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## LIST OF SYMBOLS AND ABBREVIATIONS USED

%	:	per cent
$\sigma^2_g$	:	Genotypic variance
$\sigma^2_p$	:	Phenotypic variance
ANOVA	:	Analysis of variance
cm	:	Centimeter
$D^2$	:	Genetic divergence
DAS	:	Days after sowing
DOR	:	Directorate of Oilseeds Research
Fig	:	Figure
g	:	Gram
GCV	:	Genotypic coefficient of variation
GMU	:	Germplasm Management Unit
ha	:	Hectare
IPGRI	:	International Plant Genetic Resources Institute
mm	:	Millimeter
m.ha	:	Million hectare
MSS	:	Mean Sum of Squares
No.	:	Number
OIB	:	Outer involucral bract
PCV	:	Phenotypic coefficient of variation
$r_g$	:	Genotypic correlation
$r_p$	:	Phenotypic correlation

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### **ABSTRACT**

A study of the nature and degree of genetic variability present in exotic germplasm accessions forms an essential pre-requisite for its utilization in any plant breeding programme. This information aids to select desirable parents for evolving superior varieties and heterotic recombinants, based on the variability and extent of diversity present in the population. As most of exotic germplasm, which have adopted biotic and abiotic characteristic features, remains untapped, a concerted effort is needed to tap the beneficial genes through conventional hybridization techniques.

The present study consisting of sixty germplasm accessions and four check varieties was laid in Simple Lattice design replicated twice at College Farm, College of Agriculture, Rajendranagar, Hyderabad. The data was recorded for nine morphological and eight quantitative characters respectively.

Morphological characterization was carried out by using descriptor guidelines developed by IPGRI. Considerable amount of variability was observed for all morphological characters.

Analysis of variance indicated significant differences among genotypes for all the characters studied indicating wide variability in the experimental material. High estimates of phenotypic and genotypic coefficients of variations for seed yield/plant, number of filled seeds in main capitulum and number of effective capitula/plant indicated adequate variability for these characters among the genotypes studied while low variability estimates were observed for days to 50% flowering.

The extent of genetic divergence between genotypes in the experimental material was assessed by Mahalanobis  $D^2$  analysis. The clustering analysis had partitioned the sixty four genotypes into nine clusters based on  $D^2$  values. The pattern of distribution of genotypes into various clusters revealed no relationship between geographical and genetic diversity. Maximum genetic divergence was found between cluster II and cluster IX followed by cluster VII and cluster IX suggesting that the genotypes in these clusters could be fully exploited to explore the wide range of heterosis and to release good recombinant lines by intermating them in a definite design.

Correlation analysis revealed that number of effective capitula/plant, number of filled seeds in main capitulum, diameter of main capitulum and 100 seed weight were significantly and positively associated with seed yield while plant height, days to 50% flowering and oil content exhibited negative association with seed yield.

Path analysis revealed that number of effective capitula/plant had maximum positive direct effect followed by number of filled seeds in main capitulum on seed yield. Days to 50% flowering and plant height exhibited negative direct effect on seed yield.



# CHAPTER I

## INTRODUCTION

Safflower (*Carthamus tinctorius* L.) originated in Southern Asia and belongs to the family Asteraceae. The Genus *Carthamus* has about 25 species with 10, 11, 12, 22 and 32 pairs of chromosomes. However, only *Carthamus tinctorius* (n=12) is cultivated as all other species are wild and weedy in nature (Dajue *et al.* 1996). Safflower is a highly branched, herbaceous, thistle like annual, usually with long sharp spines on the leaves. Plants bear globular flower heads (capitula) with either brilliant yellow, orange or red flowers. Achenes are smooth and generally lack pappus. The plant has a strong taproot, which enables it to thrive in dry climates.

Traditionally, the crop was grown as a source of Orange-red dye (Carthamin) that was used as colouring agent. However, with the advent of cheaper aniline dyes, it is now primarily grown as an edible oilseed crop. The high quality edible oil of safflower is obtained from its seed. The oil contains 55-81% Linoleic acid, 7-42% Oleic acid, 1-10% Stearic acid, 1-10% Palmitic acid with 90% unsaturated and 10% saturated fatty acids (Nagaraj 1994). Iodine index of the oil is rather high, ranging from 137 to 146 and has a saponification value ranging from 186 to 195 (Vibhakar *et al.* 1981). As an industrial oil, it is considered to be drying or semi-drying oil and is used in manufacture of paints. The oil is light in colour and does not yellow with age.

Hence, it is used in white and light coloured paints. The meal that remains after oil extraction is used as a protein supplement for livestock.

At present over 60 countries grow safflower, of which India, Mexico, Kazakhstan, USA, Ethiopia, Argentina, Australia, Iran, Pakistan, Russia and China have significant area and production (FAO, 2002). In India the crop has traditionally been grown in the '*rabi*' or winter season. Despite wide fluctuation and decreasing trend in area and production of safflower, India ranks first in area and production while USA has highest productivity (Damodaram and Hegde 2002). In area and production, Maharashtra ranks first among Indian states followed by Karnataka and Andhra Pradesh.

The vital role of plant genetic resources in the improvement of cultivated plants is well recognized. Emphasis is laid on development of crop specific characterization and evaluation programmes to identify the best available accessions and for detection of valuable genes. Assembly of germplasm representing the genetic diversity in a crop species is a prerequisite for its effective study, conservation and improvement. Therefore, characterization and evaluation of both exotic and indigenous collections would provide explicit information on useful traits, which can be utilized in crop improvement programmes. Morphological characterization is an easier and quicker method for evaluating variability in the germplasm, which is done with prescribed descriptor guidelines.

Knowledge of genetic diversity of exotic accessions and their performance against local high yielding varieties is essential to fully exploit their benefits. Therefore, it is necessary to evaluate their performance and also to study the nature and degree of variability in various yield and agronomic traits and the degree of inter-relationships among various traits. This information would be of immense value in formulating suitable breeding programmes and also in deciding most appropriate selection criterion. Mahalanobis (1936)  $D^2$  statistic based on multivariate analysis of quantitative traits is a powerful tool for measuring divergence in a set of population using the concept of statistical distances utilizing multivariate measurement. Study of genetic divergence among a set of genotypes will therefore enable a plant breeder to select genetically diverse parents, which is a crucial factor that determines the success of any hybridization programme.

Yield is a quantitative character controlled by polygenes and it is the result of combined effect of several component characters and environment. Correlation coefficients measure the magnitude and direction of association among characters. Knowledge of interaction among the characters and with environment in plant breeding is very essential to determine the extent and nature of relationship between yield and yield components.

Path analysis is a biometrical technique developed by Wright (1921) and subsequently extended for crop experiments by Dewey and Lu (1959). It

is simply a standardized partial regression analysis based on cause and effect relationship, which serves to analyze by subdividing the correlations.

Considering the above facts, the present investigation which involved 60 exotic germplasm accessions and 4 cultivated varieties (checks) of safflower was undertaken to elicit information with the following objectives:

1. Morphological characterization using descriptor guidelines developed by IPGRI.
2. To estimate genetic variability and divergence in the experimental material.
3. To study the association of characters with yield and among themselves through correlation studies.
4. To estimate the direct and indirect effects of component characters on yield by path analysis.

## **CHAPTER II**

### **REVIEW OF LITERATURE**

Exploitation of genetic diversity for crop improvement should be the ultimate objective of exploration and conservation of genetic resources. While it is important to ensure that plant genetic resources are adequately safeguarded for future generations, they simply cannot be placed in a gene bank and forgotten. The vital stages of evaluation and incorporation of valuable characters such as disease resistance or tolerance to environmental stress factors into new varieties are the justifications of genetic resources activities. The ultimate value of genetic resources depends to a considerable extent upon the ease with which a plant breeder can utilize them.

Development of improved genotypes is a continuous process and primary aim of a plant breeder. For a successful plant breeding programme, variability is the basic requirement for future genetic improvement in any crop. The estimates of different genetic parameters are important for a better understanding of the nature and magnitude of genetic variability available in the breeding material along with the association of different yield and quality attributing characters.

The literature pertaining to the present study is reviewed under the following headings.

- 1) Variability
- 2) Genetic divergence studies
- 3) Correlation studies
- 4) Path coefficient analysis

## **2.1 VARIABILITY**

Ashri *et al.* (1974) studied a collection of 903 varieties of sunflower for mean yield per plant and the three major yield components *viz.*, number of heads per plant, number of seeds per head and seed weight. Their studies revealed marked differences in the potential of lines from different origin. Due to mutual compensation of the yield components, the differences in yield were not as marked as they were for the components. The collection contained abundance of genetic variability, which was available for breeding higher yielding safflower varieties. There were regional differences in the components due to human and/or natural selection.

Abel (1976) conducted several tests involving seven cultivars. Variance components were usually significant for plant height, heads per plant and seed weight. Variance was found to be non-significant for head diameter and seeds per head.

Mathur *et al.* (1976) evaluated 15 varieties of safflower and found that the characters such as seeds per head, seed yield, heads per plant and head diameter showed a high genetic coefficient of variation.

Ghanavati and Knowles (1977) identified plants with a long rosette period in one of the local populations of safflower from northwestern Iran. Fifty one lines developed from these plants showed considerable variation in winter hardiness, seed yield, oil content, oil yield per hectare, number of heads per plant and 1000 seed weight.

Makne *et al.* (1979) selected 71 types from 1200 indigenous and exotic germplasm lines of safflower. The height, number of capitula per plant, number of seeds per capitulum, capitulum size, number of bracts per capitulum and 1000 seed weight had shown low genotypic coefficient of variability and they also showed little differences between genotypic and phenotypic coefficient of variation indicating that these characters responded less to environmental factors.

Sengupta and Bhattacharya (1979) evaluated one hundred and thirty seven accessions of safflower germplasm. The maximum variability was observed in yield per plant and capitula per plant but a study of variance present in these two characters as against plant height at maturity presented a different picture. The variance present in the latter mentioned character was observed to be maximum for both GCV and PCV among all the characters studied.

Deokar *et al.* (1985) evaluated thirty-eight indigenous and exotic varieties at Solapur in *rabi*, 1981. The estimated data of genotypic and phenotypic variances were found to be high in cases of plant height and phenotypic variances were found to high in case of plant height, number of capsules per plant and yield per plant indicating wide variability.

Mallesappa *et al.* (1990) studied F<sub>3</sub> population in Indian x Indian (S144 x A1) and Indian x Exotic (S144 x G1157) combinations. Nine quantitative characters were studied on 750 random plants in each cross. Yield per capitulum showed maximum phenotypic and genotypic coefficient of variation followed by total capitula per plant and seed yield per plant in cross S144 x A1. However, in S144 x G1157, the highest coefficient of variation both at phenotypic and genotypic levels were observed for height of branching followed by yield per capitulum.

Pandya *et al.* (1996) evaluated 66 genotypes of safflower to assess genetic variance, coefficient of variance and broad sense heritability. Genetic coefficient of variation was highest for seed yield per plant followed by number of capitula per plant, 100 seed weight and number of secondary branches per plant.

In a study comprising of 150 germplasm lines and 5 released check varieties Patil (1998) reported that difference between values of GCV and PCV for number of effective capitula per plant, seed yield per plant, number of primary branches per plant and number of secondary branches per plant was

more as compared to days to maturity, days to flowering and 100 seed weight suggesting that the later traits were less influenced by environment and these could be improved by following phenotypic selection.

Chowdary *et al.* (1999) evaluated 60 diverse safflower genotypes for assessing the variability in seven agronomic characters. Hundred seed weight and seed yield per plant recorded higher estimates with respect to genetic coefficient of variation and high heritability and they offered greater scope of selection for improvement of safflower.

Mane *et al.* (1999) reported that among 9 yield components studied in safflower, the highest phenotypic coefficient of variation was recorded for number of seeds per capitula followed by number of secondary branches.

Senapati *et al.* (1999) carried out studies on variability in seventeen safflower varieties including two checks (A-1 and CO-1). All the traits except days to maturity and branches per plant showed wide variability. Phenotypic and genotypic variances were maximum in seed volume and minimum in biological yield. The phenotypic coefficient of variation had higher estimates than genotypic coefficient of variation. Number of capitula per plant and days to maturity showed the highest and lowest PCV respectively and the same trend was observed in GCV. The minor difference between PCV and GCV for biological yield, 100 seed weight and days to maturity indicated that the variability was primarily due to genotypic differences. The least PCV and

GCV for days to 50 per cent flowering and maturity indicated less scope for selection.

Kavani *et al.* (2000) studied 35 genotypes of safflower under 4 diverse environments. Pooled analysis revealed presence of high GCV for seed yield/plant and number of seeds per capitulum in all environments. Moderate coefficients of variation were recorded for number of primary branches per plant, number of capitula per plant and harvest index.

Johnson *et al.* (2001) evaluated USDA safflower core collection consisting of 207 accessions. A significant variation among accessions was observed for all the quantitative factors *viz.*, OIB width, OIB length, days to 50 per cent flowering, plant height, weight per seed and yield per plant. The variability was maximum for plant height and minimum for yield per plant.

Reddi *et al.* (2003) reported that phenotypic and genotypic coefficient of variations were high for seed yield/plant, number of primary and secondary branches per plant and number of capitula per plant and moderate for test weight and oil content.

Venkata Gopinath (2003) evaluated 40 genotypes of safflower and reported high estimates of phenotypic and genotypic coefficient of variations for oil yield/plant and seed yield/plant and observed low variability estimates for days to 50% flowering and oil content.

## 2.2 GENETIC DIVERGENCE

Ranga Rao *et al.* (1980) studied germplasm collections of safflower involving 30 genotypes. Based on 14 characters, the entire collection formed 14 constellations in stress and 13 in non-stress environments. The composition of clusters and their cultural associations remained more or less stable in both stress and non-stress conditions. Various characters such as height of branching from ground level, size and number of capitula, seed number and weight, yield per plant and hulling per cent exerted marked influence on genetic diversity both at inter and intra cluster levels.

Agarwal *et al.* (1982) conducted an experiment with fifty lines of safflower germplasm, which were subjected to  $D^2$  analysis for quantifying degree of divergence and to assess the relative contribution of yield and yield components towards total variability. Their results suggested that the selection of lines was associated with diverse clusters and different characters contributing maximum towards total genetic divergence such as plant height, number of seeds per capitulum and oil content would be more effective in the available materials of safflower for recombination breeding.

Patil *et al.* (1984) conducted studies on 40 cultivars of safflower on eight characters using Mahalanobis  $D^2$  statistic and clustered the genotypes into nine clusters. The clustering pattern revealed that genetic divergence was not necessarily associated with geographical diversity. The characters 1000-

seed weight and oil content contributed maximum while seed number per capitulum contributed least to the genetic divergence.

Subbalakshmi and Shiva Subramanian (1986) evaluated 28 genotypes of safflower under rainfed and irrigated conditions. The  $D^2$  analysis revealed that the genotypes are grouped into nine and thirteen clusters under rainfed and irrigated conditions, respectively. There was some amount of parallelism in the genotypes not only in the clustering pattern but also in the distance between the clusters. The characters *viz.*, number of branches and number of heads per plant were the main contributing factors for yield.

Patel *et al.* (1989) showed that plant height, seed yield, branching height, and 1000 seed weight accounted for 80% of the diversity through Mahalanobis  $D^2$  analysis in a population of 60 representative genotypes (including 26 from India and 30 from other countries). The 14 clusters formed were not associated with geographical regions indicating that geographical isolation may not be the only factor causing genetic diversity.

Mandal and Banerjee (1991) studied genetic divergence in a population of 50 genotypes of safflower collected from diverse sources. Mahalanobis  $D^2$  analysis indicated the existence of substantial genetic diversity for components of the material between and within geographic regions. The strains were grouped into nine different clusters. Oil content, width of outer involucre bract (OIB), hundred-seed weight and seed yield per plant contributed to total divergence.

Patil *et al.* (1991) conducted an experiment with thirty safflower genotypes, which were grouped into fifteen clusters based on Mahalanobis  $D^2$  statistics. The canonical analysis indicated that plant height, days to flowering, number of seeds per capitulum and 100 seed weight were important source of variation. The clustering pattern revealed that geographic diversity did not necessarily represent the genetic diversity in the population.

Dingming *et al.* (1993) gave principal component analysis and cluster analysis of 21 agronomic characters of 30 safflower cultivars. Their analysis revealed that number of first effective branch, main stem diameter, diameter of main capitulum, 1000 seed weight, oil content and angle of the primary branch were the six principal components of genetic divergence.

Ghongade and Navale (1995) studied the genetic divergence for eleven characters among 41 strains of safflower representing different geographical areas by Mahalanobis  $D^2$  statistics. Their results showed that there was substantial genetic diversity. The forty-one strains were grouped into thirteen clusters. The clustering pattern was associated with geographical diversity. Among the plant attributes, number of capitula per plant, number of seeds per capitulum, number of primary and secondary branches per plant and seed yield per plant were found to be important in selection of parents.

Venkata Gopinath (2003) assessed genetic divergence among 40 genotypes of safflower by Mahalanobis  $D^2$  analysis. The pattern of distribution of genotypes in various clusters revealed no relationship between geographical

distribution and genetic diversity. Hull content contributed maximum towards genetic divergence followed by number of seeds in main capitulum.

### **2.3 CORRELATION STUDIES**

Ashri *et al.* (1974) evaluated 903 germplasm lines of safflower. A multiple stepwise regression analysis showed that the most important yield component was the number of heads per plant. The number of seeds per head was of little importance. Seed weight had no effect on yield per plant. The number of heads per plant had negative but negligible correlation with oil content. Yield per plant was not correlated with season length or oil content.

Mathur *et al.* (1976) evaluated 15 varieties of safflower, which were well adapted under local conditions and were of Indian origin. They found that seed yield per plot showed significant positive association with plant height, head diameter and seeds per head whereas it had negative significant associations with number of capitula per plant.

Makne *et al.* (1979) selected 71 types from 1200 indigenous and exotic germplasm lines of safflower. Plant height, number of capitula per plant, number of seeds per capitulum, capitulum size and 1000 seed weight exhibited positive and significant correlation with yield at genotypic level. However, yield was negatively correlated with the number of branches per plant and bracts per capitulum. A strong positive and significant correlation at genotypic level was observed for number of capitula, indicating its close association with yield.

Sengupta and Bhattacharya (1979) evaluated 137 genotypes of safflower. Correlation studies revealed that plant height, number of capitula per plant, number of primary branches per plant and number of secondary branches had positive correlation with seed yield.

Sangale *et al.* (1982) evaluated 14 promising varieties of safflower for correlation studies. He observed that relationship between 1000 seed weight and hulling content was significant and positive indicating that the hulling of seed increased with the increase in weight of the seed. Further, he observed that hulling was not important for oil production as significant negative association was observed between these two traits.

Mallesappa *et al.* (1989) evaluated fifty  $F_4$  progenies in replicated trials. The correlation coefficients suggested that total number of capitula per plant exhibited significant positive association with yield. Other characters, which had strong positive association with yield, were yield per capitulum and number of primary branches. Negative correlation between yield and height of branching indicated that increase in height of branching reduced the number of primary branches, which in turn reduced the yield through total number of capitula per plant.

Mallesappa *et al.* (1990) studied  $F_3$  population in Indian x Indian (S144 x A1) and Indian x Exotic (S144 x G1157) combinations. Nine quantitative characters were studied on 750 random plants in each cross. Total capitula per plant exhibited significant positive association with yield both at

phenotypic and genotypic levels in S144 x A1 and in S144 x G1157 crosses followed by 100 seed weight and yield per capitulum. Among component traits, height of branching was negatively correlated with number of primary branches and total capitula. Number of primary branches had strong association with total number of capitula per plant.

Patil *et al.* (1990) evaluated 30 genotypes of safflower. Days to 50 per cent flowering showed negative significant association while number of capitula per plant showed positive significant correlation with yield per plant at phenotypic level. At genotypic level, days to 50 per cent flowering and oil content recorded significant and negative association with yield per plant. Hundred seed weight showed positive and significant genotypic correlation with yield per plant.

Lakha *et al.* (1992) evaluated 22 safflower selections from F<sub>4</sub> generation for character association towards yield. Genotypic and phenotypic correlations indicated that seed yield was significantly and positively associated with plant height, number of secondary branches, number of capitula per plant and hundred seed weight.

Ghongade *et al.* (1993) evaluated forty-one safflower genotypes to study the associations and path effects. Seed yield per plant was positively correlated with number of primary and secondary capitulum at both phenotypic and genotypic levels. Yield was negatively correlated with days to 50 per cent flowering at both phenotypic and genotypic levels.

Prasad *et al.* (1993) evaluated two sets of 56 hybrid lines of safflower involving high oil testers and early maturing testers. In the set involving high oil testers exhibited significant positive association of seed yield with number of capitula was recorded and strong positive association of number of primary branches with number of capitula was also recorded. They reported significant positive correlation between seed yield and number of seed per capitulum and strong positive association of number of primary branches with number of capitula per plant in the set involving early maturing testers.

Singh *et al.* (1993) carried out character studies for eight parents and 15 F<sub>1</sub> progenies. The studies revealed that seed yield per plant had significant positive correlation with number of days to maturity and plant height.

In correlation studies involving 28 safflower hybrids conducted over two years Prasad *et al.* (1994) reported significant and positive association between number of primary branches and number of primary capitula and between plant height and number of seeds per capitulum over both years. Number of seeds per capitula had strong negative association with 100-seed weight. Seed yield per plant over two years showed considerable influence of environment with regard to association with component traits.

Patil (1997) conducted a study with 155 genotypes of safflower observed a positive association among the characters number of primary branches/plant, number of secondary branches/plant, number of capitula/plant,

and 100 seed weight, and they were positively associated with seed yield/plant and suggested that due emphasis be given to these characters.

Patil (1998) evaluated 150 germplasm collections and five released check varieties. The study revealed a strong positive genotypic association of yield with 100 seed weight, number of capitula per plant, number of primary branches per plant, number of secondary branches per plant and number of seeds per capitulum. The traits *viz.*, days to 50 per cent flowering and days to maturity were negatively associated with seed yield indicating that early flowering and early maturing safflower genotypes would give more yield.

Sharma *et al.* (1998) evaluated 32 genotypes of safflower to study the relationship among 10 quantitative traits. Their studies revealed strong positive and significant phenotypic correlation of seed yield with number of seeds per capitulum and 100 seed weight. Values of genotypic correlations for most of the character combinations were higher than the phenotypic correlation values.

Senapati *et al.* (1999) studied character association in 17 genotypes including two checks of safflower with number of capitula per plant and biological yield. Plant height, branches per plant and 100 seed weight showed positive correlation with yield whereas hulling content exhibited negative correlation.

Kubsad *et al.* (2000) estimated correlation coefficients for 9 traits viz. plant height, branches per plant, capitula per plant, seeds per main capitulum, diameter of main capitulum, 100-seed weight, hull content, dry matter per plant and seed yield in safflower cv. A-1. The highest association (0.41) was observed between seed yield and 100-seed weight.

Omidi Tabrizi (2000) evaluated 100 safflower genotypes to study the correlation of seed and oil yield with their components. For most of the characters, genotypic correlation coefficients were higher than phenotypic correlation coefficient. There was high significant positive correlation of biomass and number of heads per plant with seed yield. There was a negative correlation between seed hulling and oil content.

Bagheri *et al.* (2001) studied correlation effects of other traits on seed yield using 121 genotypes using Simple Lattice design in Tehran University. Yield was highly and positively correlated to capsule diameter, days to the first flowering, number of seeds per capsule, number of capsules per plant and seed weight of a capsule. Correlation between 1000 seed weight and seed oil content was negative.

Johnson *et al.* (2001) evaluated USDA safflower core collection consisting of 207 accessions. Significant correlation coefficients were observed between several quantitative traits. Days to 50 per cent flowering and plant height were the most strongly correlated traits and days to flowering were also correlated with head diameter and weight per seed. Higher weight

per seed was also associated with lower plant height and with wider and longer OIB. Yield was positively correlated with weight per seed and also with plant height.

Mallesappa *et al* (2003) observed that number of capitula and test weight showed a strong positive association with seed yield and reported that the characters viz. number of capitula, number of seeds and test weight were reliable components influencing seed yield directly.

Venkata Gopinath (2003) reported significant positive association of hull content, number of seeds in main capitulum and diameter of main capitulum with seed yield and negative association between days to 50% flowering and seed yield.

#### **2.4 PATH COEFFICIENT ANALYSIS**

Mathur *et al.* (1976) evaluated 15 varieties of safflower, which were well adapted under local conditions and were of Indian origin. Path coefficient analysis was done to estimate the direct and indirect effects of all components except days to bloom, which did not have significant correlation coefficient with any of the characters other than plant height. It was observed that head diameter had the highest direct effect on seed yield followed by seed weight. Plant height and seeds per head, which showed significantly positive association with seed yield, had negative direct effect. The direct effect of primary branches was negative but low in magnitude.

Malleshappa *et al.* (1989) evaluated forty F<sub>4</sub> progenies by path analysis studies. The results revealed high direct effect of total capitula per plant, which was strongly associated with seed yield. Other traits having greater direct contribution to yield were yield per capitulum and plant height.

Patil *et al.* (1990) evaluated 30 genotypes of safflower. Path analysis revealed that weight of capitulum per plant exhibited highest direct contribution towards yield per plant. Weight of capitulum per plant and weight of seeds per capitulum showed a marked indirect positive effect on yield per plant.

Ghongade *et al.* (1993) evaluated forty-one safflower genotypes to study the path effects. The results revealed high direct effect of capitula per plant, which was strongly associated with seed yield indicating the existence of true and perfect relationship among these characters. The characters, seeds per primary and secondary capitulum were the other traits directly contributing to yield per plant. The characters *viz.*, number of primary branches per plant and number of seeds per main capitulum had a negative direct effect on the seed yield but recorded a significant correlation with seed yield.

Prasad *et al.* (1993) evaluated two sets of 56 hybrid lines of safflower involving high oil testers and early maturing testers. Number of primary branches had negative direct contribution to seed yield. In the set involving high oil testers, the direct effect of number of capitula was negative in accordance with its association with seed yield. In the set involving early

maturing testers, number of seeds per capitulum had high direct contribution to seed yield. The direct effect was higher than its correlation with seed yield. This may be attributed to negative effect of number of seeds per capitulum via seed weight. Number of primary branches recorded a direct positive effect with seed yield. The direct effect of number of capitula in set II was negative and in accordance with correlation values. The direct effect of seed weight with seed yield was high and positive.

Zheng *et al.* (1993) studied nine safflower cultivars by means of path analysis for correlated characters on seed yield. Their results indicated that flowering period, number of capitula per plant, average number of capitula per plant, seed weight per capitulum, number of ineffective branches per plant, effective number of capitula per plant, height of the plant and height of branching affected yield directly and significantly in descending order of magnitude.

In path analysis involving 28 safflower hybrids conducted over two years, Patil *et al.* (1994) revealed 100 seed weight exhibited a higher positive direct effect in first year as compared to second year. Moreover, the indirect effect of 100 seed weight with number of seeds per capitulum was negative and considerable. The indirect effects of number of capitula per plant via number of primary branches exhibited considerable contribution towards seed yield in second year. Plant height also had a considerable indirect contribution towards seed yield via number of seeds per capitulum in both the years.

Patil (1998) evaluated 150 germplasm collections and evaluated them for selecting high yield genotypes. Path analysis revealed that maximum direct effect on seed yield was shown by 100 seed weight and it was followed by number of capitula per plant, number of branches per plant, number of secondary branches per plant and number of seeds per capitulum. However, it was moderate for plant height. The seed yield was negatively associated with days to flowering and days to maturity and their direct influence was also negative.

Kubsad *et al.* (2000) estimated path coefficients for 9 traits viz. plant height, branches per plant, capitula per plant, seeds per main capitulum, diameter of main capitulum, 100-seed weight, hull content, dry matter per plant and seed yield in safflower cv. A-1. Dry matter per plant had maximum contribution (0.457) towards seed yield, and was closely followed by seeds per main capitulum (0.421)

Omidi Tabrizi (2000) evaluated 100 safflower genotypes to study seed and oil yield with their components through path analysis. The results of the analysis revealed that the increase of oil yield was primarily associated with the increase of seed yield, which was in turn affected, by biomass and number of heads per plant.

Bagheri *et al.* (2001) studied direct and indirect effects of other traits on seed yield using 121 genotypes using Simple Lattice design in Tehran University. Number of capsules per plant, had the highest direct effect on yield and exerted a large indirect effect by increasing seed weight of a capsule.

Venkata Gopinath (2003) reported that hull content and number of seeds in main capitulum had a maximum direct effect on seed yield followed by number of effective capitula/plant and 100 seed weight.

## CHAPTER III

### MATERIALS AND METHODS

The details of the experimental material used and the statistical techniques adopted during the investigation were as follows

#### 3.1 MATERIALS

The experimental material consisted of 60 exotic germplasm accessions and 4 cultivated check varieties of safflower obtained from Safflower Germplasm Management Unit (GMU) of the Directorate of Oilseeds Research, Rajendranagar, Hyderabad. Details of the germplasm accessions and the checks are furnished below in Table – 1.

**Table 1 -Details of the experimental material included for the study**

S. No.	GMU No.	Accession No.	Country of origin
1.	950	EC - 181149	Ethiopia
2.	1197	EC - 181446	Israel
3.	1250	EC - 181513	Israel
4.	1251	EC - 181515	Israel
5.	1281	EC - 181556	Pakistan
6.	1306	EC - 181583	Israel
7.	1383	EC - 181667	Hungary
8.	1386	EC - 181670	Israel
9.	1394	EC - 181680	Ethiopia
10.	1790	EC - 182226	Turkey
11.	1791	EC - 182228	Turkey
12.	1792	EC - 182229	Turkey
13.	1794	EC - 182231	Turkey
14.	1796	EC - 182234	Turkey
15.	1797	EC - 182235	Turkey
16.	1805	EC – 182247	Pakistan
17.	1815	EC - 201459	USA

<b>S. No.</b>	<b>GMU No.</b>	<b>Accession No.</b>	<b>Country of origin</b>
18.	1988	EC - 210520	USA
19.	2001	EC - 210533	USA
20.	2007	EC - 210539	USA
21.	2010	EC - 337894	China
22.	2039	EC - 337989	China
23.	2040	EC - 338040	China
24.	3120	EC - 283046	Pakistan
25.	3121	EC - 283047	Pakistan
26.	3152	EC - 159676	USA
27.	4045	EC - 303239	Egypt
28.	4050	EC - 303244	Egypt
29.	4063	EC - 303260	Egypt
30.	4068	EC - 303265	Afghanistan
31.	4073	EC - 303272	Afghanistan
32.	4078	EC - 303278	Egypt
33.	4083	EC - 303283	Egypt
34.	4087	EC - 303529	Egypt
35.	4092	EC - 303534	Canada
36.	4094	EC - 303713	Ethiopia
37.	4096	EC - 303715	Ethiopia
38.	4098	EC - 303717	Ethiopia
39.	4119	EC - 338553	China
40.	4361	S - 24	Mexico
41.	4388	S - 129	Mexico
42.	4389	S - 131	Mexico
43.	4390	S - 138	Mexico
44.	4391	S - 141	Mexico
45.	4392	S - 144	Mexico
46.	4393	S - 146	Mexico
47.	4799	JLA - 1243	Pakistan
48.	4800	JLA - 1244	Pakistan
49.	4859	JLA - 1444	Afghanistan
50.	4860	JLA - 1446	Afghanistan
51.	4863	JLA - 1454	Afghanistan
52.	5122	EC - 177188	Canada
53.	5125	EC - 177192 - A	Canada
54.	5121	EC - 177186	Canada
55.	5129	EC - 1771196	Canada
56.	5131	PI - 2447	USA
57.	5132	PI - 199915	USA
58.	5133	PI - 253912	Afghanistan
59.	5151	EC - 337127	China
60.	5389	EC - 337455	China
<b>CHECK VARIETIES</b>			
61.	A-1		India
62.	Bhima		India
63.	Manjira		India
64.	NARI - 6		India

### **3.2 METHODS.**

The experiment was carried out during *rabi* 2003-04. The experimental material was sown in Simple Lattice (8x8) design with 2 replications at College Farm, College of Agriculture, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad. Each genotype was sown in 3 rows of 2m length with a spacing of 45x 20cm. Two to three seeds were sown per hill. Thinning and gap filling was done 2 weeks after sowing. Recommended agronomic practices and prophylactic measures were adopted for raising a good crop.

### **3.3 OBSERVATIONS RECORDED**

Five open pollinated plants of each genotype in each replication were randomly selected for collection of data on the following characters.

#### **3.3.1 MORPHOLOGICAL CHARACTERS.**

##### **3.3.1.1 Growth habit**

- a) Erect
- b) Bushy

##### **3.3.1.2 Location of Primary branches on Main axis**

- a) Predominantly basal
- b) Predominantly on the upper 1/3<sup>rd</sup> of the plant
- c) Predominantly on the upper 2/3<sup>rd</sup> of the plant
- d) Base to apex.

**3.3.1.3 Angle of Primary Branches on Main Axis.**

- a) Appressed –  $15^{\circ}$  to  $25^{\circ}$
- b) Semi-appressed –  $26^{\circ}$  to  $30^{\circ}$
- c) Normal –  $31^{\circ}$  to  $60^{\circ}$

**3.3.1.4 Leaf shape of upper stem leaves**

- a) Fusiform
- b) Elliptical
- c) Obovate

**3.3.1.5 Leaf margin of upper stem leaves**

- a) Entire
- b) Serrate
- c) Deeply serrate
- d) Lobed

**3.3.1.6 Flower colour at full bloom**

- a) Yellow
- b) Orange
- c) Pale yellow

**3.3.1.7 Flower colour at fading stage**

- a) Pinkish white
- b) Golden yellow
- c) Orange red
- d) Red

### **3.3.1.8 Shape of main capitulum**

- a) Conical
- b) Flattened

### **3.3.1.9 Presence of spines on outer involucre bract (OIB)**

- a) None
- b) Few
- c) Intermediate

## **3.3.2 QUANTITATIVE CHARACTERS.**

### **3.3.2.1 Days to 50 per cent flowering**

This character was recorded as the number of days taken from the sowing date to the day on which 50 per cent of the flowers opened.

### **3.3.2.2 Plant height (cm)**

Height of fully matured plants was recorded from the base of the stem to primary/main capitulum in centimeters.

### **3.3.2.3 Number of effective capitula**

Number of effective capitula put forth by the plant at maturity were counted.

### **3.3.2.4 Diameter of main capitulum (mm)**

Diameter of main capitulum was measured in millimeters with a digital vernier caliper at maturity.

### **3.3.2.5 Number of filled seeds.**

The number of completely filled seeds present in main capitulum were counted at maturity.

### 3.3.2.6 Weight of 100 seeds (g)

The weight of 100 seeds was recorded with the help of an electronic top pan balance in grams.

### 3.3.2.7 Oil content (%)

Oil content in the seeds was assessed employing Nuclear Magnetic Resonance (NMR) spectroscopy technique and expressed in per cent.

### 3.3.2.8 Seed yield per plant (g)

Total weight of the seeds from each plant was recorded in grams with the help of electronic top pan balance.

## 3.4 STATISTICAL ANALYSIS

The data recorded was subjected to the following statistical analysis

### 3.4.1 ANALYSIS OF VARIANCE

Difference between genotypes for various characters were tested for significance by using analysis of variance technique as suggested by Panse and Sukhatme (1957)

Source	d.f	SS	MSS	F value
Replication	$r-1$			
Treatments	$p^2-1$			
Blocks within Replication	$[r(p-1)]$			
Error	*			
Total	$(rp^2-1)$			

\* - By Subtraction

r = number of replications

p = square root of total treatments

### 3.4.2 Variance

The phenotypic and genotypic variance were calculated as per the formula suggested by Burton and Devane (1953)

$$\text{Genotypic variance } (\sigma^2g) = \frac{\text{MSS due to treatment (Mt)} - \text{MSS due to error (Me)}}{\text{No. of replications (r)}}$$

$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + \sigma^2e$$

$$\sigma^2e = \text{error variance}$$

Phenotypic (PCV) and Genotypic (GCV) coefficient of variation was calculated by the formula given by Burton (1952)

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation } (\sigma p)}{\text{General mean (x)}} \times 100$$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation } (\sigma g)}{\text{General mean (x)}} \times 100$$

### 3.4.3 Genetic diversity

After testing the differences between genotypes for each of the character, a simultaneous test of significance of difference between the mean values of a number of correlated variables was done by using 'V' statistic, which in turn utilizes Wilk's criterion (Wilk, 1932). The sum of squares and sum of products of error and error + genotypes were used for this purpose. The estimation of  $\Lambda$  (Wilk's criterion) was done by using the following relationship:

$$\Lambda = W/s$$

Where,  $\Lambda$  = Wilk's criterion  
W = Determinant of error matrix  
s = Determinant of (error + genotype) sum of squares and sum of product matrix

The genetic diversity in 64 genotypes for characters was estimated using Mahalanobis's (1936)  $D^2$  statistic technique. The  $D^2$  value between  $i^{\text{th}}$  and  $j^{\text{th}}$  genotypes for P character was calculated as follows:

$$D_{ij}^2 = P_t = \sum (y_{it} - y_{jt})^2$$

Where,

$$D_{ij}^2 = D^2 \text{ between } i^{\text{th}} \text{ and } j^{\text{th}} \text{ genotypes}$$

$y_{it}$  = uncorrelated mean value of the  $i^{\text{th}}$  genotype for 't' character

$y_{jt}$  = uncorrelated mean value of the  $j^{\text{th}}$  genotype for 't' character

The various types involved in estimation of  $D^2$  values are given below:

$$V(\text{stat}) = -mg \log_e \Lambda'$$

Where,

$$m = n - (P+Q+1)/2$$

$$P = \text{Number of characters or variable observations}$$

$$Q = \text{Number of genotypes-1 (or degree of freedom for population)}$$

$$n = \text{degree of freedom for error + genotypes at base of natural log i.e., 2.7183}$$

$$‘V’ \text{ (stat)} = \text{is distributed as } \chi^2 \text{ with PQ degrees of freedom}$$

#### **3.4.3.1 Transformation of correlated variables**

Computation of  $D^2$  values was reduced to simple summation of differences in mean values of various characters of the two genotypes i.e.,  $D_i^2$ . Therefore, the transformation of correlated variables to uncorrelated ones was done before working out the  $D^2$  values. Transformation was done by using pivotal condensation mean.

#### **3.4.3.2 Computation of $D^2$ values**

For a given combination of i and j genotypes, the mean deviation i.e.,  $y_{it} - y_{jt}$  for  $t = 1, 2, \dots, P$  variables are computed and the  $D^2$  values were calculated as sum of squares of the deviation i.e.,

$$P_{et} = \sum (Y_{ie} - Y_{je})^2$$

### 3.4.3.3 Testing the significance of $D^2$ values:

The  $D^2$  values obtained for a pair of genotypes as the calculated value of  $\chi^2$  and were tested against tabulated value of  $\chi^2$  at 'P' degrees of freedom. Where "P" is the number of variables or characters considered.

### 3.4.3.4 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of its contribution towards divergence between two entries ( $d_i = y_{it} - y_{jt}$ ). Rank-I was given to the highest mean difference and rank-P to the lowest differences. P is the total number of characters considered. The number of cases where a particular character ranked first was counted and the proportion of this to the total number of combinations expressed in percentage had quantified the contribution of character to the overall genetic divergence between the genotypes:

$$X = \frac{N \times 100}{M}$$

Where,

X = Per cent contribution of character

N = Number of genotype combinations where the character ranked first

M = All possible combinations of the genotypes considered

#### **3.4.3.5 Clustering of genotypes into various clusters**

Clustering of genotypes into different clusters was done by using Euclidean method. The criterion used in clustering by this method was that any two genotypes belonging to the same cluster should at least on an average show a smaller  $D^2$  value among themselves than those belonging to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose,  $D^2$  values of all the combinations in each genotype were arranged in the increasing order of their magnitude as described by Singh and Chaudhary (1977). To start with two genotypes having the smallest distance from each other was considered first to which third population having the smallest average  $D^2$  value from the first two genotypes and so on. At certain stage when it was felt that after adding a particular variety there was a disrupt increase in the average  $D^2$  value, then that genotype was not considered for inclusion in that cluster. Similarly, a second cluster was formed. Thus, the process was continued till all the genotypes were included in one or the other cluster.

#### **3.4.3.6 Intra and inter cluster distances**

Based on  $D^2$  values, average intra and inter cluster distances were calculated as per Euclidean method.

### 3.4.3.7 Average intra cluster distance

For the measurement of intra cluster distances, the formula used was  $ED^2_i/n$  where,  $D^2_i$  was the sum of distance between all possible combinations and 'n' is number of the genotypes included in a cluster.

### 3.4.3.8 Average inter cluster distance

Cluster is taken one by one and their distances from other clusters were calculated. The distance between the two clusters was calculated as the sum of  $D^2$  value between the numbers of one cluster to each of the members of other clusters divided by the product of number of genotypes in both clusters under consideration. The square root of the average  $D^2$  value gave the genetic distance 'D' between the clusters.

### 3.4.4. Phenotypic correlation

The phenotypic correlation coefficients were calculated by working out the variance components for each character and the covariance components for each pair of characters using the formula suggested by Al-jibouri *et al.* (1979).

$$\text{Phenotypic correlation (rp)} = \frac{\text{Cov. (X}_p, \text{Y}_p)}{\sigma X_p \sigma Y_p}$$

Where,

$\sigma X_p$  = phenotypic standard deviation of character X

$\sigma Y_p$  = phenotypic standard deviation of character Y

$$\text{Phenotypic covariance} = \frac{\text{Phenotypic covariance} - \text{Error covariance}}{\text{Number of replications}}$$

To test the significance of the correlation coefficients at the genotypic levels, the estimated values were compared with the table values of correlation coefficients (Fisher and Yates, 1967) at 0.005 and 0.001 and probability level of significance with (n-2) degrees of freedom.

### 3.4.5 Path coefficient analysis

The direct and indirect effects at genotypic level for genotypes were estimated by taking seed yield as dependent variable, using path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959). The following equations were formed and solved simultaneously for estimating the various direct and indirect effects.

$$r_{1y} = P_{1y} r_{11} + P_{2y} r_{12} + P_{3y} r_{13} \dots \dots \dots + P_{ny} r_{1n}$$

$$r_{2y} = P_{1y} r_{21} + P_{2y} r_{22} + P_{3y} r_{23} \dots \dots \dots + P_{ny} r_{2n}$$

$$r_{ny} = P_{1y} r_{n1} + P_{2y} r_{n2} + P_{3y} r_{n3} \dots \dots \dots + P_{ny} r_{nn}$$

Where,

- 1, 2 . . . . . n = Independent variable
- y = Dependent variable (yield per plant)
- $r_{1y} r_{2y} \dots \dots \dots r_{ny}$  = coefficient of correlation between casual factors '1' to 'n' on dependent character 1
- $p_{1y} P_{2y} \dots \dots P_{ny}$  = Direct effect of characters 1 to n on character Y

The above equations can be written in matrix form as:

$$\begin{matrix}
 \mathbf{A} & & \mathbf{C} & & \mathbf{B} \\
 \left( \begin{array}{c} r_{1y} \\ r_{2y} \\ \vdots \\ r_{ny} \end{array} \right) & & \left( \begin{array}{cccc} 1 & r_{12} & r_{13} & \dots\dots r_{1n} \\ r_{21} & 1 & r_{23} & \dots\dots r_{2n} \\ \vdots & \vdots & \vdots & \\ \vdots & \vdots & \vdots & \\ r_{n1} & r_{n2} & r_{n3} & \dots\dots 1 \end{array} \right) & & \left( \begin{array}{c} p_{1y} \\ p_{2y} \\ \vdots \\ p_{ny} \end{array} \right)
 \end{matrix}$$

Then

$$\mathbf{B} = [\mathbf{C}]^{-1} \mathbf{A} \text{ where } \mathbf{C}^{-1} = \left( \begin{array}{cccc} c_{11} & c_{12} & c_{13} & \dots\dots c_{1n} \\ c_{21} & c_{22} & c_{23} & \dots\dots c_{2k} \\ \vdots & \vdots & \vdots & \\ \vdots & \vdots & \vdots & \\ c_{n1} & c_{n2} & c_{n3} & \dots\dots c_{nn} \end{array} \right)$$

Direct effects were as follows:

$$p_{1y} = \sum_{i=1}^k c_{1i} r_{iy}$$

$$p_{2y} = \sum_{i=1}^k c_{2i} r_{iy}$$

$$p_{ny} = \sum_{i=1}^k c_{nj} r_{iy}$$

Residual effect, which measures the contribution of characters not considered, was obtained as:

$$p_{ry} = \sqrt{1 - (p_{1y} r_{1y} + p_{2y} r_{2y} + \dots + p_{ny} r_{ny})}$$

Where,  $p_{ny}$  = Direct effect of  $x_n$  on Y  
 $r_{iy}$  = Correlation coefficient of  $x_n$  on y.

**Table 1 -Details of the experimental material included for the study**

---

<b>S. No.</b>	<b>GMU No.</b>	<b>Accession No.</b>	<b>Country of origin</b>
1.	950	EC - 181149	Ethiopia
2.	1197	EC - 181446	Israel
3.	1250	EC - 181513	Israel
4.	1251	EC - 181515	Israel
5.	1281	EC - 181556	Pakistan
6.	1306	EC - 181583	Israel
7.	1383	EC - 181667	Hungary
8.	1386	EC - 181670	Israel
9.	1394	EC - 181680	Ethiopia
10.	1790	EC - 182226	Turkey
11.	1791	EC - 182228	Turkey
12.	1792	EC - 182229	Turkey
13.	1794	EC - 182231	Turkey
14.	1796	EC - 182234	Turkey
15.	1797	EC - 182235	Turkey
16.	1805	EC - 182247	Pakistan
17.	1815	EC - 201459	USA
18.	1988	EC - 210520	USA
19.	2001	EC - 210533	USA
20.	2007	EC - 210539	USA
21.	2010	EC - 337894	China
22.	2039	EC - 337989	China
23.	2040	EC - 338040	China
24.	3120	EC - 283046	Pakistan
25.	3121	EC - 283047	Pakistan
26.	3152	EC - 159676	USA
27.	4045	EC - 303239	Egypt
28.	4050	EC - 303244	Egypt
29.	4063	EC - 303260	Egypt
30.	4068	EC - 303265	Afghanistan
31.	4073	EC - 303272	Afghanistan
32.	4078	EC - 303278	Egypt
33.	4083	EC - 303283	Egypt
34.	4087	EC - 303529	Egypt
35.	4092	EC - 303534	Canada
36.	4094	EC - 303713	Ethiopia
37.	4096	EC - 303715	Ethiopia
38.	4098	EC - 303717	Ethiopia

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<b>S. No.</b>	<b>GMU No.</b>	<b>Accession No.</b>	<b>Country of origin</b>
39.	4119	EC - 338553	China
40.	4361	S - 24	Mexico
41.	4388	S - 129	Mexico
42.	4389	S - 131	Mexico
43.	4390	S - 138	Mexico
44.	4391	S - 141	Mexico
45.	4392	S - 144	Mexico
46.	4393	S - 146	Mexico
47.	4799	JLA - 1243	Pakistan
48.	4800	JLA - 1244	Pakistan
49.	4859	JLA - 1444	Afghanistan
50.	4860	JLA - 1446	Afghanistan
51.	4863	JLA - 1454	Afghanistan
52.	5122	EC - 177188	Canada
53.	5125	EC - 177192 - A	Canada
54.	5121	EC - 177186	Canada
55.	5129	EC - 1771196	Canada
56.	5131	PI - 2447	USA
57.	5132	PI - 199915	USA
58.	5133	PI - 253912	Afghanistan
59.	5151	EC - 337127	China
60.	5389	EC - 337455	China
<b>CHECK VARIETIES</b>			
61.	A-1		India
62.	Bhima		India
63.	Manjira		India
64.	NARI - 6		India



## **CHAPTER IV**

### **RESULTS**

The experimental findings obtained from the present study on evaluation of 60 safflower germplasm lines along with the 4 check varieties for nine morphological characters and eight quantitative characters are presented below under following heads:

- i. Morphological characterization
- ii. Analysis of variance
- iii. Mean performance
- iv. Variability
- v. Genetic divergence
- vi. Correlation studies
- vii. Path coefficient analysis

#### **4.1 MORPHOLOGICAL CHARACTERIZATION**

60 safflower germplasm accessions along with 4 check varieties were characterized for their morphological characters using descriptor guidelines developed by IPGRI. These descriptors were unambiguous and easily identifiable. Characterization was done for each genotype to establish their diagnostic features.

The experimental material exhibited great variability for all of the morphological characters. (Table –2), (Plates - 1 to 6).

## **4.2 ANALYSIS OF VARIANCE**

ANOVA showed significant differences for all the traits evaluated. Significant replication difference was observed for Number of effective capitula per plant. Significant difference was observed in the blocks within replication for the character plant height. The results of ANOVA are presented in Table –3.

## **4.3 MEAN PERFORMANCE**

Mean performance for the 8 quantitative characters are presented in Table – 4.

### **4.3.1 Days to 50% flowering**

Number of days to 50% flowering ranged from 69.00 days (GMU 4388) to 89.00 (GMU 4063) days with a mean of 82.46 days. Thirty one genotypes flowered earlier when compared to grand mean (82.46) days.

#### **4.3.2. Plant height (cm)**

Plant height ranged from 53.50cm (GMU 4092) to 104.90cm (GMU 4045) with a mean of 71.53cm. Thirty two genotypes were found to be taller on comparison with grand mean (71.53cm).

#### **4.3.3 Number of effective capitula/plant**

Number of effective capitula/plant ranged from 8.30 (GMU 4083) to 27.40 (GMU 5151) with a mean value of 18.10. Thirty one genotypes had higher number of capitula when compared to grand mean (18.10).

#### **4.3.4 Diameter of main capitulum (mm)**

Diameter of main capitulum ranged from 15.30mm (GMU 4050) to 25.30mm (GMU 1815) with a mean value of 20.48mm. Thirty two genotypes had larger diameter of main capitulum on comparison with grand mean (20.48mm).

#### **4.3.5 Number of filled seeds in main capitulum**

Number of filled seeds in main capitulum ranged from 9.80 (GMU 4863) to 34.30 (GMU 1794) with a mean value of 21.25. Thirty one genotypes had more number of seeds when compared to grand mean (21.25).

#### **4.3.6 100 seed weight (g)**

100 seed weight ranged from 3.29g (GMU 4083) to 7.15g (Bhima) with a mean value of 5.31g. Thirty one genotypes had more 100 seed weight when compared to grand mean (5.31g).

#### **4.3.7 Oil content (%)**

Oil content ranged from 20.60 (GMU 4390) to 31.75 per cent (GMU 4045) with a mean value of 26.68 per cent. Thirty three genotypes had more oil content when compared to grand mean (26.68 per cent).

#### **4.3.8 Seed yield/plant (g).**

Seed yield/plant ranged from 3.96g (GMU 1805) to 35.80g (Bhima) with a mean value of 15.28g. Thirty genotypes had had recorded higher yields in comparison to grand mean (15.28g).

### **4.4 VARIABILITY**

Phenotypic and genotypic coefficients of variation for 8 characters are presented in Table-5. Among the 8 characters studied seed yield/plant (52.21%) recorded highest PCV, followed by number of filled seeds in main capitulum (29.38%) while lowest PCV was recorded by days to 50% flowering (4.56%). Highest GCV was recorded by seed yield/plant (49.96%) and the least GCV by days to 50% flowering (4.31%). However, the

difference between the PCV and GCV values were low indicating minimum effect of environment.

#### **4.5 GENETIC DIVERGENCE**

The quantitative assessment of genetic divergence was made by adopting Mahalanobis  $D^2$  statistic for yield and its contributing characters.

##### **4.5.1 TEST WITH WILK'S CRITERION**

The Wilk's criteria obtained were used in calculation of "V" statistic. The "V" statistic exhibited highly significant differences among the genotypes for the aggregate effect of all the characters indicating the existence of considerable genetic divergence in the experimental material.

##### **4.5.2 MAHALANOBIS GENERALIZED DISTANCE ( $D^2$ )**

In order to assess genetic divergence among 64 genotypes  $D^2$  statistic was carried out following the procedure given by Rao (1952). Since all the 8 variables were correlated, they were transformed into uncorrelated linear combination through Pivotal Condensation Method.

### 4.5.3 GROUPING OF GENOTYPES INTO VARIOUS CLUSTERS

64 genotypes were grouped into 9 clusters based on  $D^2$  values such that genotypes belonging to same cluster had on an average smaller  $D^2$  values than those belonging to different clusters. The distribution of 64 genotypes of safflower into different clusters is presented below in Table-6.

**Table 6 – Distribution of 64 genotypes of safflower in different clusters**

Cluster No.	No. of Genotypes	Genotypes/Check Varieties
I	20	GMU 950, 1197, 1251, 1281, 1386, 1791, 1796, 1797, 1805, 1988, 2007, 3121, 4083, 4094, 4119, 4361, 4390, 4391, 4859, 4860.
II	1	GMU 4388.
III	9	GMU 1306, 1394, 3152, 4092, 4393, 4799, 4800, 5133, 5389.
IV	6	GMU 1794, 1815, 3120, 4096, 4392, 5129.
V	8	GMU 1383, 2010, 2039, 2040, 4389, 5121, 5125, 5132.
VI	4	GMU 4050, 4863, 5131, A-1
VII	8	GMU 1250, 1790, 2001, 4087, 5122, 5151, Bhima, Manjira
VIII	5	GMU 1792, 4063, 4068, 4078, NARI-6
IX	3	GMU 4045, 4073, 4098.

### 4.5.4 CLUSTER MEANS OF THE CHARACTERS

The data on cluster means is presented in Table –7. From the data it was observed that considerable differences existed among the clusters. The cluster

mean for days to 50% flowering was highest in IX cluster (87.66) and least in cluster II (69.00). Cluster IX recorded the highest value (94.4) for plant height while cluster II had the least value (61.30) Cluster VII had the highest mean value for number of effective capitula/plant (23.43) while cluster IX recorded the least value (12.00). Highest diameter of main capitulum was recorded in IX cluster (23.08) whereas least was recorded in cluster III (17.68). Maximum number of filled seeds was recorded in cluster IV (29.66) whereas least was recorded in cluster VI (11.42). Maximum 100 seed weight was recorded in cluster VI (6.55) whereas least was recorded in cluster VIII (4.34). Highest oil content was recorded in cluster II (29.75) whereas lowest was recorded in cluster VI.

**Table 7 – Cluster means for eight characters of 64 safflower genotypes.**

<b>Cluster</b>	<b>Days to 50% flowering</b>	<b>Plant Height (cm)</b>	<b>No. of effective Capitula/plant</b>	<b>Diameter of main capitulum (mm)</b>	<b>No. of filled seeds in main capitulum</b>	<b>100 seed weight (g)</b>	<b>Oil content (%)</b>	<b>Seed yield per plant (g)</b>
<b>I</b>	79.57	68.82	16.66	20.66	22.71	5.25	26.41	11.83
<b>II</b>	69.00	61.30	17.30	21.35	19.45	5.50	29.75	15.75
<b>III</b>	83.33	65.17	21.11	17.68	16.63	5.25	26.00	12.96
<b>IV</b>	85.66	69.23	18.08	22.27	29.66	4.54	27.60	15.65
<b>V</b>	86.06	71.06	18.46	22.01	21.90	6.01	26.90	19.52
<b>VI</b>	81.25	75.32	15.90	18.61	11.42	6.55	25.68	14.62
<b>VII</b>	80.75	72.61	23.43	21.63	25.90	5.33	26.74	30.72
<b>VIII</b>	86.10	80.90	14.93	18.03	13.60	4.34	26.52	6.90
<b>IX</b>	87.66	94.40	12.00	23.08	20.91	5.45	28.50	6.69
<b>Mean</b>	82.46	71.53	18.10	20.48	21.25	5.31	26.68	15.28

(25.68). The cluster mean for seed yield was highest in cluster VII (30.72) and lowest in cluster IX (6.69)

#### **4.5.5 AVERAGE INTRA AND INTER CLUSTER DISTANCES**

The average Intra and Inter cluster  $D^2$  values are presented in Table – 8. Intra cluster values ranged from 0 (cluster II) to 58.76 (cluster VII).

From the Inter cluster distances it can be inferred that highest divergence occurred between cluster II and cluster IX (495.09) while it was least between cluster IV and V (56.35)

#### **4.5.6. RELATIVE CONTRIBUTION OF CHARACTERS TOWARDS DIVERGENCE**

The number of times that each of the 8 quantitative characters appeared in combination and its respective percent contribution towards diversity is presented in Table – 9.

Seed yield contributed maximum (29.96%) towards diversity followed by days to 50% flowering (22.17%), 100 seed weight (12.10%), plant height (11.90%), diameter of main capitulum (9.33%), number of effective

capitula/plant (6.70%), number of filled seeds in main capitulum (6.35)% and oil content (1.49%).

#### **4.6. CORRELATION STUDIES**

The phenotypic correlation coefficients of the seven component traits of seed yield per plant viz. days to 50% flowering, plant height, number of effective capitula/plant, number of filled seeds in main capitulum, diameter of main capitulum, 100 seed weight and oil content were calculated with seed yield per plant as well as among themselves and are furnished in Table – 10.

Number of effective capitula/plant (0.662\*\*), number of filled seeds in main capitulum (0.399\*\*), diameter of main capitulum (0.367\*\*) and 100 seed weight (0.268\*) exhibited significant positive association with seed yield while plant height (-0.138), days to 50% flowering (-0.110) and oil content (-0.025) exhibited negative association with yield.

Days to 50% flowering exhibited significant positive association with plant height (0.274\*) and positive association with oil content (0.031), number of filled seeds in main capitulum (0.007) while it exhibited negative association with seed yield (-0.110), number of effective capitula/plant (-0.128) and 100 seed weight (-0.054).

Plant height exhibited significant positive association with days to 50% flowering (0.274\*) and positive association with oil content (0.188) and diameter of main capitulum (0.044), while it exhibited negative association with seed yield (-0.138), number of filled seeds in main capitulum (-0.138), number of effective capitula/plant (-0.089) and 100 seed weight (-0.069).

Number of effective capitula/plant exhibited significant positive association with seed yield (0.662\*\*) and positive association with number of filled seeds in main capitulum (0.191), diameter of main capitulum (0.189) and 100 seed weight (0.110), plant height (0.044) while it exhibited negative association with days to 50% flowering (-0.128) and oil content (-0.088).

Diameter of main capitulum exhibited significant positive association with number of filled seeds in main capitulum (0.651\*\*), and seed yield (0.367\*\*) and positive association with number of effective capitula/plant (0.189), 100 seed weight (0.110), oil content (0.105) and plant height (0.044).

Number of filled seeds in main capitulum exhibited significant positive association with diameter of main capitulum (0.651\*\*) and seed yield (0.399\*\*) and positive association with number of effective capitula/plant (0.191), oil content (0.061), and days to 50% flowering (0.007) while it exhibited negative association with 100 seed weight (-0.158) and plant height (-0.138).

100 seed weight exhibited significant positive association with seed yield (0.268\*) and positive association with diameter of main capitulum (0.110), number of effective capitula/plant (0.110), while it exhibited negative association with oil content (-0.175), number of filled seeds in main capitulum (-0.158), plant height (-0.069) and days to 50% flowering (-0.054).

Oil content exhibited positive association with plant height (0.188), diameter of main capitulum (0.105), number of filled seeds in main capitulum (0.061) and days to 50% flowering (0.031) while it exhibited negative association with 100 seed weight (-0.175), number of effective capitula/plant (-0.088), and seed yield (-0.025).

#### **4.7 PATH COEFFICIENT ANALYSIS**

The path coefficient analysis was worked out taking seed yield associated characters to find out the direct and indirect contribution of these important traits to seed yield per plant. The results are presented in Table- 11

Among the eight quantitative characters studied, the maximum direct effect on seed yield per plant was of number of effective capitula/plant (0.570), followed by number of filled seeds in main capitulum (0.305), 100 seed weight (0.257), oil content (0.055) and diameter of main capitulum

(0.026). Days to 50% flowering (-0.017) and plant height (-0.034) recorded negative direct effects on seed yield per plant.

Days to 50% flowering had indirect positive effect through number of filled seeds in main capitulum (0.002) followed by oil content (0.001) while it exhibited negative indirect effect through number of effective capitula/plant (-0.073), 100 seed weight (-0.014), days to 50% flowering (-0.001) and plant height (-0.009).

Plant height had indirect positive effect through oil content (0.010) followed by diameter of main capitulum (0.001). However, negative effect on seed yield was observed through number of effective capitula/ plant (-0.051), number of filled seeds in main capitulum (-0.042) and 100 seed weight (-0.017).

Number of effective capitula/plant had highest indirect positive effect through number of filled seeds in main capitulum (0.058), followed by 100 seed weight (0.028), diameter of main capitulum (0.005), plant height (0.003) and days to 50% flowering (0.002). It exhibited negative indirect effect through oil content (-0.004).

Diameter of main capitulum had highest indirect positive effect through number of filled seeds in main capitulum (0.199) followed by number of effective capitula/plant (0.108), 100 seed weight (0.028), plant height (0.001)

and oil content (0.005). It exhibited negative indirect effect through days to 50% flowering (-0.001).

Number of filled seeds in main capitulum had highest indirect positive effect through number of effective capitula/plant (0.109), followed by diameter of main capitulum (0.017), plant height (0.004) and oil content (0.003). However, negative effect on seed yield was observed through 100 seed weight (-0.040).

100 seed weight showed highest indirect positive effect through number of effective capitula/plant (0.063), followed by diameter of main capitulum (0.003), plant height (0.002) and days to 50% flowering (0.001). It exhibited negative indirect effect through number of filled seeds in main capitulum (-0.048) followed by oil content (-0.009).

Oil content recorded highest indirect positive effect through number of filled seeds in main capitulum (0.018), followed by diameter of main capitulum (0.002). It exhibited negative indirect effect through number of effective capitula/plant (-0.050) followed by 100 seed weight (-0.045) and plant height (-0.006).

**Table 2 - Morphological characterization of qualitative characters of safflower genotypes**

S. No.	Qualitative characters	Frequency	Check varieties
1.	<b>Growth habit</b>		
	a) Erect	57	GMU 950, 1197, 1250, 1251, 1281, 1306, 1383, 1386, 1394, 1790, 1791, 1792, 1794, 1796, 1797, 1805, 1815, 2001, 2007, 2010, 2039, 2040, 3120, 3121, 3152, 4045, 4050, 4063, 4068, 4073, 4078, 4083, 4087, 4092, 4094, 4096, 4098, 4119, 4388, 4390, 4391, 4392, 4799, 4800, 4859, 4863, 5121, 5122, 5125, 5129, 5132, 5133, 5151, 5389, A-1, Manjira, NARI-6
	b) Bushy	7	GMU 1988, 4361, 4389, 4393, 4860, 5131, Bhima
2.	<b>Location of primary branches on main axis</b>		
	a) Predominantly basal.	2	GMU 5121, Bhima.
	b) Predominantly on Upper 1/3 <sup>rd</sup>	24	GMU 950, 1197, 1251, 1306, 1386, 1394, 1790, 1791, 1792, 1805, 2039, 2040, 3121, 4050, 4063, 4068, 4073, 4073, 4390, 4391, 4392, 4799, 4863, 5129, 5389, A-1
	c) Predominantly on upper 2/3 <sup>rd</sup>	35	GMU 1250, 1281, 1383, 1790, 1791, 1794, 1796, 1797, 1815, 1988, 2001, 2007, 3120, 3152, 4045, 4078, 4083, 4087, 4092, 4094, 4096, 4119, 4388, 4800, 4859, 4860, 5121, 5122, 5125, 5131, 5132, 5133, 5151, Manjira, NARI-6
	d) Base to apex	3	GMU 4361, 4389, 4393

**Table 2 – contd.**

<b>S. No.</b>	<b>Qualitative characters</b>	<b>Frequency</b>	<b>Genotypes/Check varieties</b>
3.	<b>Angle of primary branches on main axis.</b>		
	a) Appressed ( $15^{\circ}$ – $25^{\circ}$ )	1	GMU 4078
	b) Semi appressed ( $26^{\circ}$ – $30^{\circ}$ )	6	GMU 1197, 1386, 4045, 4063, 4073, 4393
	c) Normal ( $31^{\circ}$ – $60^{\circ}$ )	57	GMU 950, 1250, 1251, 1281, 1306, 1383, 1394, 1790, 1791, 1792, 1794, 1796, 1797, 1805, 1815, 2001, 2007, 2010, 2039, 2040, 3120, 3121, 3152, 4050, 4068, 4083, 4087, 4092, 4094, 4096, 4098, 4119, 4361, 4388, 4389, 4390, 4391, 4392, 4399, 4799, 4800, 4859, 4860, 4863, 5121, 5122, 5125, 5129, 5131, 5132, 5133, 5151, 5389, A-1, Bhima, Manjira, NARI-6
4.	<b>Shape of upper stem leaves</b>		
	a) Elliptical	13	GMU 1790, 1792, 1797, 1815, 2007, 3152, 4119, 4799, 4800, 4859, 4860, 5121, 5189
	b) Fusiform	36	GMU 1250, 1281, 1306, 1383, 1386, 1394, 1791, 1794, 1805, 1988, 2010, 2039, 2040, 3120, 3121, 3152, 4050, 4063, 4068, 4073, 4078, 4083, 4092, 4094, 4096, 4098, 4388, 4390, 4392, 4393, 4800, 4863, 5122, 5125, 5129, 5133, 5151, NARI-6
	c) Obovate	15	GMU 950, 1197, 1251, 1796, 2001, 4045, 4087, 4361, 4389, 4391, 5131, 5132, A-1, Manjira, Bhima.

**Table 2 – contd.**

<b>S. No.</b>	<b>Qualitative characters</b>	<b>Frequency</b>	<b>Genotypes/Check varieties</b>
5.	<b>Margin of upper stem leaves</b>		
	a) Entire	3	GMU 4063, 4068, 4078
	b) Serrate	24	GMU 1250, 1790, 1791, 1794, 1805, 3121, 3152, 4045, 4050, 4083, 4087, 4092, 4094, 4096, 4392, 4393, 4799, 4859, 4863, 5122, 5125, 5129, 5131, NARI-6
	c) Deeply Serrate	34	GMU 950, 1197, 1251, 1281, 1306, 1383, 1394, 1792, 1796, 1797, 1815, 1988, 2001, 2007, 2010, 2039, 2040, 3120, 4098, 4119, 4361, 4388, 4390, 4391, 4800, 4860, 5121, 5132, 5151, 5389, A-1, Bhima, Manjira.
	d) Lobed	4	GMU 1386, 4073, 4389, 5133
6.	<b>Flower colour at full bloom stage.</b>		
	a) Pale Yellow	1	Bhima
	b) Yellow	56	GMU 950, 1197, 1251, 1281, 1306, 1383, 1386, 1394, 1790, 1791, 1792, 1794, 1797, 1805, 1815, 1988, 2001, 2010, 2039, 2040, 3120, 3121, 3152, 4050, 4063, 4078, 4083, 4087, 4092, 4094, 4096, 4098, 4119, 4361, 4388, 4389, 4390, 4391, 4392, 4393, 4799, 4800, 4859, 4860, 4863, 5121, 5122, 5125, 5129, 5131, 5132, 5133, 5151, 5389, A-1, Manjira,
	c) Orange	7	GMU 1250, 1796, 2007, 4045, 4068, 4073

**Table 2 – contd.**

<b>S. No.</b>	<b>Qualitative characters</b>	<b>Frequency</b>	<b>Genotypes/Check varieties</b>
7.	<b>Flower colour at fading stage.</b>		
	a) Pinkish white	1	Bhima
	b) Golden yellow	12	GMU 1383, 1386, 2040, 3120, 3121, 4098, 4119, 4361, 4859, 5129, 5151, 5389.
	c) Orange red	7	GMU 1790, 1791, 1988, 4045, 4800, 5121, A-1
	d) Red	44	GMU 950, 1197, 1250, 1251, 1281, 1306, 1394, 1792, 1794, 1796, 1797, 1805, 1815, 2001, 2007, 2010, 2039, 3152, 4050, 4063, 4068, 4073, 4078, 4083, 4087, 4092, 4094, 4096, 4388, 4389, 4390, 4391, 4392, 4393, 4799, 4860, 4863, 5122, 5125, 5131, 5132, 5133, Manjira, NARI-6
8.	<b>Shape of main capitulum</b>		
	a) Conical	56	GMU 950, 1197, 1251, 1281, 1306, 1383, 1386, 1394, 1790, 1791, 1792, 1794, 1796, 1797, 1805, 1815, 1988, 2001, 2007, 2010, 2039, 2040, 3120, 3121, 3152, 4050, 4078, 4087, 4092, 4094, 4096, 4098, 4119, 4361, 4388, 4389, 4390, 4391, 4392, 4393, 4799, 4800, 4859, 4860, 4863, 5121, 5122, 5125, 5129, 5131, 5132, 5133, 5389, A-1, Bhima Manjira,
	b) Flattened	8	GMU 1250, 4045, 4063, 4068, 4073, 4083, 5151, NARI-6

**Table 2 – contd.**

<b>S. No.</b>	<b>Qualitative characters</b>	<b>Frequency</b>	<b>Genotypes/Check varieties</b>
9.	<b>Presence of spines on OIB</b>		
	a) None	6	GMU 4045,4063, 4068, 4078, 4087, NARI-6
	b) Few	10	GMU 1250, 1394, 2010, 4050, 4073, 4083, 4092, 4388, 4389, 5151
	c) Intermediate	48	GMU 950, 1197, 1251, 1281, 1306, 1383, 1386, 1790, 1791, 1792, 1794, 1796, 1797, 1805, 1815, 1988, 2001, 2007, 2039, 2040, 3120, 3121, 3152, 4094,4096, 4098, 4119, 4361, 4390, 4391, 4392, 4393, 4799, 4800, 4859, 4860, 4863, 5121, 5122, 5125, 5129, 5131, 5132, 5133, 5389, A-1, Bhima, Manjira

**Table 3: Analysis of variance for eight characters in 64 safflower genotypes.**

Source	Degrees of freedom	Days to 50% flowering	Plant Height (cm)	No. of effective capitula/plant	Diameter of main capitulum (mm)	No. of filled seeds in main capitulum	100 seed weight (g)	Oil content (%)	Seed yield per plant (g)
Replications	1	0.070	13.11	42.89*	0.28	3.56	0.00	9.29	5.05
Treatments	63	26.84**	176.17**	44.73*	10.11**	68.42**	1.91*	7.63**	121.96*
Blocks within replication	14	2.15	26.36*	4.88	1.25	7.12	0.16	2.16	4.16
Error	49	1.26	11.97	5.66	1.52	10.30	0.25	3.13	5.69

\* - Significant at 5% level

\*\* - Significant at 1% level

**Table 4 - Mean values of different characters for 64 safflower genotypes**

S.No.	GMU No.	Days to 50% flowering	Plant height (cm)	No. of effective capitula/plant	Diameter of main capitulum (mm)	No. of filled seeds in main capitulum	100 seed weight (g)	Oil content (%)	Seed yield/plant (g)
1	950	79.50	72.80	16.60	21.10	28.30	5.41	26.10	13.56
2	1197	79.00	76.90	18.20	20.10	18.10	4.86	25.05	6.55
3	1250	79.00	85.75	27.00	18.95	22.80	4.69	24.30	29.60
4	1251	80.50	59.80	17.70	20.75	26.60	5.03	27.60	14.80
5	1281	78.00	67.30	19.40	20.75	26.60	5.03	27.60	14.80
6	1306	84.00	65.30	14.80	16.85	17.30	4.67	25.80	8.15
7	1383	87.00	61.60	13.70	19.95	16.30	5.95	26.70	11.85
8	1386	78.00	72.00	12.80	19.25	19.45	4.90	26.35	5.11
9	1394	82.00	57.80	16.00	18.20	19.45	5.73	26.50	16.28
10	1790	80.50	68.60	21.70	24.30	28.50	5.02	26.90	26.72
11	1791	81.50	73.90	19.80	20.45	19.00	5.50	28.30	17.15
12	1792	86.00	75.10	15.70	18.85	12.45	4.64	27.70	7.52
13	1794	85.00	72.50	18.80	24.40	34.30	4.40	27.70	16.94
14	1796	82.50	74.30	20.30	22.40	27.95	5.35	26.30	18.47
15	1797	77.00	64.50	14.50	21.40	21.15	6.03	27.45	11.49
16	1805	79.50	61.80	8.90	19.90	15.80	4.32	27.30	3.96
17	1815	85.50	56.50	22.50	25.30	33.15	5.46	24.75	17.37
18	1988	77.00	66.90	21.60	20.35	16.80	6.03	28.70	18.47
19	2001	80.00	71.00	22.00	19.55	23.95	6.64	24.10	35.10
20	2007	82.00	69.80	14.60	19.50	21.50	6.81	27.65	9.96
21	2010	87.00	66.80	22.50	22.05	25.60	6.20	26.30	24.90
22	2039	88.00	74.60	17.70	20.85	19.10	4.72	27.65	17.45
23	2040	84.50	66.50	11.00	22.00	19.30	6.70	26.30	18.53
24	3120	87.00	71.50	17.50	19.60	27.65	3.30	30.90	15.09
25	3121	78.00	74.40	14.00	18.65	21.60	4.01	25.60	6.35

**Table 4 – Contd.**

<b>S.No.</b>	<b>GMU No.</b>	<b>Days to 50% flowering</b>	<b>Plant height (cm)</b>	<b>No. of effective capitula/plant</b>	<b>Diameter of main capitulum (mm)</b>	<b>No. of seeds in main capitulum</b>	<b>100 seed weight (g)</b>	<b>Oil content (%)</b>	<b>Seed yield/plant (g)</b>
26	3152	84.50	60.80	19.90	19.60	17.60	5.03	24.05	16.27
27	4045	86.50	104.9	15.10	23.70	15.30	5.77	31.75	4.43
28	4050	80.00	84.10	9.40	15.30	9.95	5.98	26.80	8.27
29	4063	89.00	80.20	14.40	17.90	14.30	3.75	24.25	7.75
30	4068	83.00	79.20	12.40	19.45	12.45	4.92	23.70	4.10
31	4073	88.50	88.40	9.50	24.60	26.30	5.15	26.55	6.66
32	4078	86.50	74.10	14.40	15.75	12.80	4.14	29.40	9.48
33	4083	82.50	70.10	8.30	20.10	25.05	3.29	27.60	6.27
34	4087	80.00	73.10	18.30	22.85	29.45	4.36	30.15	25.20
35	4092	81.00	53.50	26.60	18.00	15.20	4.79	26.30	17.80
36	4094	81.00	70.40	17.20	21.00	26.10	5.11	27.10	9.08
37	4096	87.50	60.90	16.30	22.60	30.80	5.95	26.55	13.80
38	4098	88.00	89.90	11.40	20.95	21.15	5.45	27.20	9.00
39	4119	77.00	73.80	23.40	23.05	23.10	4.35	28.35	17.37
40	4361	76.00	72.00	25.90	23.55	23.95	4.48	24.95	15.25
41	4388	69.00	61.30	17.30	21.35	19.45	5.50	29.75	15.75
42	4389	85.00	78.30	24.30	22.60	25.15	6.34	28.40	27.80
43	4390	81.00	61.00	18.30	21.55	28.50	5.04	20.60	14.45
44	4391	81.00	71.95	13.60	20.50	22.60	6.11	27.00	10.98
45	4392	84.00	75.90	14.50	20.45	26.45	3.86	27.40	16.30
46	4393	84.00	82.75	25.30	18.55	16.45	5.36	24.45	12.50
47	4799	84.00	66.40	20.00	17.00	19.30	5.12	27.75	10.69
48	4800	83.00	63.60	24.90	18.25	13.30	6.50	27.25	16.59
49	4859	81.00	59.70	11.80	19.50	27.45	5.05	28.30	10.82
50	4860	79.50	63.10	16.30	19.70	20.30	6.95	21.80	15.51

**Table 4 – Contd.**

S.No.	GMU No.	Days to 50% flowering	Plant height (cm)	No. of effective capitula/plant	Diameter of main capitulum (mm)	No. of seeds in main capitulum	100 seed weight (g)	Oil content (%)	Seed yield/plant (g)
51	4863	83.00	75.70	19.90	18.15	9.80	6.79	22.65	15.15
52	5122	81.50	69.20	21.30	20.65	25.80	4.69	27.40	27.40
53	5125	84.00	69.50	19.90	23.40	20.50	6.69	24.85	21.76
54	5121	86.00	74.30	16.20	23.40	23.15	5.86	26.65	13.88
55	5129	85.00	78.10	18.90	21.30	25.65	4.31	28.35	14.41
56	5131	80.50	64.70	17.20	20.85	12.15	6.64	26.35	14.41
57	5132	87.00	76.90	22.40	21.85	26.15	5.67	28.40	19.95
58	5133	83.00	71.50	23.10	15.45	15.15	5.90	25.80	9.19
59	5151	80.50	59.30	27.40	22.55	30.45	3.49	26.05	34.25
60	5389	84.50	64.90	19.40	17.25	15.95	4.15	26.10	9.18
<b>CHECK VARIETIES</b>									
61	A-1	81.50	76.80	17.10	20.15	13.80	6.81	26.95	18.40
62	Bhima	83.50	78.70	25.30	21.35	24.80	7.15	28.45	35.80
63	Manjira	81.00	75.30	24.50	22.90	21.50	6.60	26.60	31.70
64	NARI-6	86.00	95.90	17.75	18.20	16.00	4.27	27.55	5.65
<b>Mean</b>		82.46	71.53	18.10	20.48	21.25	5.31	26.68	15.28
<b>C.V.</b>		1.46	5.44	12.94	5.91	14.57	9.09	6.55	15.14
<b>S.E.</b>		0.85	2.75	1.65	0.85	2.19	0.34	1.23	1.63
<b>C.D.5%</b>		2.42	7.84	4.68	2.42	6.19	0.96	3.49	4.62
<b>C.D.1%</b>		3.12	10.34	6.22	3.21	8.22	1.28	4.64	6.14

**Table 5 –Range and Coefficient of variability for eight characters in safflower genotypes.**

	Degrees of freedom	Days to 50% flowering	Plant Height (cm)	No. of effective capitula / plant	Diameter of main capitulum (mm)	No. of filled seeds in main capitulum	100 seed weight (g)	Oil content (%)	Seed yield per plant (g)
Range	Minimum	69.00	53.50	8.30	15.30	9.80	3.29	20.60	3.96
	Maximum	89.00	104.90	27.40	25.30	34.30	7.15	31.50	35.80
Coefficient of Variation (%)	Phenotypic	4.56	13.67	27.47	11.75	29.38	19.50	8.66	52.21
	Genotypic	4.31	12.54	24.68	10.15	25.51	17.25	5.67	49.96

**Table 6 – Distribution of 64 genotypes of safflower in different clusters**

<b>Cluster No.</b>	<b>No. of Genotypes</b>	<b>Genotypes/Check Varieties</b>
I	20	GMU 950, 1197, 1251, 1281, 1386, 1791, 1796, 1797, 1805, 1988, 2007, 3121, 4083, 4094, 4119, 4361, 4390, 4391, 4859, 4860.
II	1	GMU 4388.
III	9	GMU 1306, 1394, 3152, 4092, 4393, 4799, 4800, 5133, 5389.
IV	6	GMU 1794, 1815, 3120, 4096, 4392, 5129.
V	8	GMU 1383, 2010, 2039, 2040, 4389, 5121, 5125, 5132.
VI	4	GMU 4050, 4863, 5131, A-1
VII	8	GMU 1250, 1790, 2001, 4087, 5122, 5151, Bhima, Manjira
VIII	5	GMU 1792, 4063, 4068, 4078, NARI-6
IX	3	GMU 4045, 4073, 4098.

**Table 7 – Cluster means for eight characters of 64 safflower genotypes.**

<b>Cluster</b>	<b>Days to 50% flowering</b>	<b>Plant Height (cm)</b>	<b>No. of effective Capitula/plant</b>	<b>Diameter of main capitulum (mm)</b>	<b>No. of filled seeds in main capitulum</b>	<b>100 seed weight (g)</b>	<b>Oil content (%)</b>	<b>Seed yield per plant (g)</b>
<b>I</b>	79.57	68.82	16.66	20.66	22.71	5.25	26.41	11.83
<b>II</b>	69.00	61.30	17.30	21.35	19.45	5.50	29.75	15.75
<b>III</b>	83.33	65.17	21.11	17.68	16.63	5.25	26.00	12.96
<b>IV</b>	85.66	69.23	18.08	22.27	29.66	4.54	27.60	15.65
<b>V</b>	86.06	71.06	18.46	22.01	21.90	6.01	26.90	19.52
<b>VI</b>	81.25	75.32	15.90	18.61	11.42	6.55	25.68	14.62
<b>VII</b>	80.75	72.61	23.43	21.63	25.90	5.33	26.74	30.72
<b>VIII</b>	86.10	80.90	14.93	18.03	13.60	4.34	26.52	6.90
<b>IX</b>	87.66	94.40	12.00	23.08	20.91	5.45	28.50	6.69
<b>Mean</b>	82.46	71.53	18.10	20.48	21.25	5.31	26.68	15.28





**Table 9 – Contribution of different characters towards genetic divergence ( $D^2$ ) in 64 genotypes of safflower.**

<b>Source</b>	<b>No. of times ranked first</b>	<b>Percent contribution toward divergence</b>
Days to 50% flowering	447	22.17
Plant height (cm)	240	11.90
No. of effective capitula/plant	135	6.70
Diameter of main capitulum (mm)	188	9.33
No. of filled seeds in main capitulum	128	6.35
100 seed weight (g)	244	12.10
Oil content (%)	30	1.49
Seed yield per plant (g)	604	29.96

**Table 10 – Estimation of Correlation coefficient between seed yield and its contributing characters**

	<b>Days to 50% flowering</b>	<b>Plant height (cm)</b>	<b>No. of effective capitula/plant</b>	<b>Diameter of main capitulum (mm)</b>	<b>No. of filled seeds in main capitulum</b>	<b>100 seed weight (g)</b>	<b>Oil content (%)</b>	<b>Seed yield per plant (g)</b>
<b>Days to 50% flowering</b>	1.000	0.274*	-0.128	0.000	0.007	-0.054	0.031	-0.110
<b>Plant height(cm)</b>		1.000	-0.089	0.044	-0.138	-0.069	0.188	-0.138
<b>No. of effective capitula/plant</b>			1.000	0.189	0.191	0.110	-0.088	0.662**
<b>Diameter of main capitulum(mm)</b>				1.000	0.651**	0.110	0.105	0.367**
<b>No. of filled seeds in main capitulum</b>					1.000	-0.158	0.061	0.399**
<b>100 seed weight(g)</b>						1.000	-0.175	0.268*
<b>Oil content(%)</b>							1.000	-0.025

\* - Significant at 5% level

\*\* - Significant at 1% level

**Table 11 – Estimation of Path coefficient between seed yield and its contributing characters**

	<b>Days to 50% flowering</b>	<b>Plant height (cm)</b>	<b>No. of effective capitula/plant</b>	<b>Diameter of main capitulum (mm)</b>	<b>No. of filled seeds in main capitulum</b>	<b>100 seed weight (g)</b>	<b>Oil content (%)</b>	<b>Seed yield per plant (r)</b>
<b>Days to 50% flowering</b>	<b>-0.017</b>	-0.009	-0.073	-0.001	0.002	-0.014	0.001	-0.110
<b>Plant height(cm)</b>	-0.004	<b>-0.034</b>	-0.051	0.001	-0.042	-0.017	0.010	-0.138
<b>No. of effective capitula/plant</b>	0.002	0.003	<b>0.570</b>	0.005	0.058	0.028	-0.004	0.662**
<b>Diameter of main capitulum(mm)</b>	-0.001	-0.001	0.108	<b>0.026</b>	0.199	0.028	0.005	0.367**
<b>No. of filled seeds in main capitulum</b>	0.000	0.004	0.109	0.017	<b>0.305</b>	-0.040	0.003	0.399**
<b>100 seed weight(g)</b>	0.001	0.002	0.063	0.003	-0.048	<b>0.257</b>	-0.009	0.268*
<b>Oil content(%)</b>	0.000	-0.006	-0.050	0.002	0.018	-0.045	<b>0.055</b>	-0.025

**Residual value = 0.644**

\* - Significant at 5% level

\*\* - Significant at 1% level

## **CHAPTER V**

### **DISCUSSION**

The success of safflower as a commercial crop in traditional areas and its expansion into new areas will largely depend on the extent of improvement made in its yield and oil content. The selections made in the field based on phenotypic expression are less efficient. Studies on the relative magnitude of heritable and non-heritable variability exhibited for various traits are, therefore, likely to be useful in line selection. Partitioning the total variance into phenotypic, genotypic and environmental components will be helpful in making efficient selection. Knowledge of nature and extent of character association and an understanding of direct and indirect forces that influence a particular character association are essential to obtain information on these aspects and results are discussed in this chapter.

Success in any plant breeding programme depends largely on the extent of genetic variability available to a breeder. Even though India is one of the primary centres of origin and diversity of safflower, the great indigenous variability in safflower was not subjected to detailed genetic studies. The above argument is reflected in the number of varieties and hybrids released in India, even though this crop has ample number of benefits in medicine as well as for edible purposes. However, a detailed study on exotic collections is also a pre-requisite for plant breeders to extend their search world wide for selection of parents with wide genetic divergence or better quality traits, which

are absent in the landraces. Evaluation and characterization of exotic accessions will enable us to identify and describe new and useful genetic traits. Therefore, the exotic accessions along with improved indigenous varieties were evaluated for qualitative and quantitative traits. In order to describe, establish diagnostic characteristics and identify genotypes with desired agronomic traits it is essential to estimate the extent of morphological variation in the collection. The exotic accessions and indigenous varieties were characterized using nine morphological descriptors developed by IPGRI.

### **5.1 ANOVA.**

Analysis of variance showed the existence of distinct genetic differences among the genotypes under study in respect of all the eight characters studied. Significant difference among the genotypes warranted grouping of the entries to identify genetically diverse ones to ensure success in recombination breeding.

### **5.1 VARIABILITY**

Variability in the population, especially for characters where improvement is sought for, is an indispensable pre-requisite for any crop improvement programme. The total variance was partitioned into phenotypic, genotypic and environmental components. The estimates of PCV and GCV were high in case of seed yield per plant, number of seeds in main capitulum, number of effective capitula per plant, in decreasing order of their magnitude.

This highlighted the presence of high genetic variation in respect of these attributes. High estimates of PCV and GCV for seed yield per plant, number of effective capitula per plant, number of seeds in main capitulum were reported in earlier studies by Ashri *et al.* (1974); Abel, (1976); Mathur *et al.* (1976); Ghanvati and Knowles, (1977); Sengupta and Bhattacharya, (1979); Deokar *et al.*, (1985); Malleshappa *et al.* (1990); Pandya *et al.* (1996); Patil (1998); Chowdary *et al.* (1999), Mane *et al.* (1999); Senapati *et al.* (1999); Kavani *et al.* (2000) and Reddy *et al.* (2003).

Low estimates of PCV and GCV were exhibited by days to fifty percent flowering and this finding was in accordance with reports given by Patil (1998) and Senapati *et al.* (1999).

The difference between PCV and GCV was less for all the traits under consideration. This suggested that the traits were less influenced by environment and hence, they could be improved by following phenotypic selection. Similar results were also reported by Makne *et al.* (1979); Pandya *et al.* (1996) and Patil (1998).

## **5.2 GENETIC DIVERGENCE**

Genetic divergence among parents is essential since, any hybridization programme involving genetically diverse parents is likely to produce high heterotic effects and also more variability could be expected in the segregating generations. Since eco-geographical divergence is not necessarily related with

the genetic diversity, phenotypic variability cannot be taken as an index of selection of diverse lines for productive heterosis breeding and evolving superior varieties. In order to quantify degree of genetic divergence, to assess relative contribution of characters to total divergence and to understand the genetic distance, the present experimental material comprising of exotic accessions and local cultivated varieties was subjected to divergence studies. Genetic diversity between population/genotypes indicates the differences in gene frequencies. Several measures of genetic distance have been proposed among which Mahalanobis's generalized distance is most widely used in plant breeding.

In the present study also, Mahalanobis  $D^2$  analysis was used to measure the distance between the genotypes. Mahalanobis  $D^2$  considers the variation produced by any character and the consequent effect that it has on other characters. This statistical tool has been widely employed to resolve genetic divergence at inter-varietal and sub-species level in classifying the crop plants (FAO, 1997). This is possible by clustering the entries based on  $D^2$  values as it represents the index of genetic diversity among genotypes and clusters.

The data on eight characters *viz.*, days to 50 percent flowering, plant height, number of effective capitula per plant, diameter of main capitula, number of seeds in main capitulum, 100-seed weight, oil content, seed yield per plant, were found to be important component traits of divergence in

safflower. Based on the  $D^2$  analysis, the sixty germplasm accessions and four check varieties were grouped into 9 clusters by using Euclidean cluster analysis. The magnitude of  $D^2$  suggested the presence of considerable amount of diversity in the material used in the present investigation. The pattern of distribution of genotypes into various clusters was at random suggesting that geographical diversity and genetic diversity were not related. This suggested that forces other than geographical origin such as genetic drift, natural and artificial selection affected the diversity. Similar results on genetic divergence in safflower were earlier reported by Ranga Rao *et al.* (1980); Patil *et al.* (1991); Dingming *et al.* (1993); Ghongade and Navale (1995) and Venkata Gopinath (2003).

The classification of the experimental material into different clusters following the aforesaid method was utilised for determining genetic closeness or divergence among the germplasm accessions as well as between accessions and indigenous varieties.

The analysis of dispersion for the test of significance of difference in the mean values based on Wilk's criterion revealed highly significant differences between the genotypes for the aggregation of eight characters.

Euclidean cluster method grouped the experimental material into nine clusters based on  $D^2$  distances (Fig-1). Cluster II (0.00) displayed the least intra cluster divergence while the maximum intra cluster distance was recorded in cluster VII (58.76) and this might have been due to limited gene exchange or selection practices among the genotypes for diverse characters. The genotypes of this cluster were high yielding (30.21g), had more number of effective capitula /plant (23.43) as compared to other clusters.

Based on inter cluster distance, it was found that cluster IX was highly divergent from cluster II (495.09) followed by cluster IX and cluster VII (384.65) suggesting that the genotypes in these clusters could be fully exploited to explore the wide range of heterosis and to release good recombinant lines by intermating them in a definite design. Cluster IV was least divergent from cluster V (56.35)

Greater emphasis should be laid on the characters contributing maximum to the  $D^2$  values in the clusters for the purpose of further selection and choice of parents for hybridization. Highest contribution in this regard was put forth by seed yield per plant (29.96%) followed by days to 50 percent flowering (22.17%), 100-seed weight (12.10%), plant height (11.09%) and diameter of main capitulum (9.33%). Insignificant contributions were put forth by number of effective capitula per plant (6.70%), number of filled seeds in

main capitulum (6.35%) and oil content (1.29%). Similar results were earlier reported by Patil *et al.* (1991) and Ghongade and Navale (1995).

### **5.3 CORRELATION STUDIES**

Yield is a quantitative character controlled by polygenes and it is the result of combined effect of several component characters and environment. Correlation coefficients measure the magnitude and direction of association among characters. Correlation between different characters of the plant could be due to linkage, pleiotrophy or developmentally induced functional relationships (Ginzberg, 1973 and Harlan, 1939). Knowledge of interaction among the characters is very essential in plant breeding to determine the extent and nature of relationship between yield and yield components. An attempt has been made in the present study to ascertain the association of different characters in safflower.

The components traits *viz.*, number of effective capitula/plant, number of seeds in main capitulum, diameter of main capitulum and 100 seed weight exhibited significant positive association with yield. This association was in concurrence with earlier reports given by Mathur *et al.* (1976); Makne *et al.* (1979; Prasad *et al.* (1993); Patil (1998); Sharma *et al.* (1998) and Venkata Gopinath (2003). Therefore, selection may be focused on these characters, which have strong association with seed yield per plant.

Days to 50 % flowering, exhibited significant positive association with plant height, negligible positive association with oil content and negligible negative association with seed yield. Similar findings were reported earlier by Patil *et al.* (1990); Ghongade *et al.* (1993); Patil (1998) and Venkata Gopinath (2003).

Plant height showed negative association with seed yield in the study while it showed positive association with oil content.

Number of effective capitula/plant showed highly significant positive association with seed yield indicating its importance in selection but it exhibited negative association with oil content. Similar findings were reported earlier by Ashri *et al.* (1974); Makne *et al.* (1979); Malleshappa *et al.* (1989,1990) and Malleshappa *et al* (2003).

Diameter of main capitulum exhibited highly significant positive association with number of filled seeds in main capitulum and seed yield. It showed positive association with oil content.

Number of filled seeds in main capitulum exhibited significant positive association with seed yield. Similar finding was reported earlier by Sharma *et al.* (1998) and Bagheri *et al.* (2001).

100 seed weight showed significant positive association with seed yield but showed negative association with oil content. Similar finding was reported earlier by Patil *et al.* (1990).

#### **5.4 PATH ANALYSIS**

The correlation values denote only the nature and degree of association existing between the pairs of characters. A dependent character like seed yield is controlled by several mutual associated characters of correlation between dependent and independent characteristics arise due to direct effect of a character, it reflects a true association/ relationship between them. Selection can be done for each character to improve the dependent character. This analysis is simply a standardized partial regression analysis based on cause and effect relationship, which serves to analyse by partitioning the correlation.

Days to 50 % flowering has a negative direct effect and negative association with seed yield. It had positive indirect effects through number of filled seeds in main capitulum and oil content. It had negative indirect effects through plant height, number of effective capitula, diameter of main capitulum, and 100 seed weight. Hence, selection could be focused on

genotypes, which were early flowering due to its negative direct and negative indirect effects. Similar reports were revealed by Zheng *et al.* (1993) and Patil (1998).

Plant height had a negative direct effect and negative association with seed yield. It exhibited negative indirect effects through days to 50 % flowering, number of effective capitula per plant and 100-seed weight. It exhibited positive indirect effects on diameter of main capitulum, and oil content. Hence, selection through these characters may bring about an improvement in yield. These reports were in concurrence with that of Mathur *et al.* (1976); Malleshappa *et al.* (1989) and Zheng *et al.* (1993).

Number of effective capitula/plant has positive direct effect and significant positive association with yield. It had positive indirect effects through diameter of main capitulum, number of filled seeds in main capitulum, plant height, days to 50 percent flowering, 100-seed weight and negative indirect effect through oil content. Hence, number of effective capitula/plant could play an important role in selection process for yield. The above findings are in conformity with Malleshapa *et al.* (1989); Ghongade *et al.* (1993); Zheng *et al.* (1993) Patil (1997); Bagheri *et al.* (2001) and Venkata Gopinath (2003).

Diameter of main capitulum and number of seeds in main capitulum had positive direct effect and significant positive association with yield. Both had negative indirect effects through days to 50% flowering. Both had positive indirect effects through number of effective capitula per plant, and oil content. However, indirect effect of diameter of main capitulum and 100-seed weight was positive while its negative for plant height but indirect effect of number of seeds in main capitulum with that of 100-seed weight was negative and positive with that of plant height. As both the characters share similar direct and indirect effects except for 100-seed weight and plant height they could play an important role in selection process for yield. Similar reports were put forth earlier by Mathur *et al.* (1976); Prasad *et al.* (1993) and Venkata Gopinath (2003).

100 seed weight had positive direct effect and significant positive association with yield. It expressed negative indirect effects through number of seeds in main capitulum and oil content. It exhibited positive direct effects through plant height, number of effective capitula per plant, diameter of main capitulum, 100 seed weight. The results were in agreement with the findings of Mathur *et al.* (1976); Prasad *et al.* (1993); Prasad *et al.* (1994) and Patil *et al.* (1998).

Oil content had negligible positive direct effect and negative association with seed yield. It had negative indirect effects through days to 50% flowering, plant height, number of effective capitula per plant and 100-seed weight. It had positive direct effects through diameter of main capitulum and number of seeds in main capitulum.

The path residual value was 0.644, which implied that other traits, which were not evaluated in the present study, also influenced seed yield considerably. Hence, more number of characters should be included in future studies for estimating their direct and indirect effects on yield.

## **CHAPTER VI**

### **SUMMARY**

In the present investigation, an attempt was made to characterize and evaluate exotic germplasm accessions along with local check varieties obtained from Germplasm Management Unit at Directorate of Oilseeds Research, Rajendranagar, Hyderabad. The experimental material in the study consisted of sixty exotic germplasm accessions and four check varieties. The experiment was laid out in Simple Lattice design with two replications at College Farm, College of Agriculture, Rajendranagar, Hyderabad.

Morphological characterization was done using IPGRI descriptors to describe and establish diagnostic characteristics of each genotype. Abundant morphological variation was observed in the experimental material. Distinct morphotypes were observed for shape of upper stem leaves, margin of upper stem leaves, spininess on outer involucre bract and flower colour at full bloom and at fading stages. These would serve as useful markers in hybridization programme as well as in the development of different plant types suited to different cropping systems or regions.

Analysis of variance revealed significant genotypic differences for eight quantitative characters studied suggesting the presence of considerable amount of variability among the genotypes.

A perusal of variability revealed high PCV and GCV values for seed yield per plant, oil yield per plant, number of effective capitula per plant and number of seeds in main capitulum. The difference between PCV and GCV values were minimal indicating that the traits were less influenced by environment and these could be improved by following phenotypic selection.

The exotic germplasm accessions and check varieties were subjected to  $D^2$  analysis, which revealed the presence of substantial amount of genetic variability among them. The pattern of distribution of genotypes into various clusters was random showing that geographical and genetic diversity were not related. Therefore, the experimental material was partitioned into nine clusters. Maximum genetic divergence was found between cluster II and cluster IX. Seed yield contributed maximum towards genetic divergence followed by days to 50% flowering. Therefore a plant breeder may keep in mind the above aspects to obtain superior hybrids and good set of recombinants.

Correlation analysis revealed that number of effective capitula per plant, number of seeds in main capitulum, diameter of main capitulum and 100 seed weight had significant positive association with seed yield. These characters also exhibited strong positive association among themselves.

Path analysis revealed higher magnitude of positive direct effects by number of effective capitula per plant, number of seeds in main capitulum while other traits exhibited positive direct effects but of lower magnitude on seed yield. Days to 50 per cent flowering exhibited negative association with seed yield and as well as with most of the characters. Hence more emphasis should be laid on characters like number of effective capitula/plant, number of filled seeds in main capitulum, diameter of main capitulum and 100 seed weight, for bringing further about improvement in seed yield of the crop.

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