“Genetic Divergence for yield & its attributes in Safflower (*Carthamus tinctorius* L.)”

THESIS

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RAJMATA VIJAYARAJE SCINDIA KRISHI VISHWA VIDYALAYA
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by

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CERTIFICATE–I

This is to certify that the thesis entitled “**Genetic divergence for yield and its attributes in Safflower (Carthamus tinctorius L.)”** submitted in partial fulfillment of the requirement for the degree of **Master of Science in Agriculture** (Plant Breeding & Genetics) of the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bona-side research work carried out by **Mr. Manoj gurjar** I.D.No. **RA/IN/041/2012** under my guidance and supervision. The subject of the thesis has been approved by Student’s Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any degree or diploma (Certificate awarded etc.) or has been published. All the assistance and help received during the course of investigation have been acknowledged by the scholar.

Place- Indore Signature
Date - **Dr. Jagdish Singh**
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Chairman - Dr. Jagdish Singh ___________

Member - Dr.(Smt.) Indu Swarup ___________

Member - Sh. H.L. Khapediya ___________

Member - Dr. M. Qureshi ___________

CERTIFICATE–II

This is to certify that the thesis entitled **"Genetic divergence for yield and its attributes in Safflower (Carthamus tinctorius L.)"** submitted by Mr. **Manoj Gurjar** I.D.No**. RA/IN-041/2012** to the R. V. S. Krishi Vishwa Vidyalaya, Gwalior in partial fulfillment of the requirements for the degree of Master of Science in Agriculture (Plant Breeding & Genetics) in the Department of Plant Breeding & Genetics, College of Agriculture, Indore has been, after evaluation, approved by the External Examiner and by the Student's Advisory Committee after an oral examination of the same.

Place- Indore Signature
Date - **Dr. Jagdish Singh**
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Chairman - Dr. Jagdish Singh ___________

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Place: Indore
Date:

Manoj Gurjar

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LIST OF SYMBOLS

Symbol	Stands for
et al.	Allied (and others)
%	Percentage
/	Per
@	At the rate of
&	And
^{0}c	Degree centigrade
cm	Centimeters
m	Meter
m^{2}	Square meter
cm^{2}	Square centimeters
Mm	Millimeter
Km/hr	Kilometer per hour
Fig.	Figure
Kg	Kilograms
Cv	Cultivars
N	North
S	South
E	East
W	West
g or gm	Gram (s)
FYM	Farm yard manure
Ha	Hectare
Q	Quintal
Ml	Milliliter
Lit	Liter
No.	Number
DAS	Days after sowing
SSP	Single Super Phosphate
MOP	Murate of Potash
t/ha	Tones/hectare
COV	Co-Variance
CV	Coefficient of variation
DF	Degrees of freedom
ESS	Error sum of squares
EMSS	Error Mean sum of squares

GA	Genetic Advance
GAM	Genetic Advance as per cent of Mean
GCV	Genotypic Coefficient of Variation
PCV	Phenotypic Coefficient of Variation
h^2(b)	Heritability in broad sense
MSS	Mean Sum of Squares
RSS	Replication Sum of Squares
RMSS	Replication Mean Sum of Squares
SE(d)	Standard error difference
S.Em	Standard error mean
t	Treatments
TrSS	Treatment Sum of Squares
TSS	Total Sum of Squares
TrMSS	Treatment Mean Sum of Squares
NPK	Nitrogen, phosphorus and potash
SMW	Standard meteorological week
ANOVA	Analysis of variance
CD	Critical Difference

CHAPTER-I

INTRODUCTION

Safflower [Carthamus tinctorius (L.)],Commonly known as Kusum (Hindi) or Kardi (Marathi), is an important Rabi oilseed crop and has generated considerable interest in recent years due to its versatile nature and good yield potential under limited moisture conditions. It belongs to the family Compositeae (Asteraceae). It is predominantly self-pollinated crop. There are 36 wild species in the genus found in many part of the world namely, Asia, Africa and Mediterranean regions. Out of which, only Carthamus tinctorius(L.) (2n = 24) is cultivated in India. It is mainly cultivated for seeds which are a source of oil. Carthamus is the latinised version of the Arabic work "Quartum" or "Gurtum" which, alludes to the colour of the dye often from florets and the modern Arabic name "Usfar" is probably version of the English name "Safflower" through various written form of Usfar, affore, asfiore, Saffiore finally to Safflower.

Safflower, a multipurpose crop, has been grown for centuries in India for the orange-red dye (carthamin) extracted from its brilliantly colored petals and for its quality oil rich in polyunsaturated fatty acids (linoleic acid, 78%). In addition to its precious oil is known to have many medicinal properties i.e. Beneficial in several chronic diseases, and are widely used in Chinese herbal preparations. The tender leaves are rich in vitamin A, iron, phosphorus, and calcium. India occupies first position in area (40%) and production (29%) of safflower grown in the world.

Safflower is one of the nine edible oil crops of the country and the area is 127 thousand hectares with its annual production of 53 thousand tonnes and productivity of 416 kg per hectare in India during 2015-16(Anonymous). It is mainly cultivated in Maharastra and Karnataka states accounting for 72% and 23% area and 63% and 35% production respectively in India. It is also grown to a limited extent in Andhra Pradesh, Madhya Pradesh, Orissa, Bihar and West Bengal etc, which together account for about 5% and 2% of the total safflower area and production in the country. It is cultivated in Rabi season under limited soil moisture condition of vertisol. There is tremendous scope for expansion of area due to its peculiar ability to perform better under adverse environments like limited soil moisture conditions. Safflower is drought tolerant because of its strong and deep penetrating tap root system. It remains succulent in early stages of growth and assumes xerophytic nature at later stages and thus considerably reduces moisture loss by the plant.

The existence of genetic variability in the experimental material is pre-requisite for any crop improvement programme. The heritable portion of genetic variability is more important for increasing the frequency of desirable genotypes in the population. It is judged by genetical parameter heritability. The genetic improvement in the population for desired trait through selection is estimated by genetic advance. It is well known fact that the seed yield is a complex quantitative trait as it is governed by a large number of genes. The expression of these genes is highly influenced by the environmental factors. Thus, component of yield characters exhibiting high heritability and genetic advance can be identified by the knowledge of the relationship between the component and seed yield, so that the, yielding potential of genotypes can be achieved indirectly through practicing selection for its component traits.

The crossing between diverse parents is essential for obtaining desirable genotypes. Hence before going for hybridization programme the information regarding genetic divergence is also required.

Keeping the above mentioned facts, the present work was carried out with the following objectives:

1. To study the genetic variability present in the experimental material.
2. To estimate the heritable portion of genetic variability transferred to the next generations.
3. To identify yield contributing traits by association analysis.
4. To study genetic divergence through D^2 statistic technique for selection of genotypes to be used as parents in hybridization prog

CHAPTER- II

REVIEW OF LITERATURE

The relevant literatures related to various aspects of present study are reviewed under the following heads.

2.1 Genetic variability

2.2 Heritability

2.3 Expected genetic advance

2.4 Correlation coefficient

2.5 Path coefficients analysis

2.6 Divergence analysis

2.1 Genetic variability:

Kavani *et al*. (2001) found high genotypic coefficient of variation for seed yield per plant and number of seeds per capitulum in all the environments. Moderate coefficient of variation for number capitula per plant, number of primary branches per plant, number of secondary branches per plant and harvest index was observed in pooled analysis.

Reddy *et al.*(2003) studied high estimates of genotypic and phenotypic coefficients of variation for seed yield per plant, number of seeds per capitulum, number of primary and secondary branches and number of capitula per plant and moderate for test weight and oil content.

Sarang *et al*.(2004a) found high genotypic and phenotypic variances for plant height followed by yield per plant and lower branch height. Yield per plant and number of secondary branches showed high genotypic and phenotypic coefficients of variation estimates.

Anjani (2005) conducted an experiment to assess the feasibility of transfering desirable traits from wild safflower (C. oxyacantha) to cultivated safflower (C. tinctorius) and to understand the extent of variability in wild safflower. High degree of variability was recorded for days to 50% flowering, days to maturity, plant height, height of branching from base, branches per plant, capitula per plant, 100-seed weight, seed yield per plant and for oil content.

Choulwar *et al*.(2005) revealed that the estimates of phenotypic coefficient of variation were higher in comparison to genotypic coefficient of variation for yield and its contributing characters.

Lakshyadeep *et al.(*2005) assessed genetic variability for days to flowering, days to maturity, number of primary branches per plant, plant height, number of leaves on main axis before and after branching, number of capitula per plant, number of seeds per capitulum ,weight per capitulum, 100-seed weight, seed yield per plant and oil content in 150 germplasm lines of safflower. Analysis of variance was significant for all traits except for number of leaves on main axis after branching, oil content and 100-seed weight. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits. The germplasm lines showed high GCV and PCV for number of capitula per plant and seed yield per plant.

Ichanal *et. al.* (2010) reported a wide range of variation for almost all the characters under study. The phenotypic coefficient of variation (PCV) was found to be higher than genotypic coefficient of variation (GCV) for all the study traits.

Safavi *et.al.(*2011) founded significant difference among the genotypes for all characters. Genotypic and phenotypic coefficient of variations were high for plant height, capitula per plant and seed yield per plant.

Pandey and Singh (2012) reported that analysis of variance for all the character studied, exhibited high degree of variability.

Biradar *et al.(*2012) releaved high Genotypic and Phenotypic Coefficient of Variation for number of capitulum per plant, number of seed per capitulum, 100 seed weight and Oil content.

Safavi *et al.(*2012) studied that safflower genotypes were significantly different for all of the studied characters except 100-seed weight.

Mohammad *et al*.(2014) studied significant variance for all the studied traits.

Rampure *et al.* (2014) observed higher genetic variability for the characters like plant height, days to 50%flower, 100 seed weight, and oil content. But for the characters like fatty acid profile, flower color, the variability was narrow.

Motamedi *et al.* (2015) reported that significant variability was observed for all the traits like grain yield, number of capsules per plant, number of grains per capsule, plant height and 100-seed weight.

Gopal *et al.* (2015) studied 150 safflower germplasm lines along with five checks for yield and its related components. Significant differences among all the germplasm lines for all characters were observed.

Parveen (2016) found significant variability for characters namely days to 50% flowering, days to maturity, plant height and height of primary branch from the base. She also reported number of primary branches, biological yield (kg), seed yield (kg/plot), number of effective capitula and oil content.

Pavithra *et al.* (2016) studied 150 germplasm accessions obtained from the Directorate of Oilseeds Research, Hyderabad and seven check varieties. A wide range of variability for all the traits was observed. The genotypic and phenotypic coefficient of variations were low for rosette period, plant height, days to 50 % flowering, days to maturity, test weight, volume weight, capitulum diameter, oil content and hull percentage. Low GCV as compared to PCV was observed for all the traits. However, there was relatively a wider gap between GCV and PCV for the traits *i.e*. capitula per plant, number of seeds per capitulum, petal yield, biological yield, harvest index and seed yield indicating the higher magnitude of environmental effect on these traits.

Belete (2017) identified germplasm accessions with desirable agro morphological characters among the thirty six accessions evaluated at 2 locations. The combined analysis of variance showed that the accessions were significantly different in characters recorded and also advocated that seed yield can be improved through early generation selection, but other characters should be improved through advanced generation selection.

2.2 Heritability:

Kavani *et al*.(2001) observed high heritability for number of capitula per plant, number of seeds per capitulum, number of secondary branches per plant, days to maturity, seed yield per plant, hull content and harvest index.

Reddy *et al*.(2003) reported high estimates of heritability for all the traits viz; number of primary and secondary branches, number of capitula per plant, seed yield per plant, number of seeds per capitulum, and moderate for test weight and oil content. High heritability coupled with high genetic advance was observed for seed yield per plant, test weight, and number of seeds per capitulum, the moderate heritability and high genetic advance were recorded for number of capitula per plant. However low heritability estimates and low genetic advance were recorded for plant height.

Sarang *et al*.(2004a) found medium to high heritability for all the characters studied. Test weight, yield per plant and lower branch height showed high heritability estimates. High heritability estimates coupled with high expected genetic advance were observed for yield per plant followed by number of capitula per plant and number of secondary branches.

Choulwar *et al.* (2005) studied that the estimates of heritability for plant height was highest and lowest for test weight. High heritability with high expected genetic advance was observed for number of capitula per plant, plant height, number of secondary branches, number of seeds per capitulum and seed yield per plant.

Lakshyadeep *et al*. (2005) reported high heritability for number of capitula per plant and seed yield per plant.

Beena *et al*.(2006) revealed high heritability estimates for days to 50% flowering, days to maturity, plant height , number of seeds per capitulum. Seed yield per plant and 100-seed weight.

Camas and Esendal (2006) found high heritability for lower branch height, plant height, number of seeds per capitulum and seed index.

Arslan *et al*. (2007) observed high heritability for plant height, primary branches per plant, capitula diameter, capitula per plant, number of seeds per capitulum, 100-seed weight and seed yield.

Safavi *et al.* (2011) reported High heritability estimates for plant hight, days of 50% flowering, diameter of primary head and seed yield per plant.

Mohammad et al. (2014) observed high heritability for main capitula diameter, number of seeds per capitulum, 100-seed weight and plant height.

Tariq et al. (2014) reported that the high heritability coupled with high genetic advance for number of heads per plant, biological yield per plant, harvest index and seed yield, On the other hand, days to 50% flowering, days to physiological maturity, seed index and number of seeds per head showed low heritability with low genetic advance.

Belete (2017) studied that broad sense heritability estimates was moderate for days to flower initiation, seed yield, plant height and primary branches per plant. While, low heritability in broad sense was revealed for days to maturity.

Pushpavalli *et al.* (2017) reported that Broad sense heritability estimates were highest for 100-seed weight followed by, number of seeds per capitulum, days to 50% flowering and days to maturity.

2.3 Expected genetic advance:

Reddy *et al.* (2003) revealed high genetic advance for number of seeds per capitulum, seed yield per plant and test weight. Moderate to high genetic advance was recorded for number of capitula per plant.

Sarang *et al.* (2004) reported high expected genetic advance for yield per plant followed by number of secondary branches and number of capitula per plant.

Choulwar *et al.* (2005) observed high expected genetic advance for number of secondary branches, plant height, number of seeds per capitulum, seed yield per plant and number of capitula per plant.

Ichanal *et al*. (2010) studied that traits like seed yield per plant, 100-seed weight, harvest index and number of seeds per capitulum exhibited high heritability coupled with high expected genetic advance.

Safavi *et al.* (2011) reported high genetic gain for head number, seed yield per plant, seed number, plant height, 100-seed weight and diameter of primary head. High heritability estimates associated with high genetic advance as percent of mean were reported for number of seeds per plant, capitula number, plant height and seed yield per plant.

Lande and Deshmukh (2012) releaved high expected genetic advance for seed yield per plant.

Mohammad *et al*.(2014) observed that capitula diameter and plant height posses higher values of genetic advance. High genetic advance coupled with heritability was observed for main capitol diameter and plant height traits.

Tariq *et al*. (2014) reported that the high heritability coupled with high genetic advance was measured for number of heads per plant, biological yield plant, harvest index and seed yield per plant. On other hand, days to 50% flowering, days to physiological maturity, number of seeds per head, and 100-seed weight showed low heritability with low genetic advance.

Bahmankar *et al.* (2014) studied broad-sense heritability for main capitulum diameter, plant height, number of seeds per capitulum, and 100-seed weight traits and reported its higher values. High genetic advance coupled with high heritability was observed for main capitula diameter and plant height traits.

Belete (2017) studied that genetic advance as percent of mean was high for seed yield followed by primary branches per plant, plant height and days to flower initiation

Pushpavalli *et al. (*2017) studied that estimated genetic advance was high for seed yield and moderate for 100-seed weight and number of seeds per capitulum. Genetic advance as percentage of mean was moderate for seed yield per plant, plant height, height of branching from base and 100-seed weight.

2.4 Correlation coefficient:

Tabrizi (2002) observed that most of the characters, genotypic correlation coefficients were higher than phenotypic correlation coefficients and there were highly significant positive correlations between biomass and number of capitula per plant with seed yield.

Dalvi *et al.* (2005) reported that the number of primary branches, number of secondary branches, and number of effective capitula per plant showed significant and positive correlations with seed yield at both phenotypic and genotypic levels while, test weight showed positive significant correlation with seed yield at the genotypic level. The association between number of seeds per capitulum and test weight was negative significant at the genotypic level. Days to 50% flowering showed positive significant correlation with plant height, height of first primary branch, days to maturity and number of seeds per capitulum. The number of primary branches exhibited positive significant correlation with the number of secondary branches, number of effective capitula per plant at genotypic and phenotypic levels both. The number of seeds per capitulum showed negative correlation with test weight at both the levels.

Ali *et al.* (2006) studied that seed yield was positively and significantly correlated with flowering duration, total biomass, seed weight per capitulum, stem yield, capitulum diameter, seed index, number of days to the beginning of branching.

Alizadeh and Carapetian (2006) observed positive association of the average number of seeds per head with grain yield. A negative significant correlation between grain yield and number of days to flower initiation was recorded.

Diwakar *et al.* (2006) recorded significant and positive correlation of number of effective capitula per plant, number of filled seeds in main capitulum, diameter of main capitulum and 100-seed weight with seed yield while plant height, days to 50% flowering and oil content exhibited negative association with seed yield.

Jawanjal *et al.* (2006) studied that the number of secondary branches per plant, days to 50% flowering, number of seeds per capitulum number of capitula per plant and number of primary branches per plant had strong positive association with seed yield.

Arslan *et al.* (2007) found positive and significant correlation between seed yield and all the evaluated traits except number of primary branches per plant.

Ahmadzadeh *et al.* (2008) revealed that grain yield was significantly correlated with hectoliter weight, plant height and biological yield.

Mukta *et al*. (2008) observed that genotypic correlation coefficients were higher than phenotypic correlation coefficients and there were highly significant positive correlations between biomass and number of capitula per plant with seed yield.

Salamati (2011) reported that seed yield per plant had significant and positive correlations with biological yield, capitula number per plant, seed number per capitula and oil yield.

Maryam *et al.* (2012) studied that seed yield had positive correlation with number of seed per head. There was a positive correlation between head and branch number but negative correlation between capitula diameter and 100-seed weight.

Safavi *et al.* (2012) observed positive correlation between oil yield and seed yield.

Nezhad and Talebi (2015) reported that two significant differences among genotypes for all traits in both irrigated and rainfed environments. Grain yield showed high significant positive correlation with number of head per plant, number of seeds per head and seed index in both irrigated and rainfed environments.

Kurhade and Charjan (2016) observed that seed yield per plant had positive significant correlation with number of capitula per plant, number of primary branches per plant and number of seeds per capitulum and negative correlated with days to 50% flowering. Days to 50% flowering had significant negative correlation with number of capitula per plant, seed yield per plant, 100 seed weight and significant and positive correlation with plant height. Plant height exhibited significant positive correlation with days to maturity and oil content. The number of primary branches per plant exhibited significant positive correlation with number of capitula per plant.

Pavithra *et al*.(2016) studied and found significant positive correlation between seed yield per plant and other characters like plant height, capitula per plant, number of seeds per capitulum, biological yield and harvest index. However significant negative correlation was also observed with rosette period, days to 50% flowering and days to maturity.

2.5 Path coefficients analysis:

Reddy *et al.* (2004) observed that number of seeds per capitulum followed by number of capitula per plant, number of secondary branches and number of primary branches exhibited the highest positive direct effect on seed yield. The characters number of secondary branches and number of primary branches also contributed indirectly through each other.

Sarang *et al.* (2004) found that number of capitula per plant exerted the highest positive direct effect on yield followed by seed index and height of first primary branch. The highest positive indirect effect on the yield was observed due to the number of effective capitula per plant at genotypic level.

Dalvi *et al.* (2005) reported that the number of effective capitula exerted the highest positive direct effect on seed yield, followed by days to 50% flowering, seed density, number of secondary branches, test weight and plant height. The number of secondary branches showed positive direct effect on seed yield. The indirect effect of number of secondary branches through number of effective capitula was highest.

Ali *et al.* (2006) revealed that total biomass, first fertile branch, 100-seed weight and flowering duration had substantial direct effects on enhancement of seed yield.

Diwakar *et al.* (2006) reported that number of effective capitula per 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.

Arsal (2007) found that seed yield was determined by capitulum diameter, number of capitula per plant, and number of seeds per head as these characters had highly positive direct effects on seed yield.

Ahmadzadeh *et al.* (2008) studied correlation and path analysis used thirty safflower genotypes and reported that hectoliter weight, 100- seed weight and plant height had the highest positive direct effect on grain yield.

Mukta *et al*. (2008) revealed that increase of oil yield was primarily associated with increasing seed yield, which was affected by biomass and number of capitula per plant.

Topal *et al.* (2010) observed direct and indirect effects estimated with parametric and non-parametric path analysis exhibited similarity but parametric path analysis was preferred to nonparametric path analysis because residual effects of parametric path analysis has lower than that of non-parametric path analysis. Furthermore, determination coefficients of parametric path analysis were higher than that of non-parametric path analysis in both the years. The direct effect of oil yield and indirect effect of number of seeds per capitulum on seed yield *via* oil yield were found large by parametric and non-parametric path analysis.

Tamoor *et al.* (2014) studied path analysis that showed highest and positive direct effect of number of seeds per capitulum followed by 100- seed weight and plant height on seed yield.

Gopal (2015) observed direct effect on seed yield per plant was exhibited positively by the character, number of effective capitula per plant followed by days to maturity and number of secondary branches per plant.

Pavithra *et al.* (2016) revealed that plant height, number of capitula per plant, number of seeds per capitulum, biological yield and harvest index exhibited positive direct effect on seed yield except days to maturity.

Pushpavalli *et at.* (2017) reported that direct effect of number of capitula per plant was more pronounced followed by test weight, plant height and capitulum diameter on seed yield per plant.

2.6 Divergence analysis:

Reddy *et al.* (2004) studied 61 genotypes of safflower for D^2 analysis and grouped them into 9 clusters. Cluster I was biggest with 19 genotypes while, cluster II had 7 genotypes. The average intra and inter cluster D^2 values among 61 genotypes showed that cluster I showed minimum inter D^2 values and cluster XV showed maximum intra cluster D^2 values. Minimum inter cluster D^2 values were observed between cluster III and I.

Jarad *et al.* (2006) studied phenotypic diversity for quantitative and qualitative traits in a salt-tolerant subset of the international safflower germplasm collection from eleven countries in three regions. Phenotypically, the germplasm, among and within regions, was highly variable, especially for rosette and yield related traits. Frequency of desirable variants of seven agronomically important traits ranged from 14% for long rosette period to 50% for number or few spines. Level of population differentiation was high for number of capitula per plant, whereas most traits partitioned their diversity within populations.

Mukta *et al.* (2008) used Euclidean cluster analysis for the characterization of thirty six exotic germplasm accessions of different geographical origin and four check varieties of safflower. A quantitative assessment of genetic divergence for 11 characters using Mahalanobis' D^2 statistic observed the presence of considerable genetic diversity. The forty genotypes were grouped into 7 well defined clusters with variable number of genotypes. The inter-cluster distances (D value) ranged from 8.27 to 25.68.

Among the plant attributes number of effective capitula, hull content, number of seeds in main capitulum, seed yield per plant were found to be important in the present study.

Harish Babu *et al*. (2012) estimated genetic divergence of genotypes of one handrat fifty four genotypes of safflower using D^2 analysis. The genotypes under study were grouped into nine clusters. The number of capitula per plant contributed maximum towards genetic divergence followed by 100 seed weight and number of seeds per capitulum.

Safavi *et al*. (2012) reported the genetic diversity and relationships among traits using twenty genotypes of safflower under rain-fed condition and data were recorded for days to 50% flowering, days to finish flowering, days to physiological maturity, plant height, number of capitula per plant, number of seeds per capitulum, seed index, seed yield, oil per cent and oil yield.

Ingole *et al*. (2013) evaluated forty genotypes and grouped into six clusters. The cluster-I was the largest containing twenty nine genotypes followed by cluster-II (five genotypes) and cluster-V (three genotypes). The average inter cluster distance was maximum between clusters III and VI, followed by clusters II and III, clusters IV and VI, clusters I and VI, clusters I and V. The seed yield per plant contributed maximum towards genetic divergence followed by oil content and days to maturity.

Shivani *et al*. (2013) studied ninety genotypes of safflower for genetic divergence using Mahalanobis' D^2 statistics. The genotypes were grouped into twelve clusters. Seed yield contributed maximum to the total divergence. The maximum inter cluster distance was observed between cluster VIII and cluster XI whereas minimum distance between the clusters IV and XII.

Pavithra et al. (2016) studied fifteen quantitative characters among 150 accessions of safflower representing different geographical areas by Mahalanobis D^2 statistical showed that there is a substantial genetic diversity. The D^2 values of accessions ranged between 10.90 and 84.32. The intra cluster distances were ranged from 18.94 to 30.87. These accessions were grouped into 24 clusters the clustering pattern necessarily associated with geographical diversity in the set of germplasm. Among the character attributed the maximum divergence were biological yield, harvest index, plant height, volume weight, number of seeds per capitulum and capitula per plant.

Pushpavalli *et al* (2017) evaluted forty seven genotypes of safflower for Genetic divergence.The genotypes were clustered into ten different groups based on Mahalonobis D^2 statistics. Genotypes in cluster VI recorded highest mean values for number of effective capitula per plant and cluster IX for number of seeds per capitulum. However 100-seed weight contributed to maximum genetic divergence followed by days to 50% flowering among the genotypes studied.

CHAPTER-III

MATERIAL AND METHODS

The present study on **"Genetic Divergence for yield & its attributes in safflower (*Carthamus tinctorius* L.)"** was carried out at College of Agriculture, Indore during the *rabi* season of 2017-18. With a view of obtaining high precision in the results, the material used and the techniques adopted for the study was considered as most important one. The details of material and methods were used to carry out experiment and statistical procedures followed are presented in this chapter.

3.1 Site of the experiment:

The experiment was conducted in the research form of All India Coordinated Research Project on Safflower, College of Agriculture, Indore (M.P.). Indore, which is situated between latitude $22^0$43' N and longitude $76^0$54' E and at an altitude of 567 metre above the mean sea level.

3.2 Climate and weather conditions:

Indore, belongs to western part of Madhya Pradesh. It has sub-tropical and semi arid climate with an average annual rainfall of 954 mm. Mostly rains received in Indore through south west monsoon during rainy season (mid June to September end). The minimum and maximum mean temperature ranges from 6^0 to 25^0 c and from 23^0 to 43^0 c respectively. December and January are the coldest month while, the temperature attains its highest level at the end of may. The weekly maximum and minimum relative humidity, temperatures and rainfall during crop growth period are described in Table 3.1.

3.3 Experimental material:

The experimental material for present study comprised of forty genotypes. The experiment was conducted in Randomized Block Design with three replications. Each entry was sown in five rows of 5 m length with a spacing of 45 cm between rows and 20 cm between the plants. The material was sown on November 14 &15, 2017. All recommended package of practices were followed during the conduction of experiment to raise a good crop. The details of experimental material are given in Table 3.2

3.4 Observations recorded:

Observations were recorded on plot as well as single plant basis. Observations on plot basis were recorded for days to flower initiation, days to 50% flowering and days to maturity. For recording observations on single plant basis, five plants from each plot were randomly selected. Average of these five plants in respect of number of capitula per plant, number of primary branches per plant, plant height, lower branch height, days to maturity, number of seeds per capitulum, 100-seed weight, biological yield per plant (g), seed yield per plant (g), harvest index (%), vegetative phase (days), and reproductive phase (days).The data recorded as above subjected to statistical analysis.

The recorded observations were as below:

3.4.1 Days to flower initiation:

The Number of days from the date of sowing to the date of first flower initiation was observed on plot basis.

3.4.2 Days to 50% flowering:

The Number of days from the date of sowing to the date when 50% plants of a plot was flowered.

3.4.3 Days to maturity:

Number of days from sowing to physiological maturity was recorded.

3.4.4 Vegetative phase:

Table 3.1: Meteorological data during crop season 2017-18

S.No.	Genotype	Specific characters

SMW	Date	Temperature(^{0}C)		RH (%)		Wind velocity (Km/hr)	Rainfall (mm)
		Max.	Min.	morning	evening		
44	29 Oct – 04 Nov	32.9	12.9	78.4	63.6	0.2	0.00
45	05 Nov – 11 Nov	30.4	13.1	82.6	61.0	0.2	0.00
46	12 Nov – 18 Nov	29.3	12.4	83.0	64.4	0.1	0.00
47	19 Nov – 25 Nov	27.9	12.4	78.7	60.5	0.1	0.00
48	26 Nov – 02 Dec	29.4	10.3	78.9	58.5	0.2	0.00
49	03 Dec – 09 Dec	26.0	10.9	85.5	68.1	0.3	0.00
50	10 Dec – 16 Dec	27.9	11.5	79.0	61.3	0.2	0.00
51	17 Dec – 23 Dec	25.6	9.8	81.0	64.9	0.3	0.00
52	24 Dec – 31 Dec	26.8	7.5	89.7	70.5	0.1	0.00
1	01 Jan – 07 Jan	26.79	7.79	87.93	66.74	0.29	0.00
2	08 Jan – 14 Jan	26.21	9.36	86.34	62.19	0.25	0.00
3	15 Jan – 21 Jan	29.71	10.64	90.33	67.94	0.20	0.00
4	22 Jan – 28 Jan	27.64	8.29	91.80	65.26	0.36	0.00
5	29 Jan – 04 Feb	30.93	9.93	91.01	70.77	0.21	0.00
6	05 Feb – 11 Feb	30.57	11.50	87.69	65.46	0.43	0.00
7	12 Feb – 18 Feb	30.79	10.64	90.53	69.00	0.56	0.00
8	19 Feb – 25 Feb	34.50	13.86	81.41	61.89	0.28	0.00
9	26 Feb – 04 Mar	35.71	16.86	79.77	64.59	0.48	0.00
10	05 Mar – 11 Mar	35.14	17.14	74.10	65.74	0.62	0.00
11	12 Mar – 18 Mar	36.86	17.79	65.44	58.94	0.67	0.00
12	19 Mar – 25 Mar	36.43	18.36	58.40	56.51	1.12	0.00
13	26 Mar – 01 Apr	39.93	18.21	61.69	55.60	0.97	0.00
14	02 Apr – 08 Apr	40.86	21.64	62.99	61.34	1.28	0
15	09 Apr – 15 Apr	39.50	22.36	55.96	57.73	0.74	0
16	16 Apr – 22 Apr	41.50	24.07	57.41	55.73	1.72	0

Source: Meteorological observatory, AICRPDA, College of Agriculture, Indore

1.	IVT-I-1	Tall, Yellow at blooming and Red at fading.
2.	IVT-I-2	Dwarf, Red at blooming and at fading both.
3.	IVT-I-3	Dwarf, Red at blooming and at fading both.
4.	IVT-I-4	Dwarf, White at blooming and White at fading.
5.	IVT-I-5	Dwarf, Red at blooming and Red at fading.
6.	IVT-I-6	Tall, Yellow at blooming and Red at fading.
7.	IVT-I-7	Tall, Yellow at blooming and Red at fading.
8.	IVT-I-8	Tall, Yellow at blooming and Red at fading.
9.	IVT-I-9	Tall, Yellow at blooming and Red at fading.
10.	IVT-I-10	Dwarf, Yellow at blooming and Red at fading.
11.	IVT-I-11	Tall, Yellow at blooming and Orange at fading.
12.	IVT-I-12	Tall, Yellow at blooming and Red at fading.
13.	IVT-I-13	Tall, Yellow at blooming and Red at fading.
14.	IVT-I-14	Dwarf, Yellow at blooming and Red at fading.
15.	IVT-I-15	Tall, Red at blooming and at fading both.
16.	IVT-I-16	Tall, Yellow at blooming and Red at fading.
17.	IVT-II-1	Tall, Yellow at blooming and Red fading.
18.	IVT-II-2	Dwarf, Yellow at blooming and Red at fading.
19.	IVT-II-3	Tall, Yellow at blooming and Red at fading.
20.	IVT-II-4	Dwarf, Yellow at blooming and Red fading.
21.	IVT-II-5	Dwarf, Yellow at blooming and Red at fading.
22.	IVT-II-6	Dwarf, Yellow at blooming and Red at fading.
23.	IVT-II-7	Dwarf, Yellow at blooming and Orange at fading.
24.	IVT-II-8	Dwarf, Yellow at blooming and Red at fading.
25.	IVT-II-9	Tall, Yellow at blooming and Red at fading.
26.	IVT-II-10	Tall, Yellow at blooming and Red at fading.
27.	IVT-II-11	Dwarf, Yellow at blooming and Red fading.
28.	IVT-II-12	Dwarf, Yellow at blooming and Orange at fading.
29.	IVT-II-13	Dwarf, Yellow at blooming and Orange at fading.
30.	IVT-II-14	Dwarf, Yellow at blooming and Red at fading.
31.	IVT-II-15	Dwarf, White at blooming and White at fading.
32.	IVT-II-16	Dwarf, Yellow at blooming and Red at fading.
33.	AVT-I-1	Tall, Yellow at blooming and Red at fading.
34.	AVT-I-2	Dwarf, Yellow at blooming and Red at fading.
35.	AVT-I-3	Tall, Yellow at blooming and Red at fading.
36.	AVT-I-4	Dwarf, Yellow at blooming and Red at fading.
37.	AVT-I-5	Tall, Yellow at blooming and Red at fading.
38.	AVT-I-6	Tall, Yellow at blooming and Orange at fading.
39.	AVT-I-7	Dwarf, Yellow at blooming and Orange at fading.
40.	AVT-I-8	Dwarf, Yellow at blooming and Red at fading.

Table 3.2: List of safflower along with their specific characteristics in brief.

Number of days from the date of sowing to the date of first flower initiation was noted.

3.4.5 Reproductive phase:

Number of days from the date of first flower initiation to physiological maturity was calculated in a plot.

3.4.6 Plant height (cm):

Height of the plant was measured from ground level to the tip of the main shoot at maturity.

3.4.7 Lower branch height (cm):

Height was measured from ground to first branch of the main stem at maturity.

3.4.8 Number of primary branches per plant:

Number of primary branches emerged from main stem were recorded at the time of maturity.

3.4.9 Number of capitula per plant:

Numbers of capitula from each of the five randomly selected plants were counted prior to crop harvest and averaged.

3.4.10 Number of seeds per capitulum:

A random sample of 25 capitula was drawn from each plot to workout the average number of seeds per capitulum.

3.4.11 100-seed weight (g):

A composite sample was drawn from the seed yield of the selected plants and hundred seeds counted and weighed.

3.4.12 Biological yield per plant (g):

Weight of total biomass of five selected plants was recorded in grams and averaged.

3.4.13 Harvest index (%):

The harvest index was calculated by the following formula:

Harvest index (%) = (Economic yield/Biological yield) x100

3.4.14 Seed yield per plant (g):

Seed obtained from selected five plants was weighed in grams and averaged.

3.5 Statistical procedures:

3.5.1. Analysis of variance and covariance:

The data on various characters were subjected to statistical analysis by using appropriate method of analysis of variance and covariance as described by Panse and Sukhatme (1954). The range and estimates of mean, phenotypic, genotypic and environmental variances and co-variances, coefficient of variation, standard error and critical difference were calculated for all the fourteen traits. The significant differences between genotypes were tested for the characters under study.

Analysis of variation			
Source of variation	**D.f**	**S.S.**	**M.S.**
Replication	**(r-1)**	**SSr**	**Mr**
Genotypes	**(g-1)**	**SSg**	**Mg**
Error	**(r-1) (g-1)**	**SSe**	**Me**

Where,

r = Number of replications

g = Number of genotypes

Mr = Mean sum of replication

Mg = Mean sum of genotypes

Me = Mean sum of error

$$\text{Genotypic variance} = \frac{(Mg - Me)}{r}$$

Phenotypic variance = $\frac{(Mg - Me)}{r} + Me$

Environmental variance = Me

3.5.2. Estimation of phenotypic and genotypic coefficients of variation:

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formula suggested by Burton (1952).

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

3.5.3. Estimation of heritability and genetic advance:

Heritability:

The following formula given by Singh and Choudhary (1977) was used for estimation of heritability in broad sense.

$$\text{Heritability } h^2 \text{ (Bs)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Genetic advance:

The estimates of expected genetic advance from selection, G(s), was estimated by the formula given by Robinson, Comstock, and Harvey (1949).

$G(s) = k \times h_b^2 \times \sigma_p$

Where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h_b^2 = Heritability coefficient (broad sense) and

σ_p= Phenotypic standard deviation

3.5.4. Estimation of correlations:

Phenotypic, genotypic and environmental correlation coefficients between characters were computed utilizing respective components of variance and co-variance, by following formula suggested by Miller et al. (1958).

$$r_{xy} = \frac{\text{Cov.}_{x,y}}{\sqrt{V_x \times V_y}}$$

Where,

r_{xy} = Correlation coefficient between character x and y,

$\text{Cov}_{x,y}$ = Co-variance of character x and y,

V_x = Variance of character x and

V_y = Variance of character y.

To test the significance of phenotypic and environmental correlation coefficients, the calculated values were compared with the tabulated values of Fisher and Yates (1938) at n-2 degree of freedom at two levels of probability, viz., 5% and 1%.

3.5.5 Path coefficient analysis:

Correlation does not provide an exact picture of the relative importance of influence of each of the component characters. The correlation coefficients between yield and its components were further partitioned into direct and indirect effects with the help of path coefficient analysis originally suggested by Wright (1921, 1934) and further outlined by Dewey and Lu (1959).

Path coefficient is a standardized partial regression, that measures the direct influence of one variable upon other one and allows partition of correlation coefficient into components of direct and indirect effects.

For estimation of various direct and indirect effects, the following set of simultaneous equations were formed and solved.

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

$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots + r_{2n}P_{ny}$

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

Where,

r_{1y} to r_{ny} = Coefficient of correlation between causal factor 1 to n and dependent character y,

r_{12} to $r_{n-1,n}$ = Coefficient of correlation among causal factors themselves, and

P_{1y} to P_{ny} = Direct effects of characters 1 to n on character y.

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

Residual effect (P_{RY}) = $\sqrt{1 - R^2}$

(a) Estimation of Wilk's (Λ) criterion:

To test the significance of difference between lines, taking all the characters simultaneously, 'V' statistic was estimated which was based on Wilk's (Λ) criterion (Wilks, 1932). The sum of squares and sum of products of error and error + variety were utilized for estimation of "Λ".

Following equation was used to estimate the value of "Λ":

$$\text{"}\Lambda\text{"} = \frac{|E|}{|E + V|}$$

Where,

$|E|$ was the determinant of error sum of squares and sum of products matrix and $|E + V|$ was the determinant of the "error + variety' sum of squares and sum of products matrix.

χ^2 test was used to test the significance of "Λ" as

$$\chi^2_{pq} = V = -\,m \log_e \Lambda$$

Where,

$$m = n - \frac{p + q + 1}{2} \text{ with pq d.f.}$$

Where,

n = total number of observations –1,

p = number of characters,

q = k – 1, and

k = number of lines

(b) Estimation of D^2-statistic:

To estimate divergence between two lines, Mahalanobis (1936) D^2-statistic was used. He defined generalized distance between two lines as:

$$\Delta^2 = \sum\sum \lambda^{ij} \delta_i \delta_j$$

Where,

λ^{ij} = Reciprocal matrix of the common dispersion matrix λ_{ij},

δ_i = Difference between mean values of the two lines for the ith character, and

δ_j = Difference between mean values of the two lines for the jth character.

D^2-statistic is the sample estimate of the generalized distance which is estimated as:

$$D^2 = \sum_{i,j=1}^{p} s^{ij} d_i d_j$$

Where, s^{ij} and d_i are the sample estimates of λ^{ij} and δ_i, respectively. For calculating D^2 values inversion of matrix was required which is quite cumbrous. To overcome this type of difficulty original , correlated unstandardized character means (X_i) were transformed to uncorrelated standardized variables (Y_i) by Pivotel condensation method (Rao, 1952). D^2 between any pairs of populations, for example population 1 and 2, was then estimated as:

$$D_p^2 = \sum_{i=1}^{p} (Y_{i1} - Y_{i2})^2$$

Where, p = number of characters used for estimation of divergence.

(c) Determination of population constellations:

Population constellations were determined by Tocher's method described by Rao(1952). No formal rules can be laid down for finding the clusters because a cluster is not well defined term. The only criteria appeared to be that any two

Groups belonging to same cluster should at least on an average show a smaller D^2 than those belonging to the two different clusters. Rao (1952) suggested that two closely related populations of low D^2 value be pooled together and then a third population of similar D^2value be added to this group such that it did not increase the average D^2value considerably. This process is continued. Any population, which sharply increases in the average D^2 value, should not be included in that group. After formation of first cluster, the process is repeated to form second, third, etc., clusters using remaining populations until all populations are included in one or the other clusters. After the formation of cluster average intra and inter-cluster distances were calculated. The square root of corresponding average D^2 values represents the distance within and between groups.

CHAPTER-IV

EXPERIMENTAL RESULTS

The experimental results of the present study entitled "Genetic Divergence for yield and its attributes in Safflower (*Carthamus tinctorius* L*).*" are presented under the following headings:

- Analysis of variance
- Mean performance and range
- Phenotypic and genotypic coefficients of variation
- Heritability in broad sense
- Genetic advance
- Correlation coefficient estimates
- Path analysis
- D^2 statistic

4.1. Analysis of variance:

The data for all the fourteen traits among forty genotypes were analyzed and presented in Table 4.1. The analysis of variance indicated that component of variance for genotypes was highly significant for all the characters studied *viz.,* days to flower initiation, days to 50% flowering, days to maturity, vegetative phase, reproductive phase, plant height, lower branch height, number of primary branches per plant, number of capitula per plant, number of seeds per capitulum, biological yield per plant, 100-seed weight, harvest index, and seed yield per plant..

4.2. Mean performance and range:

The mean values for fourteen characters and their range for forty genotypes are given in Appendix and Table 4.2.

Table 4.1 ANOVA showing mean sum of squares for different traits

S. No.	Characters	Mean Sum of squares		
		Replication (2) df	Treatment (39) df	Error (78) df
1	Flower initiation (days)	2.63	6.38**	1.96
2	Days to 50% flowering	10.03	7.92**	1.22
3	Maturity phase (days)	12.93	29.34**	2.12
4	Vegetative phase (days)	2.63	6.38**	1.96
5	Reproductive phase (days)	5.70	22.66**	4.20
6	Plant height (cm)	0.03	385.93**	5.35
7	Lower branch height (cm)	15.89	218.99**	8.67
8	Number of Primary branches per plant	0.76	3.49**	0.58
9	Number of Captiula per plant	27.48	176.04**	6.75
10	Number of seeds per capitulum	24.60	72.60**	5.21
11	100- seed weight (g)	0.40	2.64**	0.11
12	Biological yield per plant (g)	109.59	1334.25**	19.59
13	Harvest index (%)	6.91	29.11**	7.76
14	Seed yield per plant (g)	4.11	100.23**	13.97

* * Significant at 0.01 level of significance

4.2.1. Days to flower initiation:

The variation for days to flower initiation in safflower genotypes under study ranged from 94.33 (AVT-I-2) to 100 days (IVT-II-3) around a grand mean of 97.13 days. Out of 40 genotypes studied, 21 genotypes showed earliness in flower initiation.

4.2.2. Days to 50% flowering:

The substantial variation for days to 50 % flowering was recorded for material studied. It ranged between 106 (AVT-I-2) and 111.33 (IVT-II-10) days with a general mean of 108.67 days. Out of 40 genotypes studied, 17 genotypes exhibited earliness in 50% flowering.

4.2.3. Days to maturity:

The range for this character was between 138.67 (IVT-II-2) and 150.33 days (IVT-II-10) with a general mean of 143.56 days. Out of all 40 genotypes studied, 23 genotypes exhibited earliness in maturity.

4.2.4. Vegetative phase (days):

The range for vegetative phase was from 94.33 days (AVT-I-2) to 100.00 days (IVT-II-3) with a general mean 97.13 days. Out of 40 genotypes studied, 21 genotypes exhibited low vegetative phase.

4.2.5. Reproductive phase (days):

The mean value for this character ranged from 41.33 days (IVT-II-3) to 52.33 days (IVT-II-12) around a population mean of 46.43. Out of all 40 genotypes studied, 18 genotypes exhibited long reproductive phase.

4.2.6. Plant height (cm):

The plant height for the genotypes under study ranged between 93.00 cm to 133.47 cm with a general mean of 111.90 cm. The genotype IVT-I-13 was the tallest genotype having plant height of 133.47 cm followed by IVT-I-

11 (133.27cm). However, the genotype IVT-II-6 was dwarfest with only 93.00 cm height. Out of all 40 genotypes studied, 17 genotypes exhibited tall type.

4.2.7. Lower branch height (cm):

Genotype IVT-I-3 had the lowest node to start branching *i.e.* 36.60 cm (IVT-I-3) and that of highest was of genotype AVT-I-1(69.80). Lower branch has mean of 49.47 cm. Out of 40 genotypes studied, 20 genotypes showed low lower branch height.

4.2.8. Number of primary branches per plant:

Number of primary branches per plant was ranged from 5.27 (AVT-I-2) and 9.13 (IVT-I-3) with a grand mean of 6.8. Out of all genotypes studied, 18 genotypes showed higher number of branches per plant.

4.2.9. Number of capitula per plant:

It ranged from 19.07 (IVT-II-5) to 54.00 (IVT-I-3) with a general mean of 28.09. Out of 40 genotypes studied, 17 genotypes showed higher number of capitula per plant.

4.2.10. Number of seeds per capitulum:

The substantial amount of variation for number of seeds per capitulum was recorded for 40 genotypes. The range for number of seeds per capitulum was from 14.27 (IVT-I-8) to 36.4 (IVT-II-8) with a general mean of 21.93. Out of 40 genotypes studied, 12 genotypes exhibited higher number of seeds per capitulum in relation to general mean.

4.2.11. 100-seed weight (g):

The mean value for 100-seed weight ranged between 2.8g (IVT-II-9) and 6.2 g (IVT-I-6) with a general mean of 4.84 g. Out of 40 genotypes studied, 25 genotypes showed higher seed index in relation to general mean (4.84g).

4.2.12. Biological yield per plant (g):

The mean value for this character ranged between 40.90 (AVT-I-7) and 135.37 g (AVT-I-6) with a grand mean of 76.95 g. Out of 40 genotypes studied, 20 genotypes showed higher biological yield per plant than population mean.

4.2.13. Harvest index (%):

Harvest index for 40 safflower genotypes ranged between 12.07 (AVT-I-6) and 26.43% (IVT-I-14) with a general mean of 20.14 per cent. Out of all 40 genotypes studied, 21 genotypes exhibited higher harvest index value in relation to general mean..

4.2.14 Seed yield per plant (g):

Out of 40 genotypes studied, 16 genotypes showed higher seed yield than population mean (19.45g). The range for seed yield per plant was from 9.4 g (AVT-I-7) to 36.10 g (IVT-I-3) with a grand mean of 19.45 g.

Table: 4.2 Estimate of various parameters of genetic variability for different traits in safflower

S. No.	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability (Broad sense %)	Genetic advance	Genetic advance as % of mean
			Mini.	Maxim.					
1	Flower initiation (days)	97.13	94.33	100	1.91	1.25	42.85	1.64	1.69
2	Days to 50% flowering	108.61	106	111.33	1.71	1.38	64.68	2.48	2.28
3	Maturity phase (days)	143.56	138.67	150.33	2.33	2.10	81.05	5.59	3.89
4	Vegetative phase (days)	97.13	94.33	100	1.91	1.25	42.85	1.64	1.69
5	Reproductive phase (days)	46.43	41.33	52.33	6.93	5.34	59.41	3.94	8.49
6	Plant height (cm)	111.90	93	133.47	10.28	10.07	95.95	22.73	20.31
7	Lower branch height (cm)	49.47	36.60	69.80	17.94	16.93	88.99	16.27	32.89
8	Primary branches per plant (Number)	6.80	5.27	9.13	18.32	14.50	62.64	1.61	23.64
9	Captiula per plant (Number)	28.09	19.07	54.00	28.30	26.74	89.30	14.62	52.05
10	Seed per capitulum (Number)	21.93	14.27	36.40	23.99	21.61	81.60	8.80	40.11
11	100- seed weight (g)	4.84	2.80	6.20	20.22	18.98	88.03	1.78	36.67
12	Biological yield per plant (g)	76.95	40.90	135.37	27.81	27.21	95.72	42.19	54.83
13	Harvest index (%)	20.14	12.07	26.43	19.16	13.25	47.84	3.80	18.88
14	Seed yield perplant(g)	19.45	9.40	36.10	33.62	27.58	67.29	9.06	46.60

4.3. Coefficient of variation:

Estimation of phenotype coefficient of variation (PCV) and genotype coefficients of variation (GCV) were calculated and are presented in Table 4.2.

The highest PCV was estimated for seed yield per plant(33.62%), followed by, number of capitula per plant (28.30%), biological yield per plant (27.81%), number of seeds per capitulum (23.99%), 100-seed weight (20.22%), harvest index (19.16%), number of primary branches per plant (18.32%), lower branch height (17.94%). However, low PCV was observed for days to 50% flowering (1.71%), followed by, days to flower initiation (1.91%), vegetative phase (1.91%), days to maturity (2.33%), reproductive phase (6.93%) and plant height (10.28%).

The highest GCV was observed for seed yield per plant(27.58%), followed by biological yield per plant(27.21%), number of capitula per plant (26.74%), number of seeds per capitulum (21.61%), 100-seed weight (18.98%), lower branch height (16.93%), number of primary branches per plant (14.50%), harvest index (13.25%). However, low GCV was observed for days to flower initiation (1.25%), vegetative phase (1.25%), days to 50% flowering (1.38%), days to maturity (2.10 %), reproductive phase (5.34%) and plant height (10.07%).

4.4 Heritability:

Heritability estimate in broad sense was calculated for all the characters under study and the results are presented in (Table 4.2). The heritability (broad sense) ranged from 42.85 % (days to flower intiation) to 95.95 % (plant height). High heritability was observed for plant height (95.95 %), biological yield per plant (95.72%), number of capitula per plant (89.30%), lower branch height (88.99%), 100-seed weight (88.03%), number of seeds per capitulum (81.60%), days to maturity (81.05%). It was moderate for seed yield per plant (67.29%), days to 50% flowering (64.68%), number of primary branches per plant (62.64%) and reproductive phase (59.41%). While it was low for harvest index (47.84%), vegetative phase (42.85%) and days to flower initiation (42.85%).

4.5 Expected genetic advance:

Expected genetic advance was estimated for fourteen characters and the results are presented in (table 4.2).

The estimates of expected genetic advance as per cent of mean was high for biological yield per plant (54.83%), number of capitula per plant (52.05), seed yield per plant (46.60%), number of seeds per capitulum (40.11%), 100-seed weight (36.67%), lower branch height (32.89%), number of primary branches per plant (23.64%), plant height (20.31%), harvest index (18.88%), While, reproductive phase (8.49%), days to maturity (3.89%), days to 50% flowering (2.28%), days to flower initiation (1.69%) and vegetative phase (1.69%) possessed low values for expected genetic advance.

4.6 Estimates of correlation coefficients:

4.6.1 Phenotypic correlation coefficients:

Phenotypic correlation coefficients between yield and its contributing characters and among themselves were estimated and results are presented in Table 4.3.

(a) Phenotypic Correlation with seed yield:

Seed yield per plant (g) exhibited significant positive correlation with biological yield per plant (0.668), harvest index (0.527), number of capitula per plant (0.487), 100 seed weight (0.347), and days to maturity (0.259). However, lower branch height (-0.392) and plant height (-0.186) had significant negative association with seed yield per plant at phenotypic lavel.

(b) Phenotypic correlation among yield attributes:

Phenotypic correlation coefficients among all yield attributes were estimated and the results are presented in Table 4.3.

Days to flower initiation showed significant positive correlation with vegetative phase (1.000), days to 50% flowering (0.432), days to maturity (0.345), while, it was negative and significant with reproductive phase (-0.218).

Days to 50% flowering had significant positive correlation with vegetative phase (0.432) and days to maturity (0.345).

Days to maturity had significant and positive correlation with reproductive phase (0.841), number of capitula per plant (0.448) and vegetative phase (0.345) and it was significant negative correlation with lower branch height (-0.315).

Vegetative phase showed significant positive correlation with days to flowering initiation(1.000), days to 50% flowering (0.432), days to maturity (0.345), while, it was negative and significant with reproductive phase (-0.218).

Plant height exhibited significant and positive correlation with lower branch height (0.432) while, significant and negative correlation coefficient with 100– seed weight (-0.254).

Lower branch height showed positive and significant correlation with plant height (0.432). It was significant and negative correlation with number of capitula per plant (-0.556), 100- seed weight (-0.409) and maturity phase (-0.315).

Number of primary branches per plant showed significant positive correlation with number of seeds per capitulum per plant (0.644), days to maturity (0.352), reproductive phase (0.271), biological yield per plant (0.231).While, it showed significant and negative correlation with lower branch height (-0.388) at phenotypic level.

Number of capitula per plant had significant positive correlation with days to maturity (0.448), biological yield per plant (0.479) and it showed significant and negative correlation with lower branch height (-0.556).

Number of seeds per capitulum exhibited significant positive correlation with primary branches per plant (0.180) and negative significant correction with 100-seed weight (-0.310).

Hundred seed weight exhibited significant positive correlation with capitula per plant (0.364), harvest index (0.223) and negative significant correlated with lower branch height (-0.409) and plant height (-0.254).

Biological yield per plant showed positive significant correlation with number of capitula per plant (0.479), reproductive phase (0.331) and negative significant correlation with lower branch height (-0.313).

Harvest index had significant positive correlation with 100-seed weight (0.223) and significant negative correlation with biological yield per plant (-0.199).

4.6.2 Genotypic correlation coefficients:

Genotypic correlation coefficients between yield and its contributing characters and among themselves were estimated and results are presented in Table 4.4.

(a) Genotypic correlation with seed yield:

Biological yield per plant (0.713), number of capitula per plant (0.582), 100-seed weight (0.468), harvest index (0.346), and days to maturity (0.408) exhibited positive correlation while, lower branch height (-0.478) and plant height (- 0.237) had negative correlation with seed yield per plant at genotypic level (Table 4.4).

(c) Genotypic correlation among yield attributes:

Genotypic correlation coefficients among all yield attributes were estimated and the results are presented in Table 4.4.

Days to flower initiation had positive correlation with vegetative phase (1.000), days to 50% flowering (0.719), days to maturity (0.601), harvest index (0.414) and number of capitula per plant (0.289) however ,it had negative association with lower branch height (-0.225) at genotypic level.

Days to 50% flowering exhibited positive correlation with vegetative phase (0.719), days to maturity (0.483), number of primary branches per plant (0.324), while, it had negative correlation with lower branch height (-0.059) and biological yield per plant (-0.029) at genotypic level.

Days to maturity exhibited positive correlation with reproductive phase (0.920), vegetative phase (0.601), number of primary branches per plant (0.514) and negative correlation with lower branch height (-0.317) at genotypic level.

Vegetative phase had positive correlation with flowering initiation (1.000), days to 50% flowering (0.719), days to maturity (0.601) harvest index (0.414) and number of capitula per plant (0.289) however ,it had negative association with lower branch height (-0.225) at genotypic level.

Plant height had positive correlation with lower branch height (0.461) and negative correlation with 100–seed weight (-0.284) and harvest index (-0.188).

Lower branch height showed positive correlation with plant height (0.461) while, it was negative correlation with number of capitula per plant (-0.605), 100- seed weight (-0.450) and biological yield per plant (-0.328).

Number of primary branches per plant showed positive correlation with maturity phase (0.514), reproductive phase (0.480), number of seeds per capitulum (0.323), while, it had negative correlation with lower branch height (-0.478) and harvest index (-0.303)

Number of capitula per plant had positive correlation with seed days to maturity (0.503), biological yield per plant (0.502) and it showed significant and negative correlation with lower branch height (-0.605) at genotypic level .

Number of seeds per capitulum had significant positive correlation with number of primary branches per plant (0.323), days to flower initiation (0.243) and days to maturity (0.213) and negative correction with 100-seed weight (-0.368).

100–seed weight exhibited positive correlation with number of capitula per plant (0.427), harvest index (0.377) and negative significant correlated with lower branch height (-0.450) and plant height (-0.284).

Biological yield per plant had positive correlation with number of capitula per plant (0.502), reproductive phase (0.439) and negative significant correlation with lower branch height (-0.328) at genotypic level.

Harvest index showed significant positive correlation with flowering initiation (0.414), 100-seed weight (0.377) and it was negative correlation with biological yield per plant (-0.413).

4.7. Path coefficient analysis at genotypic level:

The path coefficient analysis was estimated for considering seed yield per plant as dependent character and yield attributes as independent characters at genotypic level. The genotypic correlation was devided into direct effects, indirect effects and residual effects and the results are presented in (Table 4.5)**.**

a) Direct effect:

In the present investigation it was observed that number of capitula per plant (1.280) had very high positive direct effects on seed yield. However, 100-seed weight (0.104), days to flower initiation (0.104) showed low positive direct effects and days to 50% flowering (0.075) exhibited positive but negligible direct effects on seed yield. Harvest index (-0.701) had high negative direct effect on seed yield. While, primary branches per plant (-0.275), vegetative phase (-0.245) expressed moderate negative direct effects on seed yield. Lower branch height (-0.094) and Number of seeds per capitulum (-0.053) showed negative and negligible direct effects on seed yield per plant.

(b) Indirect effect

Days to flower initiation had high positive indirect effect via harvest index (0.808), number of primary branches per plant (0.479).While, reproductive phase (0.117) had low indirect effect on seed yield. However, high negative indirect effects on seed yield were recorded via vegetative phase (-0.305) and capitula per plant (-0.302).

Days to 50% flowering showed high positive indirect effect on seed yield through number of primary branches per plant (0.528) and harvest index (0.470). Moderate negative indirect effects on seed yield were recorded through days to flower initiation (-0.243) and vegetative phase (-0.219). Negative and negligible indirect effect was observed on seed yield via plant height (-0.010) on seed yield.

Days to maturity recorded high positive indirect effect on seed yield via primary branches per plant (0.837), biological yield per plant (0.624).While, high negative indirect effect was found on seed yield through number of capitula per plant (-0.527) and days to flower initiation (-0.407).

Vegetative phase exhibited high positive indirect effect on seed yield via harvest index (0.808) and number of primary branches per plant (0.479).While, it showed high negative indirect effects on seed yield via days to flower initiation (-0.305) and number of capitula per plant (-0.302).

Reproductive phase recorded high positive indirect effect on seed yield via biological yield per plant (0.746), number of primary branches per plant (0.782). While, negative and high indirect effect on seed yield was observed through number of capitula per plant (-0.491) and harvest index (-0.430).

Plant height showed positive and moderate indirect effect on seed yield through lower branch height (0.265) and number of primary branches per plant (0.254). Negligible positive indirect effect on seed yield was exhibited through vegetative phase (0.014). However, negative and high indirect effect on seed yield through harvest index (-0.367). Negative and moderate indirect effect showed through days to flower initiation (-0.204).

Lower branch height observed the high positive indirect effect on seed yield through number of capitula per plant (0.632) and days to flower initiation (0.576), while, negligible positive indirect effect exhibited on seed yield through days to maturity (0.014) and negative and high indirect effect on seed yield was showed via number of primary branches per plant (-0.777), biological yield per plant (-0.557).

Number of primary branches per plant exhibited very high and positive indirect effect on seed yield per plant was observed via days to flower initiation (1.628) and high positive indirect effect on seed yield showed through biological yield per plant (0.507). While, high and negative indirect effect was observed on seed yield through number of capitula per plant (-0.822) and harvest index (-0.591).

Number of capitula per plant exhibited high positive indirect effect on seed yield per plant was through biological yield (0.854) and moderate was recorded via plant height (0.229). While, very high and negative indirect effect on seed yield was showed through flower initiation (-1.046).However, it was high and negative indirect effect on seed yield exhibited via number of primary branches per plant (-0.348).

Number of seeds per capitulum had high positive indirect effect on seed yield via capitula per plant (0.526).While it was negligible positive indirect effect observed on seed yield through days to 50% flowering (0.025).

Negative and moderate indirect effect observed on seed yield through harvest index (-0.293).

100-seed weight showed high and positive indirect effect on seed yield per plant via harvest index (0.733). Moderate and positive indirect effect was observed on seed yield through biological yield per plant (0.294). While, it was negative and high indirect effect on seed yield through number of seeds per capitulum (-0.449) and negative and moderate indirect effects exhibited on seed yield though days to flower initiation (-0.270).

Biological yield per plant showed very high positive indirect effect on seed yield via days to flower initiation (1.699).Moderate and positive indirect effect on seed yield showed through plant height (0.214) and negative and high indirect effect was observed on seed yield via harvest index (-0.805) and number of seeds per capitulum (-0.525).

Harvest index recorded very high and positive indirect effect on seed yield via days to flower initiation (1.952).While, it showed negative and high indirect effects on seed yield via number of capitula per plant (-0.493). Negative and low indirect effect on seed yield was showed through reproductive phase (-0.126).

Residual effect was found to be low that is 0.1918.

4.8.1 Divergence analysis:

Genetic divergence study is a vital tool for the assessment of genotypes and selection of parents for the hybridization programme. So, present study was aimed at analysis of genetic divergence among the forty genotypes and to identify the superior and divergent lines for formulating the crossing programme. Wilk’s lambda criterion was used for simultaneous test of significance for differences in the mean values of the fourteen characters and the pooled effect was found significant indicating a broad range of diversity among the genotypes.

(i) D^2 statistic:

Generalized distance was calculated through Mahalanobis D^2 – statistic. D^2 values were estimated for all the 40 genotypes. The maximum divergence (D = 9.84) was recorded between genotypes AVT-I-6 and AVT-I-7, while minimum divergence (D = 2.64) between IVT-II-13 and AVT-I-8.

Clusters of genotypes and estimates of intra and inter cluster distance:

The cluster formation was done by using Tocher’s method, as suggested by Rao (1952). All the forty genotypes under study were grouped into eight clusters.(table 4.6). Cluster I comprised of maximum number of genotypes (19 genotypes), followed by cluster IV (7 genotypes), cluster II (4 genotypes), cluster III (3 genotypes), cluster V, VI and VII (2 genotypes each) and cluster VIII contained only 1 genotype (Table 4.6).

The average distance within and between clusters and average inter and intra cluster D^2 values are presented in Table no. 4.7. In this table, the diagonal values (bold) are mean intra cluster and off the diagonal values are inter cluster distances.

Table 4.3: Estimates of phenotypic correlation coefficient

Characters	Flower initiation (days)	Days to 50% flowering	Maturity phase (days)	Vegetative phase (days)	Reproductive phase (days)	Plant height (cm)	Lower branch height (cm)	Primary branches per plant (Number)	Captiula per plant (Number)	Seed per capitulum (Number	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Flower initiation (days)	1													
Days to 50% flowering	0.432**	1												
Maturity phase (days)	0.345**	0.345**	1											
Vegetative phase (days)	1.000**	0.432**	0.345**	1										
Reproductive phase (days)	-0.218*	0.110	0.841**	-0.218*	1									
Plant height (cm)	-0.024	0.044	0.018	-0.024	0.032	1								
Lower branch height (cm)	-0.149	-0.053	-0.315**	-0.149	-0.242**	0.432**	1							
Primary branches per plant (Number)	0.164	0.137	0.352**	0.164	0.271**	0.125	-0.388**	1						
Captiula per plant (Number)	0.154	0.124	0.448**	0.154	0.377**	0.056	-0.556**	0.644**	1					
Seeds per capitulum (Number)	0.145	0.045	0.114	0.145	0.035	0.101	0.153	0.180*	0.042	1				
100- seed weight	0.052	0.122	0.194*	0.052	0.172	-0.254**	-0.409**	0.133	0.364**	-0.310**	1			
Biological yield per plant (g)	0.001	-0.009	0.318**	0.001	0.331**	-0.094	-0.313**	0.231*	0.479**	-0.022	0.153	1		
Harvest index (%)	0.084	0.157	-0.082	0.084	-0.133	-0.132	-0.146	-0.149	0.045	-0.141	0.223*	-0.199*	1	
Seed yield per plant (g)	0.099	0.161	0.259**	0.099	0.212*	-0.186*	-0.392**	0.107	0.487**	-0.082	0.347**	0.668**	0.527**	1

Table 4.4: Estimates of Genotypic correlation coefficients

Characters	Flower initiation (days)	Days to 50% flowering	Maturity phase (days)	Vegetative phase (days)	Reproductive phase (days)	Plant height (cm)	Lower branch height (cm)	Primary branches per plant (Number)	Captiulam per plant (Number)	Seeds per capitulum (Number)	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Flower initiation (days)	1													
Days to 50% flowering	0.719	1												
Maturity phase (days)	0.601	0.483	1											
Vegetative phase (days)	1.000	0.719	0.601	1										
Reproductive phase (days)	0.240	0.234	0.920	0.240	1									
Plant height (cm)	-0.047	0.048	0.020	-0.047	0.048	1								
Lower branch height (cm)	-0.225	-0.059	-0.317	-0.225	-0.275	0.461	1							
Primary branches per plant (Number)	0.294	0.324	0.514	0.294	0.480	0.156	-0.478	1						
Captiula per plant (Number)	0.289	0.161	0.503	0.289	0.470	0.063	-0.605	0.786	1					
Seeds per capitulum (Number)	0.243	0.064	0.213	0.243	0.140	0.101	0.140	0.323	0.051	1				
100- seed weight (g)	0.040	0.170	0.201	0.040	0.225	-0.284	-0.450	0.168	0.427	-0.368	1			
Biological yield per plant (g)	0.014	-0.029	0.367	0.014	0.439	-0.106	-0.328	0.298	0.502	-0.011	0.173	1		
Harvest index (%)	0.414	0.241	-0.015	0.414	-0.220	-0.188	-0.202	-0.303	0.030	-0.150	0.377	-0.413	1	
Seed yield per plant (g)	0.305	0.203	0.408	0.305	0.346	-0.237	-0.478	0.165	0.582	-0.046	0.468	0.713	0.346	1

Table 4.5: Genotypic path analysis of various characters

Characters	Flower initiation (days)	Days to 50% flowering	Maturity phase (days)	Vegetative phase (days)	Reproductive phase (days)	Plant height (cm)	Lower branch height (cm)	Primary branches per plant (Number)	Captiula per plant (Number)	Seeds per capitulum (Number)	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Genotypic correlation with seed yield
Flower initiation (days)	**0.104**	-0.174	-0.245	-0.305	0.117	0.01	-0.13	0.479	-0.302	-0.069	-0.011	0.023	0.808	0.305
Days to 50% flowering	-0.243	**0.075**	-0.196	-0.219	0.114	-0.01	-0.034	0.528	-0.168	-0.018	-0.046	-0.049	0.47	0.203
Maturity phase (days)	-0.407	0.063	**-0.117**	-0.183	0.449	-0.004	-0.183	0.837	-0.527	-0.06	-0.055	0.624	-0.029	0.408
Vegetative phase (days)	-0.305	0.104	-0.174	**-0.245**	0.117	0.01	-0.13	0.479	-0.302	-0.069	-0.011	0.023	0.808	0.305
Reproductive phase (days)	0.488	0.025	-0.057	-0.375	**-0.073**	-0.01	-0.158	0.782	-0.491	-0.04	-0.061	0.746	-0.43	0.346
Plant height (cm)	-0.204	-0.005	-0.012	-0.008	0.014	**0.023**	0.265	0.254	-0.066	-0.028	0.077	-0.181	-0.367	-0.237
Lower branch height (cm)	0.576	-0.024	0.014	0.129	0.069	-0.134	**-0.094**	-0.777	0.632	-0.04	0.121	-0.557	-0.394	-0.478
Primary branches per plant (Number)	1.628	0.031	-0.079	-0.209	-0.09	0.234	-0.032	**-0.275**	-0.822	-0.091	-0.046	0.507	-0.591	0.165
Captiula per plant (Number)	-1.046	0.03	-0.039	-0.205	-0.088	0.229	-0.013	-0.348	**1.28**	-0.014	-0.116	0.854	0.058	0.582
Seeds per capitulum (Number)	-0.282	0.025	-0.016	-0.087	-0.074	0.068	-0.021	0.081	0.526	**-0.053**	0.099	-0.019	-0.293	-0.046
100- seed weight (g)	-0.27	0.004	-0.041	-0.083	-0.012	0.111	0.058	-0.259	0.278	-0.449	**0.104**	0.294	0.733	0.468
Biological yield per plant (g)	1.699	0.001	0.007	-0.15	-0.004	0.214	0.022	-0.189	0.486	-0.525	0.003	**-0.047**	-0.805	0.713
Harvest index (%)	1.952	0.043	-0.058	0.006	-0.126	-0.108	0.038	-0.116	-0.493	-0.031	0.042	-0.101	**-0.701**	0.346

Residual effect =0.1918

The highest (D=10.30) inter cluster distance was recorded between cluster III and IV indicating highest heterogeneous character, followed by, cluster I and IV (8.74), cluster II and III (8.67), cluster III and VI (8.53), cluster III and VII (7.45), cluster VI and VIII (7.42), cluster III and V (6.78) and cluster III and VIII (6.78) showed wide diversity between genotypes in these clusters. The lowest (D = 2.54) distance between cluster II and VI ,followed by, cluster VI and VII (2.72), cluster VII and VIII (3.02), cluster V and VI (3.13), cluster V and VII (3.18), cluster II and VIII(3.38) showed close relationship between genotypes in these clusters. The highest (D = 2.25) intra cluster distance was recorded for cluster VIII and lowest (D = 0.03) for cluster III.

Table 4.6: Clustering pattern of forty genotypes on the basis of genetic divergence in safflower:

Cluster	Genotypes	Number of genotypes
I	**IVT-I-1, IVT-I-2, IVT-I-4, IVT-I-7, IVT-I-14, IVT-II-1, IVT-II-1, IVT-II-2, IVT-II-3, IVT-II-5, IVT-II-7, IVT-II-11, IVT-II-12, IVT-II-13, IVT-II-14, IVT-II-15, IVT-II-16, AVT-I-4, AVT-I-8,**	**19**
II	**IVT-I-11, IVT-I-13, IVT-II-9, AVT-I-1,**	**4**
III	**IVT-I-6, IVT-I-12, AVT-I-7**	**3**
IV	**IVT-I-8, IVT-I-9, IVT-I-10, IVT-I-15, IVT-I-16, IVT-II-10, AVT-I-3,**	**7**
V	**IVT-I-3, IVT-I-5**	**2**
VI	**IVT-II-4, IVT-II-8**	**2**
VII	**AVT-I-2, AVT-I-6**	**2**
VIII	**AVT-I-5**	**1**

Cluster mean:

Clusters means of 14 characters are presented in Table 4.8.

1. Days to flower initiation:

Cluster mean for days to flower initiation ranged from cluster VII (95.17) to cluster VIII and VI (99.00).

2. Days to 50% flowering:

Cluster mean for this character ranged from cluster VII (106.33) to cluster VI (110.33).

3. Days to maturity:

Cluster mean for days to maturity ranged between cluster II (140.83) and cluster VI (149.17).

4. Vegetative phase:

Cluster mean for vegetative phase was maximum for cluster VI and VIII (99.00) and minimum for cluster VII (95.17).

5. Reproductive phase:

Cluster mean for reproductive phase was highest for cluster VI (50.17) and lowest for cluster II (44.42).

6. Plant height:

Cluster mean for plant height at maturity ranged from cluster VI (96.57) to cluster II (131.75).

7. Lower branch height:

Cluster mean for lower branch height was highest for cluster VIII (64.07) and lowest for cluster VI (38.20).

8. Number of primary branches per plant:

Cluster mean for number of primary branches ranged from cluster VIII (5.73) to cluster V (8.17).

9. Number of capitula per plant:

Cluster mean was highest for cluster V (49.73) and lowest for cluster VIII (19.27).

10. Number of seeds per capitulum:

Cluster mean for number of seeds per capitulum was maximum for cluster VIII (32.00) and minimum for cluster VII (17.80).

11. 100 – seed weight:

Cluster mean for 100-seed weight ranged from cluster VIII (3.13) to cluster V (6.33).

12. Biological yield per plant:

Cluster mean for biological yield per plant was maximum for cluster VII (123.24) and minimum for cluster III (54.52).

13. Harvest index:

Cluster mean for harvest index ranged between cluster VII (14.44) and cluster V (22.57).

14. Seed yield per plant:

Cluster mean for seed yield per plant ranged from cluster II (13.83) to cluster V (35.25).

Cluster characteristics: (Table 4.8)

Cluster I was characterized by lower height and high harvest index.

Cluster II was characterized by early flowering (96.42), early maturity (140.83), and highest plant height (131.75)

Cluster III was characterized by higher harvest index (21.89).

Cluster IV showed high reproductive phase (48.24), high number of primary branches per plant (7.89).

Cluster V was characterized by highest primary brachesh per plant (8.17) ,high number of capitula per plant (49.73) , high 100- seed weight (6.33) ,highest seed yield per plant (35.25) and highest harvest index (22.57).

Cluster VI was characterized by highest maturity phase (50.17), lower branch height (38.20) and high number of primary branches per plant (8.13).

Cluster VII was characterized by early flowering and lower vegetative phase (95.17) and high seed yield per plant (20.64)

Cluster VIII was characterized by highest seeds per capitulum (32) and high reproductive phase (47.67)

4.7 (a) Average inter and intra (in bold) cluster D^2 distance

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**2.15**	36.35	18.72	76.42	16.75	35.65	32.41	16.58
II		**2.46**	75.26	26.34	16.57	6.50	25.01	11.45
III			**0.001**	106.11	46.10	72.77	55.65	45.98
IV				**3.57**	45.95	22.75	36.3	22.37
V					**2.96**	9.84	10.53	12.56
VI						**2.98**	8.96	7.42
VII							**1.46**	9.16
VII								**5.07**

4.7 (b) Average intra (in bold) and inter cluster distance (D=√D2 values)

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**1.66**	6.02	4.32	8.74	4.09	5.97	5.69	4.07
II		**1.56**	8.67	5.13	4.07	2.54	5.0	3.38
III			**0.03**	10.30	6.78	8.53	7.45	6.78
IV				**1.93**	6.77	5.07	6.02	4.72
V					**1.72**	3.13	3.18	3.54
VI						**1.72**	2.72	7.42
VII							**1.20**	3.02
VII								**2.25**

Table: 4.8: Cluster means for fourteen characters

Characters	Clusters							
	I	II	III	IV	V	VI	VII	VIII
Flower initiation (days)	96.84	96.42	98.33	97.29	98.50	99.00	95.17	99.00
Days to 50% flowering	108.18	108.75	108.56	109.19	109.50	110.33	106.33	109.67
Maturity phase (days)	142.18	140.83	144.78	145.52	146.17	149.17	143.67	146.67
Vegetative phase (days)	96.84	96.42	98.33	97.29	98.50	99.00	95.17	99.00
Reproductive phase (days)	45.33	44.42	46.44	48.24	47.67	50.17	48.50	47.67
Plant height (cm)	106.60	131.75	110.91	120.81	106.73	96.57	110.90	118.73
Lower branch height (cm)	49.89	64.00	47.24	46.38	38.37	38.20	51.90	64.07
Primary Branches per plant (Number)	6.13	6.55	7.20	7.89	8.17	8.13	6.40	5.73
Captiula per plant (Number)	24.26	23.52	29.11	34.16	49.73	33.57	26.67	19.27
Seeds per capitulum (Number)	21.02	24.27	20.36	22.20	19.70	29.37	17.80	32.00
100- seed weight (g)	4.97	3.78	5.62	4.99	6.33	4.53	4.73	3.13
Biological yield per plant (g)	70.64	58.14	54.52	89.29	120.48	90.09	123.24	77.78
Harvest index (%)	21.50	19.55	21.89	18.59	22.57	17.11	14.44	17.34
Seed yield per plant (g)	19.54	13.83	15.22	21.20	35.25	19.45	20.64	16.35

CHAPTER – V

DISCUSSION

Plant breeding played an important role in any crop improvement programme. The breeder tries to breed progressively better adopted genotypes to the existing conditions or to altered conditions. Success or failure of such attempts depends on the provision of recombinational variability and genetic diversity.

Safflower is popularly known as “Rain fed crop‟ owing to its high adaptability in moisture stress conditions. Therefore, its production in entire world is mainly confined to areas with low rainfall.

The present investigation, entitled “Genetic Divergence for yield and its attributes in Safflower (*Carthamus tinctorius* L.) was carried out to study the genetic variability for fourteen characters among the forty genotypes, the correlation between the dependent and independent variables along with their direct and indirect effects on yield and genetic divergence among all genotypes. The results of the present study for variability, association and genetic divergence are briefly discussed in following heads in the light of available literature:

5.1 Genetic Variability
5.2 Heritability in broad sense and Expected Genetic advance:
5.3. Correlation analysis:
5.4. Path analysis
5.6. Genetic divergence:

Genetic Variability:

Genetic variability and its quantification for characters of economic importance are pre-requisite for crop improvement programme. A wide spectrum of variability is a key factor for success of crop improvement programme as it provides an opportunity to the plant breeder for producing desired improvement in population by increasing the frequency of desirable individuals. Broad range of variability for traits is also required to isolate significantly superior genotypes for commercial cultivation as variety or to be used as parents in hybridization programme for combination breeding or to develop useful genetic variability for further improvement.

Wide range of genetic variability was observed in the present study for all the fourteen characters. The values of mean and range exhibited that there is broad variability among genotypes for most of the traits. The value of mean sum of squares due to genotypes was significant for all the fourteen characters and suggested that existence of sufficient genetic variability for all the traits under study in the experimental population and it can be exploided for further improvement.

High estimates of PCV were recorded for seed yield per plant, followed by, number of capitula per plant, biological yield per plant, number of seeds per capitulum, 100-seed weight, harvest index, number of primary branches per plant and lower branch height. Similar trend was observed at genotypic level also. Thus, the present investigation showed that the presence of sufficient genetic variability in the population and there is good of scope for achieving desirable improvement through simple selection procedure.

The difference between PCV and GCV was negligible/ low for number of capitula per plant, biological yield per plant, number of seeds per capitulum, 100-seed weight, number of primary branches per plant and lower branch height indicated that the expression of these characters was least affected by the environmental factors and their phenotype is the true representative of their genotype and the selection on the basis of *per se* performance will be effective.

On the other hand days to maturity (1.01), days to 50% flowering (1.02), days to flower initiation (1.44), vegetative phase (1.44), plant height (2.07) and reproductive phase (4.42) was found to be compatible in its behavior at both, phenotypic and genotypic levels having low coefficient of variation. It suggested that these were minimum influenced by non – genetic factors and hence, were absolutely stable. The range was also quite wide for these characters and there was massive scope for selecting parents to develop an early and dwarf strains.

Similar results were also reported by Anjani (2005), Choulwar *et al.*(2005), Lakshyadeep *et al*. (2005), Ichanal *et al*. (2010), Safavi *et al.*(2012), Mohammad *et al.* (2014) and Rampure *et al.* (2014), Motamedi et.al.(2015) Gopal *et. al.(*2015), Parveen (2016), Pavithra *et. al*. (2016) and Belete (2017) for seed yield per plant, number of capitula per plant, lower branch height, days to flower initiation, number of seeds per capitulum, 100 Seed weight ,harvest index and biological yield per plant in safflower.

Heritability:

The coefficient of variation indicates the range of variability present for different traits and it does not indicate the heritable and non-heritable portion of genetic variability.

The total variability present in the population was not transmitted as such only its heritable portion was transmitted to the next generation. To obtain the knowledge of heritable portion of variability, it is essential to understand the heritability of different traits.

Heritability estimates in broad sense is the proportion of genotypic variance to the phenotypic variance and is expressed in percentage. It is an index of transmission of a character from parents to their progeny. It helps to the plant breeders for the selection of superior genotypes from the genetically variable population. Robinson *et al*. (1949) had classified heritability estimates (broad sense) as low (below 50%). medium (50-70%) and high (above 70%).

The estimation of heritability is effected by various elements like sample size, sampling methods, method of estimation, effects of linkage and population density etc. and other biotic and abiotic factors that influence expression of the characters in the population. So, heritability estimation is not only the property of the characters alone but it is the property of population and environmental factors. When the estimate of heritability was high denoting the phenotypic appearance would provide a close measure of genotypic value and thus, a breeder can make selection on the basis of virtual performance of the individuals.

In the present study, the high magnitude of heritability was observed for plant height (95.95%) followed by biological yield per plant (95.72%), number of capitula per plant (89.30%), lower branch height (88.99%) 100-seed weight (88.03%), number of seeds per capitulum (81.60%), maturity period (81.05%) and these traits may be used to make selection indices so that the progress made through them would be high

Similar results were also reported by Kavani *et al.* (2001) for number of capitula per plant, number of seeds per capitulum, days to maturity, Reddy *et al.* (2003) for number of seeds per capitulum, test weight, number of capitula per plant, Choulwar *et al.* (2005) for plant height, Beena *et al.* (2006) for days to maturity, plant height, number of seeds per capitulum and 100-seed weight. Çamaş and Esendal (2006) for plant height, number of seed per head and 100-seed weight, capitula per plant, Arslan *et. al*.(2007) for plant height, capitula per plant, number of seeds per capitulum and 100-seed weight. Mohammad (2014),Belete (2017) Pushpavalli *et.at* (2017) for number of seeds per capitulum, 100 seed weight and plant height in safflower.

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Expected Genetic advance:

Expected genetic advance is the product of heritability, selection intensity and phenotypic standard deviation. Heritability in conjunction with genetic advance would give a more reliable index for making selection. High genetic advance could be expected from a population with wide variability and high heritability estimates.

In the present study, the estimation of the expected genetic advance expressed as percentage of mean were high for biological yield per plant, number of capitula per plant, seed yield per plant, number of seeds per capitulum ,100-seed weight, lower branch height , number of primary branches per plant , plant height. The occurrence of high heritability with high genetic advance for these characters indicated predominance with additive gene action for the expression of these characters. Hence, these traits would be improved through direct selection procedures.

Reproductive phase and days to 50% flowering had moderate heritability with moderate to low genetic advance as percentage of mean, which indicated that the predominance of non-additive gene action for expression of these character and moderate heritability was due to favorable effect of environment condition rather than genetic element. Hence, these characters can be improved by a breeding method which can exploit the non-additive gene action like heterosis breeding etc.

Similar results were also reported by Reddy *et al.* (2003), Sarang *et al*. (2004), Choulwar *et a*l. (2005) and Lande and Deshmukh (2012), Mohammad *et al*.(2014), Bahmankar et al. (2014), Tariq *et al*. (2014), Belete (2017), Pushpavalli *et.at* (2017) found high heritability with high genetic advance as percent of mean for biological per plant, plant height, number of capitula per plant.

Correlation analysis:

Correlation is the relationship between the two attributes and the strength of relationship is measured in terms of correlation coefficient whose limits range from -1 to +1. If increase in one variable result in the increase of other variable, the association is positive and if it results in the decrease of other variables, the relationship is negative. The two variables are uncorrelated if the increase or decrease of one trait does not affect the other trait. The phenotypic and genotypic correlations have their own importance in breeding programme. The phenotypic correlation coefficients helps in determining selection index, while, genotypic correlation provides a close measure of association between characters in overall improvement of the crops. They may also help to identify characters that have little or no importance in making selection.

In the present investigation estimates of phenotypic correlation coefficients showed that seed yield per plant was significant positive correlation with biological yield per plant, harvest index, number of capitula per plant, 100- seed weight, and days to maturity. However, lower branch height and plant height had significant negative association with seed yield per plant. Suggesting the characters showing positive significant and strong correlation with seed yield and improvement in any one of them by indirect selection would result in improvement in seed yield. Also, These results are supported by Tabrizi (2002), Ali *et al.*(2006), Dalvi *et.al.(*2005), Diwakar *et al*. (2006), Arslan *et al*. (2007), Ahmadzadeh *et al*. (2008), Mukta *et al*. (2008), Salamati (2011) Nezhad and Talebi (2015) , Kurhade and Charjan (2016) and Pavithra *et.al*.(2016)

The inter-correlations between days to flower initiation with vegetative phase, days to 50% flowering, days to maturity ; of Days to 50% flowering with vegetative phase and days to maturity; of number of primary branches per plant with number of seeds per capitulum, days to maturity , reproductive phase, biological yield per plant; of number of capitula per plant with days to maturity, seed yield per plant, biological yield per plant ; of plant height with lower branch height; of days to maturity with reproductive phase ,number of capitula per plant and vegetative phase; of Lower branch height with plant height; of days to maturity with reproductive phase, capitula per plant and vegetative phase; of number of seeds per capitulum with primary branches per plant; of 100–seed weight with capitula per plant, harvest index ; of biological yield per plant with number capitula per plant, reproductive phase ; of harvest index with 100-seed weight ; of vegetative phase with days to flower initiation ; of days to 50% flowering, days to maturity were also found positive and significant.

Genotypic correlation coefficients with yield showed similar trend to those of phenotypic correlation coefficients in direction. However, these were higher in measure. It suggested that these correlations were because of breeding values and therefore, more dependable.

Hence, on the basis of correlation estimates, it is obvious, that among the characters namely biological yield per plant, number of capitula per plant, 100- seed weight, harvest index and days to maturity are significant and positively correlated with seed yield and also with one another indicating their utility in selection programme.

Path analysis:

The seed yield is a complex polygenic character. It is also affected by its component traits. The inter-relationship among the component traits therefore, often limits the magnitude of yield. Correlation coefficient measures the strength of relationship among different traits but it does not exhibit contribution of each character to the resultant correlation. Thus, the information of correlation coefficient does not help in precise ranking of characters to be used in selection indices. Analysis of ultimate correlation coefficient, therefore, becomes essential to quantify the range and direction of every character.

Correlation coefficient suggests only the event and nature of association between yield and its attributes, but does not exhibit the direct and indirect effects of different independent variables on dependent trait seed yield. Seed yield is dependent traits on various component traits which are mutually associated. These will in turn impair the true relation presence between a component and seed yield and change in any one component are likely to disturb the whole network of cause and effect. Thus, each attribute has two paths of action viz., (1) The direct effect on seed yield (2) Indirect influence through other components which are not recorded from the correlation studies. The path analysis was first described by Wright (1921) provides an effective measure of direct and indirect causes of association and depicts the relative importance of each factor involved in contributing to seed yield. In order to obtain such relations, the cause and effect of relationship between yield *per se*, thirteen yield attributes was studied in safflower through path coefficient analysis and the results are discussed below.

In the present study result of path analysis based on genotypic correlation coefficients reveald that number of capitula per plant, 100-seed weight, days to flower initiation and days to 50% flowering showing significant positive correlation with seed yield per plant had substantial direct contribution to the seed yield.

Number of capitula per plant direct effect on seed yield and also strong correlation with seed yield might be ascribed to the fact that this character had positive indirect effect through biological yield per plant and plant height .100-seed weight was the character which showed positive indirect effects through harvest index and biological yield per plant. Days to flower initiation had positive indirect effect through harvest index and number of primary branches per plant. Days to 50% flowering showed high positive indirect effect on seed yield through number of primary branches per plant.

It could be concluded from the present study that the characters like number of capitula per plant, 100-seed weight, days to flower initiation and days to 50% flowering intense positive association and high magnitude of positive direct effects on seed yield. Moreover the indirect effects of most of the characters through these characters were also positive. Thus characters were conceded as the most important yield attributing traits.

The results of the present study were also supported by the findings of Reddy *et al.* (2004), Dalvi *et.al* (2005), Ali *et al.* (2006), Diwakar *et al.* (2006), Arsal (2007), Mukta *et al*. (2008) ,Pavithra et.al (2016) and Pushpavalli *et.at* (2017).

Genetic divergence:

Selection of elite genotypes with high *per se* performance for yield and yield contributing attributess with genetic divergence is important for any hybridization programme. It would be possible to identify desirable genotypes from the genetic variability estimated, but it is difficult to expect any extra ordinary results from their offspring unless we have knowledge about divergence between

them.

Mahalanobis (1936) developed the concept of D^2 statistics which acts as important tool for plant breeding. Application of this concept for the evalution of genetic diversity in plant breeding was first suggested by Rao (1952). The degree of divergence between biological population of genotypic level and the relative contribution of different components to the total divergence at both intra and inter cluster level can be evaluated by this method

The dispersion among variables for the aggregate effect of the fourteen traits as tested by Wilk's criterion was also highly significant indicating presense of considerable divergence in the material under investigation

Genetic differences among 40 genotypes were assessed by D^2 statistic. The maximum divergence (D^2= 9.84) was between genotypes AVT-I-6 and AVT-I-7. These two genotypes also exhibited significant differences between them in respect of most of the traits (Appendix). A cross between these two genotypes is expected to give a high heterotic value hybrid and broad range of variability. Therefore, these genotypes may be used as parents for hybridization. On the other hand minimum divergence (D^2 = 2.64) was observed between genotypes IVT-II-13 and AVT-I-8, which did not differ significantly from each other for most of the characters. This suggests, these genotypes may be closely related in their evolution process.

These forty genotypes were grouped into 8 clusters. Cluster I comprised of maximum number of genotypes (19 genotypes), followed by cluster IV (7 genotypes), cluster II (4 genotypes), cluster III (3 genotypes), cluster V, VI and VII (2 genotypes each) and cluster VIII contained only 1 genotype (Table 4.6).

The maximum inter cluster distance was recorded between cluster III and IV , followed by, cluster I and IV, cluster II and III, cluster III and VI, cluster III and VII ,cluster VI and VIII , cluster III and V , cluster III and VIII. Crosses between lines carefully selected from these clusters are expected to throw a wide spectrum of segregates.

Average intra – cluster distance revealed that cluster III, which contained 3 lines, had little intra – cluster distance. It indicated that these lines could be closely related in their evolutionary process and passed through similar evolutionary factors.

The maximum intra cluster distance was observed among the genotypes in the cluster-VIII (2.25), Suggesting that lines included in this cluster might has different genetical base.

In recent time a breeder is asked to improve a particular character of a variety or genotype, which is otherwise suitable. For this a donor parent is required. Information about a range of suitable donors thus becomes inevitable. Estimates of cluster mean make this information readily available.

Cluster means for the fourteen attributes of all the eight clusters were worked out. It was found that Cluster VI had lowest mean value for lower branch height and plant height while highest mean value for reproductive phase. Cluster II had lowest mean value for days to maturity. Cluster V had highest mean values for number of capitula per plant, number of primary branches per plant, seed yield per plant, 100-seed weight and Harvest index. Cluster VII had highest mean value for biological yield per plant and lowest mean value for days to flower initiation, vegetative phase and days to 50% flowering. Cluster VIII had highest mean value for seeds per capitulum. To improve any particular trait donor for hybridization could be chosen from an appropriate cluster.

The following genotypes of marked mean performance from the selected clusters may serve as parents for hybridization programmes.

Cluster	**Desirable Characters**	**Genotypes**
VI	Low lower branch height	IVT-II-8
	Low plant height	IVT-II-4
	High reproductive phase	IVT-II-4
V	High number of capitula per plant	IVT-I-3
	High number of primary branches per plant	IVT-I-3
	High seed yield per plant	IVT-I-3
VII	High biological yield per plant	AVT-I-6
	Early days to flower initiation	AVT-I-2
	Early days to 50%flowering	AVT-I-2, AVT-I-6
VIII	High seeds per capitulum	AVT-I-5
II	Early days to maturity	IVT-I-11,AVT-I-1

To improve number of seeds per capitulum a line from cluster VIII, viz., genotype AVT-I-5 would be a right option. Lines from cluster II for example genotype IVT-I-11, AVT-I-1 having earlier in maturity could be used to develop early maturing varieties. Line from cluster VII, for example genotype IVT-I-3 could be used to develop higher seed yield, number of capitula per plant and harvest index.

CHAPTER – VI

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FURTHER WORK

The present investigation entitled, "Genetic divergence for yield and its attributes in Safflower (*Carthamus tinctorius* L.)" was conducted using forty genotypes. The experiment was conducted during *Rabi* 2017-18 in randomized block design with three replications at the research farm of All India Coordinated Research Project on Safflower, College of Agriculture, Indore (M.P.).

Keeping the above mentioned facts, the present work was carried out with the following objectives:

1. To study the genetic variability present in the experimental material.
2. To estimate the heritable portion of genetic variability transferred to the next generations.
3. To identify yield contributing traits by association analysis.
4. To study genetic divergence through D^2 statistic technique for selection of genotypes to be used as parents in hybridization programme.

The observations were recorded on yield and yield contributing characters *viz.* days to flower initiation, days to 50% flowering, number of primary branches per plant, lower branch height, plant height, number of capitula per plant, days to maturity, number of seeds per capitulum, 100-seed weight, vegetative phase, reproductive phase, biological yield per plant, harvest index and seed yield per plant for collecting the information on existing genetic variability, heritability, expected genetic advance, genetic divergence, correlation coefficient , path analysis. The data on all characters were subjected to statistical analysis and following conclusions were drawn:

1. Analysis of variance showed highly significant differences among genotypes for all the traits at univariate as well as at multivariate level. Wide range was showed for mostly traits. Trend of variability at phenotypic level

was similar to that of genotypic level for most of the characters. The genotypic co–efficient of variation was highest for seed yield per plant, followed by, biological yield per plant, number of capitula per plant, number of seeds per capitulum, 100-seed weight, lower branch height, number of primary branches per plant, harvest index, plant height and low for vegetative phase, days to flower initiation, days to 50% flowering, maturity phase and reproductive phase.

2. Heritability in broad sense for most of the characters was high to moderate. High heritability were observed for plant height, biological yield per plant, number of capitula per plant, lower branch height, 100-seed weight, number of seeds per plant per plant, maturity phase and relatively moderate for seed yield per plant, days to 50% flowering, primary branches per plant. .High heritability coupled with high genetic advance were observed for biological yield per plant, lower branch height, plant height, 100-seed weight and seeds per capitulum. Thus it might be good chances of improvement of these traits through direct selection in the material.

3 Genetic advance as per cent of mean was observed. High values for the characters for biological yield per plant, number of capitula per plant, seed yield per plant, number of seeds per capitulum, 100-seed weight, lower branch height, number of primary branches per plant suggesting scope for improvement through simple selection scheme.

4. The characters biological yield per plant, harvest index, number of capitula per plant, 100- seed weight and days to maturity were positively and significantly correlated with yield. These characters which positive correlated with seed yield may be used for construction of index for selection programme. The attributes like plant height and lower branch height had negative correlation with seed yield per plant.

5 In the path analysis study observed that number of capitula per plant, 100-seed weight, days to flower initiation, days to 50% flowering recorded positive direct effect on seed yield. These characters should be given more weightage in selection of parents for hybridization for yield improvement programme.

6. Wilk's criterion showed highly significant differences among studied genotypes at multivariate level and exhibited the presence of considerable divergence among all the forty genotypes. Based on D^2 statistic, all the forty genotypes were grouped into eight clusters. Cluster I comprised maximum number of genotypes (19 genotypes), followed by cluster IV (7 genotypes), cluster II (4 genotypes), cluster III (3 genotypes), cluster V,VI and VII (2 genotypes each) and cluster VIII contained only 1 genotype (Table 4.6).The inter cluster distance was maximum recorded between cluster III and IV, followed by, cluster I and IV, cluster II and III, cluster III and VI, cluster III and VII ,cluster VI and VIII , cluster III and V and cluster III and VIII

7. The genotypes IVT-II-8, IVT-II-4, IVT-I-3, AVT-I-2, AVT-I-5, AVT-I-6, IVT-I-11, and AVT-I-1 may serve as potential for hybridization programme in the improvement of potentiality of the yield contributing traits in safflower.

Conclusion:

On the basis of present investigation the following broad conclusions can be drawn.

- The analysis of variance showed highly significant differences among genotypes for all the characters studied indicating the existence of sufficient genetic variability in the experimental population.

- High heritability coupled with high genetic advance for for biological yield per plant, number of capitula per plant, seed yield per plant, number of seeds per capitulum, 100-seed weight, lower branch height, number of primary branches per plant, plant height indicated least influence of environment on the expression of these traitss and prevalence of more additive gene action in their inheritance. Hence, these traits would be improved through direct selection procedures.

- In the present investigation estimates of phenotypic and genotypic correlation coefficients showed that seed yield per plant was significant positive correlation with biological yield per plant, harvest index, number of capitula per plant, 100- seed weight, and days to maturity, indicating dependency of seed yield per plant on these traits

- The path coefficient analysis showed that number of capitula per plant recorded magnitudinally the highest positive direct effect on the seed yield followed by, 100-seed weight, days to flower initiation and days to 50% flowering. It suggests that selection of these traits will be highly rewarding for improving the seed yield per plant.

- The maximum divergence distance (D^2 = 9.84) was recorded between genotypes AVT-I-6 and AVT-I-7. These two genotypes also had significant differences between them in respect of most of the characters. A cross between these two genotypes is expected to give a high heterotic value hybrid and wide spectrum of variability. Therefore, these genotypes may be used as parents for hybridization

- The genotypes IVT-II-8, IVT-II-4, IVT-I-3, AVT-I-2, AVT-I-5, AVT-I-6, IVT-I-11, and AVT-I-1 may serve as potential for hybridization programme in the improvement of potentiality of the yield contributing traits in safflower.

Suggestions for further work:

The following suggestions have been made for further study:-

- The genetic variability reported for different characters in relation to yield should be exploited for future genetic improvement in safflower.
- Characters showing high heritability with high genetic advance might be utilized in direct selection.
- A better crop ideotype should be developed using findings from association analysis.
- The promising diverse genotypes identified can be tested for combining ability and inheritance of yield and its contributing traits for further use in breeding programme.
- The genotypes may be tested for genetic diversity study one more year so as to drive some concrete conclusions regarding diversity spectrum.
- Genotypes from the different clusters, identified for a specific character may be used as a parent for breeding programme with an objective to improve the specific character.

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Appendix:

Mean performance for yield and its components of 40 genotypes of safflower

S. No.	Genotypes	Flower initiation (days)	Days to 50% flowering	Maturity phase (days)	Vegetative phase (days)	Reproductive phase (days)	Plant height (cm)	Lower branch height (cm)	Branches per plant (Number)	Captiulam per plant (Number)	Seed per capitulum (Number)	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
1	**IVT-I-1**	97.33	110.00	139.67	97.33	42.33	117.13	50.53	6.33	24.83	18.00	5.67	70.53	17.83	15.27
2	**IVT-I-2**	97.00	109.00	141.33	97.00	44.33	108.40	45.07	5.53	23.33	18.13	5.34	76.17	23.53	23.50
3	**IVT-I-3**	98.33	108.67	145.00	98.33	46.67	101.80	36.60	9.13	54.00	19.87	6.67	120.20	23.03	36.10
4	**IVT-I-4**	96.67	106.00	140.67	96.67	44.00	111.73	42.73	5.87	28.33	19.53	5.00	89.00	20.93	23.63
5	**IVT-I-5**	98.67	110.33	147.33	98.67	48.67	111.67	40.13	7.20	45.47	19.53	6.00	120.73	22.10	34.40
6	**IVT-I-6**	97.67	109.67	144.67	97.67	47.00	116.00	40.47	8.53	31.27	19.73	6.20	42.83	22.03	12.20
7	**IVT-I-7**	98.67	108.00	146.33	98.67	47.67	116.60	47.13	6.60	33.07	28.80	4.33	65.10	23.97	20.70
8	**IVT-I-8**	99.00	111.00	150.00	99.00	51.00	132.80	40.60	7.73	29.67	14.27	5.40	87.83	21.83	24.90
9	**IVT-I-9**	98.33	110.67	144.33	98.33	46.00	115.07	49.47	8.27	30.13	26.53	5.00	91.17	17.03	18.77
10	**IVT-I-10**	98.33	110.67	144.33	98.33	46.00	110.13	38.67	7.33	39.67	19.80	5.53	90.07	23.07	27.07
11	**IVT-I-11**	94.67	107.33	140.33	94.67	45.67	133.27	57.53	6.87	24.20	29.53	3.60	71.50	18.50	16.33
12	**IVT-I-12**	98.67	110.00	148.67	98.67	50.00	116.33	47.40	7.27	35.87	20.00	5.33	49.23	22.17	14.13
13	**IVT-I-13**	96.67	109.00	141.33	96.67	44.67	133.47	65.20	7.13	26.20	20.40	3.60	45.53	22.67	13.47
14	**IVT-I-14**	95.33	106.00	143.00	95.33	47.67	107.27	37.80	5.87	29.67	14.67	4.93	69.10	26.43	25.13
15	**IVT-I-15**	96.00	107.00	142.33	96.00	46.33	129.73	47.87	9.00	38.33	34.73	4.47	91.80	18.57	21.03
16	**IVT-I-16**	95.00	107.00	142.67	95.00	47.67	119.73	40.53	6.73	31.47	18.07	4.60	81.00	14.73	14.17
17	**IVT-II-1**	96.67	108.00	141.67	96.67	45.00	112.73	59.73	5.33	25.13	19.20	3.80	67.63	17.70	14.77
18	**IVT-II-2**	95.67	109.00	138.67	95.67	43.00	96.07	53.27	6.07	21.13	20.80	5.20	57.97	21.50	17.77
19	**IVT-II-3**	100.00	108.00	141.33	100.00	41.33	118.60	59.07	5.67	18.07	22.67	4.20	60.53	23.17	18.40
20	**IVT-II-4**	99.00	110.00	149.33	99.00	50.33	95.60	39.00	7.53	30.40	22.33	5.27	88.27	14.67	14.57
21	**IVT-II-5**	95.67	111.00	142.33	95.67	46.67	103.00	55.40	6.73	19.07	18.53	5.00	70.17	21.70	20.83
22	**IVT-II-6**	96.00	109.00	141.67	96.00	45.67	93.00	46.53	5.53	21.67	19.47	5.07	77.63	22.97	22.37

S. No.	Genotypes	Flower initiation (days)	Days to 50% flowering	Maturity phase (days)	Vegetative phase (days)	Reproductive phase (days)	Plant height (cm)	Lower branch height (cm)	Branches per plant (Number)	Captiulam per plant (Number)	Seed per capitulum (Number)	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
23	**IVT-II-7**	98.67	106.00	141.00	98.67	42.33	100.40	53.87	5.80	20.20	21.33	5.33	71.47	21.47	19.33
23	**IVT-II-7**	98.67	106.00	141.00	98.67	42.33	100.40	53.87	5.80	20.20	21.33	5.33	71.47	21.47	19.33
24	**IVT-II-8**	99.00	110.67	149.00	99.00	50.00	97.53	37.40	8.73	36.73	36.40	3.80	91.90	19.57	24.30
25	**IVT-II-9**	98.67	111.00	141.33	98.67	42.67	127.27	63.47	6.00	20.60	23.27	2.80	67.03	19.43	15.10
26	**IVT-II-10**	98.33	111.33	150.33	98.33	52.00	117.67	56.33	7.53	32.47	20.53	5.40	102.37	19.93	28.13
27	**IVT-II-11**	96.00	109.00	141.67	96.00	45.67	111.60	48.07	6.20	27.27	19.60	5.33	81.87	20.40	20.50
28	**IVT-II-12**	95.67	107.00	148.00	95.67	52.33	110.60	53.80	6.93	23.53	26.33	4.20	79.20	17.40	18.17
29	**IVT-II-13**	97.67	110.00	143.00	97.67	45.33	109.33	53.27	5.73	22.60	22.53	5.73	58.33	23.70	18.67
30	**IVT-II-14**	98.00	108.67	144.33	98.00	46.33	93.87	39.33	6.67	25.40	28.20	5.80	78.33	22.17	23.47
31	**IVT-II-15**	96.00	107.00	138.67	96.00	42.67	102.07	50.60	5.80	19.40	21.20	3.13	77.07	20.73	18.73
32	**IVT-II-16**	95.67	107.00	142.00	95.67	46.33	97.40	54.13	6.27	22.20	19.27	5.27	67.27	19.50	14.83
33	**AVT-I-1**	95.67	107.67	140.33	95.67	44.67	133.00	69.80	6.20	23.07	23.87	5.13	48.53	17.57	10.43
34	**AVT-I-2**	94.33	106.00	144.67	94.33	50.33	108.40	54.93	5.27	25.00	19.47	5.87	111.10	16.77	22.50
35	**AVT-I-3**	96.00	106.67	144.67	96.00	48.67	120.53	51.20	8.60	37.40	21.47	4.53	80.77	14.97	14.37
36	**AVT-I-4**	96.67	108.00	142.00	96.67	45.33	106.60	43.93	7.73	31.13	21.13	5.93	61.53	19.03	14.57
37	**AVT-I-5**	99.00	109.67	146.67	99.00	47.67	118.73	64.07	5.73	19.27	32.00	3.13	77.77	17.37	16.37
38	**AVT-I-6**	96.00	106.67	142.67	96.00	46.67	113.40	48.87	7.53	28.33	16.13	3.60	135.37	12.07	18.77
39	**AVT-I-7**	98.00	108.00	141.00	98.00	43.00	98.47	41.20	7.33	23.33	19.93	3.40	40.90	18.70	9.40
40	**AVT-I-8**	96.67	108.67	144.00	96.67	47.33	109.07	53.73	5.73	24.87	19.93	4.93	63.13	24.50	20.67
Mean		**97.13**	**108.61**	**143.56**	**97.13**	**46.43**	**111.90**	**49.47**	**6.80**	**28.09**	**21.93**	**4.84**	**76.95**	**20.14**	**19.45**
S.E. M. ±		**0.81**	**0.64**	**0.84**	**0.81**	**1.18**	**1.34**	**1.70**	**0.44**	**1.50**	**1.32**	**0.19**	**2.56**	**1.61**	**2.16**
S.E.D. ±		**1.14**	**0.90**	**1.19**	**1.14**	**1.67**	**1.89**	**2.40**	**0.62**	**2.12**	**1.86**	**0.27**	**3.61**	**2.27**	**3.05**
C.D. at 5%		**2.28**	**1.80**	**2.37**	**2.28**	**3.33**	**3.76**	**4.79**	**1.24**	**4.22**	**3.71**	**0.54**	**7.19**	**4.53**	**6.08**
CV(%)		**1.44**	**1.02**	**1.01**	**1.44**	**4.42**	**2.07**	**5.95**	**11.20**	**9.25**	**10.41**	**7.06**	**5.75**	**13.84**	**19.23**

VITA

The author of the thesis **Mr. Manoj Gurjar** S/o Shri **Vasudev Gurjar** was born on 03 october, 1994 at Khargone (M.P.).

He passed his High School in the year 2009 from shri Umia bal vidhya aashram somakhedi (m.p.) with 78.83% per cent marks. After that he passed Higher Secondary in the year 2011 acquiring 74% per cent marks from Brilliant H.S. School indore (M.P.).

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He is now submitting the thesis after completing the course with 7.66 OGPA out of 10.00 point scale.

During the entire period of his education from schooling to post graduation he was very sincere and honest towards his studies.

Manoj Gurjar