ith genotype predicted have stability for general or average environments.} \]

\[ b_i > 1: \text{ith genotype predicted has stability for favorable environments.} \]

\[ b_i < 1: \text{ith genotype predicted have stability for stress or poor environments.} \]

\[ S^2 di = \text{NS: ith genotype predicted have to be stable} \]

\[ S^2 di = \text{Sig: ith genotype predicted has to be unstable, irrespective of the value for mean and regression coefficients} \]

### 2.4.1 Genotype x Environment interaction:

The interaction of genotype to the environment is a natural phenomenon irrespective of the nature of the plant material \textit{i.e.,} varietal population, pure lines, hybrids, clone populations and so on. Therefore, an understanding of genotype x environment interaction is obviously of great utility in plant breeding programme (Allard and Bradshaw, 1964). The capacity of a crop variety for yielding well over a range of environments is important as its yielding potential. This is especially so when the crop is grown under widely variable environmental conditions. A specified genotype does not exhibit the same phenotypic characteristics under all environmental conditions and the different genotypes respond differently to a specified environment. In other words the failure of a genotype to express the same phenotypic performance when grown under different environments is the reflection of genotype x environment interaction.

Environment is the sum total of physical, chemical and biological factors. Comstock and Moll (1963) classified the environments into two categories (I) Micro-environment, which is the environment of a single organism growing at the same time and in almost same place and (ii) Macro-environment, which is associated with a general location and period of time and is a collection of several micro environments.
Allard and Bradshaw (1964) coined the term predictable and unpredictable environments. The predictable environments included the permanent features of environment such as climate, soil type, day length etc. It also included the controlled variables as fertilizer level, sowing date, plant population, density etc. The unpredictable environment included the factors beyond human control i.e., weather fluctuations in terms of temperature, rain fall, etc.

Jha et al. (1986) reported significant differences among genotypes for grain yield and for genotype x environment interactions. Partitioning of genotype x environment interaction showed significant mean squares due to genotype x environment (linear) and pooled deviations. High yielding hybrids showed wide adaptation for grain yield as indicated by near unit regression coefficient and non-significant deviation from regression.

Sain et al. (1987) evaluated eight varieties of maize for stability with respect to days to 50% silking, plant height, cob length, days to maturity and grain yield. Mean squares due to genotype x environment interactions were to be significant for all the characters except cob length and days to 50% silking.

V'rchinkov (1992) reported genotype x environment interactions was significant for all traits except area of the leaf nearest to the cob and cob length. The phenotypic stability of the characters was close to the theoretical values, with no significant difference between the various hybrid types.

Pal and Prodhan (1994) studied genotype x environment interaction in maize and reported that pooled analysis of variance to be highly significant due to environments, genotypes and genotype x environment interactions for all the characters studied except cob diameter, and number of rows/cob. The results also suggest a greater influence of additive components of gene action in the expression of maturity, cob diameter and 100 grain weight.

Sedham (1994) evaluated ten maize genotypes under 8 environmental conditions to study their stability for grain yield. Significant genotypic effects and genotype x environment interactions were observed for grain yield/plant.

Reddy et al. (1998) studied stability of fodder yield in various types of maize. Result showed, the genotype x environment interaction to be significant for the linear
portion as well as on the non-linear portion but with a predominance of the former indicating that the genotypes responded in a linear manner. The high yielding genotype African Tall was better adapted to good or favorable environment, while Varun (a synthetic variety) was well adapted to poorer environments. The double-cross hybrid DHM 105 was stable over both poor and better environment having general adaptability.

2.4.2 Studies on adaptability & phenotypic stability

An adapted genotype or population is the one, which tolerates the selection pressure by surviving better than that of the stand under comparison. Adaptability is the capacity of the genotype to respond to the selection pressure and it depends on the provision of variability (Mather, 1943). Wild populations of plants and animals display a series of compromise between the two, which depends upon the present ecological circumstances, and the past evolutionary history. These compromises essentially depend upon the adjustment of recombination so that the advantages of close adaptation and disadvantages of concomitant restriction of variability are balanced.

Adaptation is the property of a genotype, which permits its survival under selection, while adaptability is the property of a genotype or the population of genotypes, which permits subsequent alteration of the norm of adaptation in response to change of the selection pressure (Simmond, 1962). In spite of the awareness of genotypic differences in adaptability, the plant breeders have not been able to exploit them fully in breeding programme, largely due to problems of defining and measuring either the adaptability itself or the complexities of natural environments. Various workers (Salmon, 1951; Horner and Frey, 1957; Sandison and Bartlett, 1958) have discussed some of the methods and problems of comparing varietal performance in several environments for several years.

Plaisted and Peterson (1959) suggested a method to characterize the stability of yield performance when several varieties were tested at a number of locations within one year. This method involved computation of a combined analysis of variance over all locations for each pair of varieties. This method has been of limited
utility because of the large number of analysis required. Finlay and Wilkinson (1963) reported a simple technique to measure adaptability of varieties based on average yield of the varieties and their regression coefficients.

Eberhart and Russell (1966) further modified the techniques and considered both the linear (bi) and nonlinear (S^2di) components of genotype x environment interaction for judging the phenotypic stability of the variety. They used corn hybrids which were a highly selected material developed from improved inbreds and suggested that an ideal variety should have high mean, linear regression and a nonlinear component (S^2di) as small as possible.

Perkins and Jinks (1968) further modified the model of the Stability estimate. Paroda and Hayes (1971) observed that the linear regression should simply be considered as measure of response of a genotype, whereas, the deviations around the regression line is a measure of stability. They also pointed out that a genotype with lowest deviation might be the most stable and vice versa.

Gamma and Hallauer (1980) reported significant association between mean yield and regression coefficient and between mean yield and deviation from regression, but these were not large enough to have predictive value.

Paradkar et al. (1995) evaluated seven genotypes of maize for phenotypic stability with respect to grain yield and its components under micro and macro environments. Genotype x environment interaction was observed for all the characters except plant height and number of grain row per cob. Genotype J3022 with the highest grain yield had average stability for most of the characters under the different environmental conditions. Early genotypes were also very stable in the different environments. Genotypes R2 and VL 88 exhibited above average stability for grain yield in poor environments, while R5 was most stable in better environments.

Gautam et al. (1998) derived information on stability from data on grain yield. They observed significant difference due to genotype, environment and genotype environment interaction. The local landrace had the highest average yield and was most suited to temperate wet locations of Himachal Pradesh.
Nirala and Jha (2003) studied the phenotypic stability for fodder traits in maize and reported highly significant mean squares due to genotypes and environments (linear) for all the traits under study indicating the presence of significant difference among genotypes and environments. Highly significant mean square due to genotype x environment (linear) for days to 50% silk and plant height revealed linear response for these traits. Highly significant mean square due to pooled deviation for all traits studied exhibited importance of non-linear component of genotype x environment interaction. The crosses GBM 84- 3 x African Tall and APFM 8 x African Tall were identified as high yielding and stable.