Screening of Safflower (*Carthamus tinctorius L.*) genotypes for drought tolerance

THESIS

Submitted to the

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In

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by

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CERTIFICATE – I

This is to certify that the thesis entitled "Screening of Safflower (*Carthamus tinctorius L.*) genotypes for drought tolerance" submitted in partial fulfillment of the requirement for the Degree of **Master of Science in Agriculture** in the Department of **Plant Breeding and Genetics** of Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bona-side research work carried out by **Mr. AJAY KUMAR BAGRI** I.D. No. RA/IN/83/2008 under my guidance and supervision. The subject of the thesis has been approved by the Students' Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any other degree or diploma or has been published. All the assistance and help received during the course of this investigation have been acknowledged by the scholar.

Place - Indore Signature

Date -

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Chairman of the Advisory Committee

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Member	-	Dr. V. K. Mishra	_____
Member	-	Dr. (Smt.) Indu Swaroop	_____

CERTIFICATE – II

This is to certify that the thesis entitled “Screening of Safflower (*Carthamus tinctorius L.*) genotypes for drought tolerance” submitted by **Mr. AJAY KUMAR BAGRI** I.D. No. RA/IN/83/2008 to the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior for the degree of **Master of Science in Agriculture** in the Department of **Plant Breeding and Genetics** has been accepted after evaluation by the External Examiner and approved by the Students’ Advisory Committee after an oral examination of the same.

Signature

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Date - Chairman Advisory Committee

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Place: Indore

Date: **Ajay Kumar Bagri**

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CHAPTER-I
INTRODUCTION

Safflower [*Carthamus tinctorius* (L.)], is an important *Rabi* oilseed crop of the country commonly known as *Kusum* (Hindi) or *Kardi* (Marathi). It belongs to the family Compositeae (*Asteraceae*). It is offen cross pollinated crop with somatic chromosome number (2n = 24). There are 36 species in the genus found in many part of the world namely, Asia, Africa and Mediterranean regions. Out of which, only *Carthamus tinctorius* (L.) is cultivated in India. It is mainly cultivated for its seed which is a source of very important edible oil. Sawflower oil is rich in poly unsaturated fatty acid (Linoleic acid 78%) which play an important role in reducing cholesterol level in blood. *Carthamus* is the latinised version of the Arabic word "Quartum" or "Gurtum" which alludes to the colour of the dye often from florets and the modern Arabic name "Usfar" is probably deversion of the English name "Safflower" through various written form of Usfar, affore, asfiore, Saffiore finally to Safflower.

The vegetable oil in India accounts for 1.5% of gross national product and 7% of value of all agricultural products with 14 million farmers involved in oilseeds cultivation and one million persons involved in processing (National seminar on oilseeds 2011). The self-sufficiency in oilseeds attained through “Yellow Revolution” in the country during early 90’S lasted for a short period. The demand for edible oils has outstripped the supply and 40% of edible oil requirements of the country is currently being met by import. In the production of vegetable oil, India has unique opportunities as wide range of agro-climates is available for cultivation of oil seed crops.

Safflower is one of the nine edible oil crops of India and the safflower area is 241 thousand hectares with its annual production of 120 thousand tonnes and productivity of 498 kg per hectare in India (Anonymous 2012). It is mainly cultivated in Maharashtra 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 safflower area and production in the country. It is cultivated in *Rabi* season under limited residual 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.

One of constraints of its low production is the crop mainly cultivated in Rabi season under residual soil moisture of vertisol and crop faces dry spell during growing season. Thus, it is necessary to screen genotypes for tolerance to drought stress condition. Its productivity is greatly influenced by the intensity and duration of dry spells faced by the crop during its growing season. To sustain its production an attempt will be made for screening the genotypes for drought tolerance and grouping the safflower genotypes on the basis of genetic diversity so that the desirable plant type with traits attributing to high yield and drought tolerance may be selected from the existing spectrum of variability.

In the background of this, the present investigation was undertaken with the following objectives:

1. To study the existence of genetic variability present in the experimental material.
2. To study genetic divergence through D^2 statistics technique for selection of genotypes to be used as parent in hybridization programme.
3. To identify yield contributing traits by Association Analysis.
4. To screen the genotypes for drought tolerance

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

2.7 Drought tolerance

2.1 Genetic variability:

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

Lakshyadeep *et al*. (2005) recorded significant variances among genotypes for all traits except for number of leaves on main axis after branching, 100-seed weight and oil content. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits. High GCV and PCV for number of capitula per plant and seed yield per plant was also observed in his study.

Biradar *et al.* (2012) reported high genotypic and phenotypic coefficient of variation for number of capitula per plant, number of seeds per capitulum, 100 seed weight and Oil content.

2.2 Heritability:

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

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

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

Camas and Esendal (2006) reported high heritability for first branch height, plant height, number of seeds per capitulum and 1000-seed weight.

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

Ichanal *et al*. (2010) observed a wide range of variation for almost all the characters understudy. The phenotypic coefficient of variation (PCV) was found to be greater than genotypic coefficient of variation (GCV). GCV and PCV ranged from 3.08 to 3.91 for number of days to 50% flowering and from 13.30 to 14.02 for seed yield per plant. Seed yield per plant, 100 seed weight, harvest index and number of seeds per capitulum exhibited high heritability coupled with high expected genetic advance.

2.3 Expected genetic advance:

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

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

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

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

2.4 Correlation coefficient:

Anjani (2005) reported that seed yield was positively associated with capitula per plant, 100 seed weight and height of branching and negatively associated with plant height, days to maturity and days to 50% flowering.

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

Lakshyadeep *et al.* (2005) reported that seed yield per plant had significant positive correlation with number of capitula per plant, weight per capitulum and number of primary branches per plant.

Ali *et al.* (2006) reported that seed yield was significantly correlated with total biomass, stem yield, capitulum diameter, 1000-seed weight, seed weight per capitulum, first fertile branch, number of days to the beginning of branching and flowering duration.

Alizadeh and Carapetian (2006) reported 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 flowering was recorded.

Beena *et al.* (2006) recorded high genotypic correlation for number of effective capitula per plant and number of branches per plant.

Bidgoli *et al*. (2006) observed that seed yield showed positive and significant correlation with total biomass, stem yield, capitulum diameter, 1000-seed weight, seed weight per capitulum, first fertile branch, number of days to the beginning of branching and flowering duration.

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) reported that the number of capitula per plant, number of primary branches per plant, number of secondary branches per plant, days to 50% flowering and number of seeds per capitulum had strong positive association with seed yield per plant.

Arsal (2007) observed positive and significant correlation between seed yield and all the traits under study except number of primary branches per plant and 1000-seed weight.

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

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

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

2.5 Path coefficients analysis:

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

Sarang *et al.* (2004) reported that number of capitula per plant exerted the highest positive direct effect on yield per plant at the genotypic level followed by test weight (g) 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 through the number of capitula per plant at the genotypic level.

Dalvi *et al.* (2005) observed that the number of effective capitula exerted the highest positive direct effect on seed yield, followed by days to 50% flowering, number of secondary branches, test weight, seed density 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) reported that total biomass, seed weight per capitulum, first fertile branch, 1000-seed weight and flowering duration had substantial direct effects on enhancement of seed yield.

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

Diwakar *et al.* (2006) observed 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) reported that seed yield was determined by capitulum diameter, number of capitula per plant, and number of seeds per head as these characters had high positive direct effects on seed yield.

Ahmadzadeh *et al.* (2008) reported that plant height, hectoliter weight and 100- seed weight had the high positive direct effect on grain yield.

Tamoor *et al.* (2014) observed that grain yield was correlated significantly and positively with plant height, capitulum diameter, number of grains per capitulum, 1000 grain weight and days to maturity. Thus these characters are the key yield contributing attributes to be given selection pressure for improving yield. The result

of path analysis showed highest and positive direct effect of number of grains per capitulum followed by 1000 grain weight and plant height on grain yield.

2.6 Divergence analysis:

Reddy and Devasenamma (2004) grouped 61 genotypes into nineteen clusters based on D^2 anaiysis. Cluster I was biggest with 19 genotypes while cluster II had seven genotypes. The average intra and inter cluster D^2 values among sixty one genotypes showed that cluster I showed minimum intra D^2 values and cluster XV showed maximum intra cluster D^2 values. The inter cluster D^2 values ranged from 18.43 to 322.26. Minimum inter cluster D^2 values were observed between cluster III and I.

Jaradat *et al,* (2006) assessed phenotypic diversity for quantitative and qualitative traits in a salt-tolerant subset of the international safflower (*Carthamus tinctorius* L.) germplasm collection from eleven countries in three regions (Central Asia, Southwest Asia and Africa) of the Middle East. 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 no or few spines. Level of population differentiation was high for number of capitula per plant (30%), whereas most traits partitioned their diversity (82-87%) 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 (*Carthamus tinctorius* L.). A quantitative assessment of genetic divergence for eleven characters using Mahalanobis' D^2 statistic revealed the presence of considerable genetic diversity. The forty genotypes were grouped into seven 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, hull content, number of seeds in main capitulum, seed yield per plant and number of effective capitula were found to be important in the present study.

Harish Babu *et al*. (2012) estimated genetic divergence of 154 genotypes of safflower using D^2 analysis. The genotypes under study were grouped into 9

clusters. The number of capitula per plant contributed maximum towards genetic divergence followed by 100 seed weight and number of seeds per capitulum.

Shivani *et al*. (2013) evaluated 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.

2.7 Drought tolerance

Blume *et al*. (1978) observed a rise in the leaf temperature associated with the decrease of the transpiration rate, reflecting the degree of water stress in sorghum and indicated the possibility of selecting for drought tolerance based on leaf temperature.

Gollan *et al.*1986, Termatt *et al.* 1985, Turner 1986 reported that plants exposed to water stress closed their stomata to maintain inner moisture content and consequently transpiration rate decreased.

Munjal and Rena (2003) reported that cool canopy during grain filling period in wheat is an important physiological principle for high crop stress tolerance.

Naderi *et al.* (2004) showed that drought stress decreases dry matter production via decreasing leaf area index. Comparison of means showed that there was no significant difference among genotypes in respect of stomata density under normal irrigation conditions whereas stomata density was affected by drought stress.

Ashkani *et al*. (2007) have reported that leaf area index at flowering and seed filling stage is an appropriate criterion for screening safflower genotypes under drought stress conditions.

Behnam *et al*. (2011) recorded significant correlation between oil and seed yield in normal and stress conditions. They also reported that the stress tolerance index, geometric mean productivity and arithmetic mean productivity could be used for selection of drought tolerant genotypes.

Golparvar, A. R. and Bahari, B. (2012) 0bserved significant difference between stress and non-stress environments for grain number, grain yield, oil yield,

biological yield, plant height and harvest index traits. The compound analysis explained that there were significant differences among all safflower cultivars for grain number, plant height, grain filling period length and grain filling rate traits.

CHAPTER-III
MATERIAL AND METHODS

The present investigation entitled “Screening of Safflower (*Carthamus tinctorius L.*) genotypes for drought tolerance” was carried out during *Rabi* 2013-2014. A detailed account of the material employed and methods followed during the course of investigation is embodied in this chapter.

3.1 Site of the experiment

The experiment was carried out at All India Coordinated Research Project on Safflower, College of Agriculture, Indore (M.P.). Indore is situated between latitude $22^{o}43'$ N and longitude 76°54' E and at an altitude of 567 meters above the mean sea level.

3.2 Climate and weather conditions

Indore is situated at western part of Madhya Pradesh. It has sub-tropical and semi arid climate with an average annual rainfall of 954.5 mm. Most of the rains received through south west monsoon during rainy season, that is, mid June to September end. The mean minimum and maximum temperature ranges between 6^{0} to 25^{0}c and between 23^{0} to 43^{0} c respectively. December and January are the coldest month while the temperature attains its peak towards the end of May. The weekly maximum and minimum temperatures, rainfall and relative humidity during crop growth period are presented in Table 3.1.

3.3 Experimental material:

The experimental material used in the present study comprised of forty genotypes. The experiment was laid down in a randomized block design with three replications. Each entry was sown in four rows of 4 m row length with a row spacing of 45 cm. and plant to plant distances were maintained as 20 cm. The material was sown on November 16, 2013. All recommended package of practices were followed during the conduction of experiment to raise a good crop. The details of experimental material are as under.

Table 3.1: Meteorological data during crop season 2013-14

SMW	Date	Temperature (^{0}C)		RH (%)	Wind velocity (Km/h)	Rainfall (mm)	No. of rainy days
		Max.	Min.				
44	1 Nov to 3 Nov 2013	30.16	15.33	81.66	1.13	0	0
45	4 Nov to 10 Nov	29.07	15.07	77.42	2.02	0	0
46	11 Nov to 17 Nov	27	12.85	77	2.11	0	0
47	18 Nov to 24 Nov	26.78	8.14	79.28	2.12	0	0
48	25 Nov to 1 Dec	27.92	11	79.85	2.51	0	0
49	2 Dec to 8 Dec	27.21	12.64	77.28	1.87	2.2	0
50	9 Dec to 15 Dec	25.35	8.5	80.57	1.58	0	0
51	16 Dec to 22 Dec	25.78	7.29	81.57	2.05	0	0
52	23 Dec to 29 Dec	24.07	6.5	81.57	3.17	0	0
53	30 Dec to 31 Dec	23.5	7.75	77	4.10	0	0
1	1 Jan to 7 Jan 2014	24.78	7.85	78.71	3.45	0	0
2	8 Jan to 14 Jan	23.35	6.92	78.57	3.52	0	0
3	15 Jan to 21 Jan	23.07	6.78	79.14	4.44	0	0
4	22 Jan to 28 Jan	20.35	7.07	85.71	3.38	0	0
5	29 Jan to 4 Feb	25.21	6.64	78.42	2.21	0	0
6	5 Feb to 11 Feb	26.78	8.14	78.71	3.01	0	0
7	12 Feb to 18 Feb	22.36	8.00	80.57	3.94	0.6	0
8	19 Feb to 25 Feb	26.57	6.79	76.29	4.00	11.6	1
9	26 Feb to 4 March	27.071	8.214	79.28	4.64	30.0	2
10	5 March to 11 March	27.79	10.14	78.29	4.01	0	0
11	12 March to 18 March	32.93	12.86	77.57	3.36	0	0
12	19 March to 25 March	34.43	14.21	80.57	4.53	0	0
13	26 March to 1 April	36.36	17.36	81.57	4.26	0	0
14	2 April to 8 April	36.5	19.07	78	4.80	0	0
15	9 April to 15 April	37.20	18.80	76.20	4.20	0	0
16	16 April to 22 April	38.4	20.9	78.00	4.200	0	0
17	23 April to 29 April	40.10	20.70	75.00	3.50	2.40	0
18	30 April to 4th May	41.30	21.70	77.40	5.10	0	0
Total						**46.8**	**3**

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

Meterological data observed during crop growth period (November 2013 to May 2014) recorded at Indore

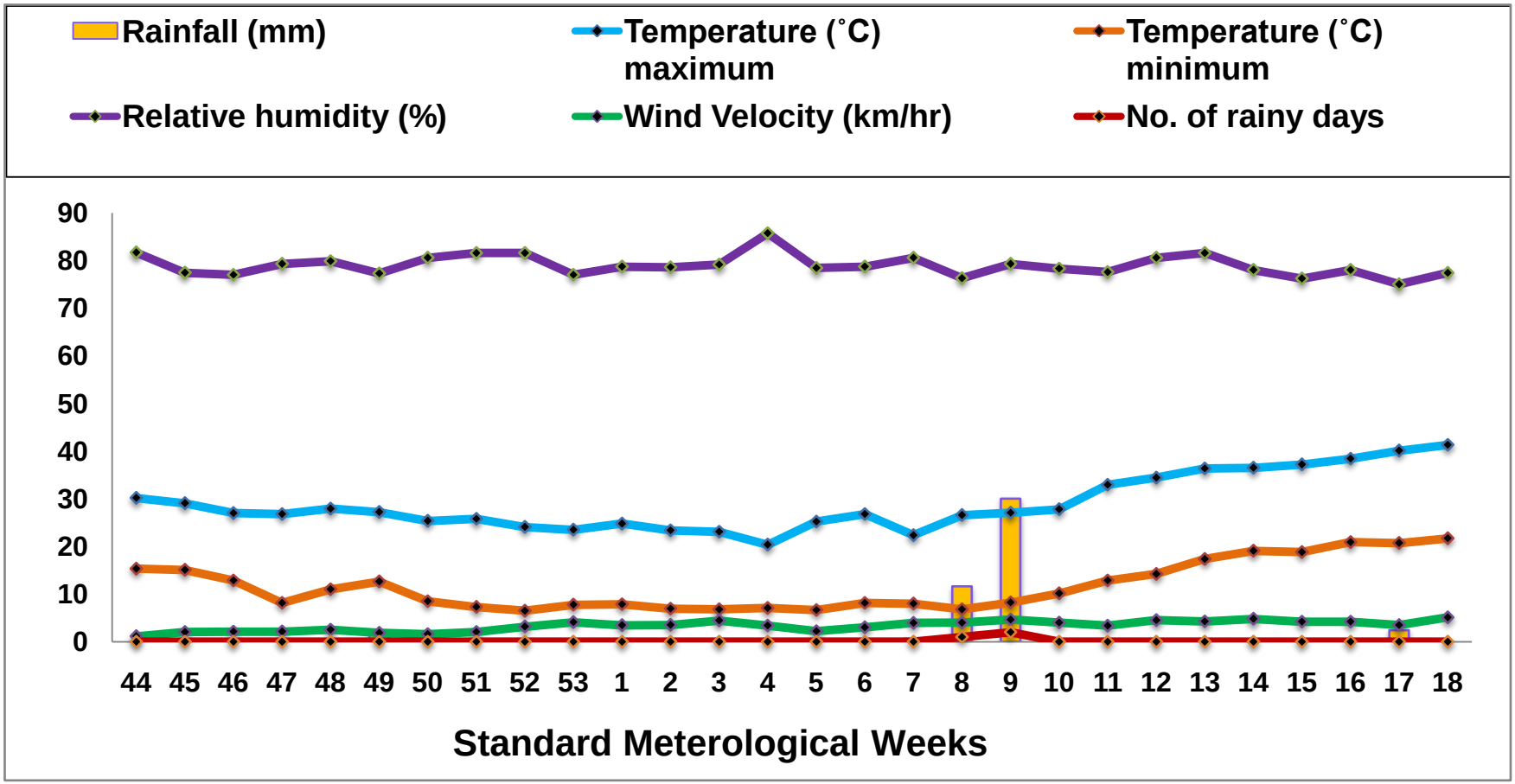

Table 3.2: List of genotypes

S. No.	Name of Genotype	S. No.	Name of Genotype
1	GMU- 2795	**21**	GMU- 4725
2	GMU- 2801	**22**	GMU- 4787
3	GMU- 2811	**23**	GMU- 4807
4	GMU- 2812	**24**	GMU- 4813
5	GMU- 2814	**25**	GMU- 4852
6	GMU- 2852	**26**	GMU- 5125
7	GMU- 2859	**27**	GMU- 5131
8	GMU- 2929	**28**	GMU- 5232
9	GMU- 2960	**29**	GMU- 5239
10	GMU- 3036	**30**	GMU- 5336
11	GMU- 3097	**31**	GMU- 5391
12	GMU- 3175	**32**	GMU- 5411
13	GMU- 4413	**33**	GMU- 5414
14	GMU-1144	**34**	GMU- 5615
15	GMU- 4452	**35**	GMU- 5740
16	GMU- 4485	**36**	GMU- 5741
17	GMU- 4490	**37**	GMU-1152
18	GMU- 4509	**38**	GMU- 5758
19	GMU- 4545	**39**	GMU- 5775
20	GMU- 4573	**40**	GMU- 6114

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, days to maturity, vegetative phase and reproductive phase. For recording observations on single plant basis, five competitive plants from each plot were randomly selected. Average of these five plants in respect of number of branches per plant, number of capitula per plant, plant height, lower branch height, number of seeds per capitulum, 100-seed weight, biological yield per plant, harvest index and seed yield per plant was used for statistical analysis. Traits for drought tolerance leaf temperature, transpiration rate and relative water content were also recorded at pre flowering stage of crop.

The following observations were recorded:

3.4.1 Days to flower initiation:

Number of days taken from the date of sowing to the date of first flower was noted on plot basis.

3.4.2 Days to 50% flowering:

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

3.4.3 Number of branches per plant:

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

3.4.4 Lower branch height (cm):

Height was measured in cm from ground level to first branch on the main stem at the time of maturity.

3.4.5 Plant height (cm):

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

3.4.6 Number of capitula per plant:

Total number of capitula were counted of the selected plants at the time of maturity and averaged.

3.4.7 Days to maturity:

Number of days taken from sowing to physiological maturity was recorded.

3.4.8 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.

3.4.9 100-seed weight (g):

100-seed from the mixture of 5 selected plants were counted at random and seed weight in grams was recorded.

3.4.10 Vegetative phase:

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

3.4.11 Reproductive phase:

Number of days from the date of first flower initiation to physiological maturity was noted on the plot basis**.**

3.4.12 Biological yield per plant (g):

Weight of total biomass of a single plant was recorded in grams.

3.4.13 Harvest index (%):

The harvest index was calculated by the following equation:

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

3.4.14 Seed yield per plant (g):

Seed obtained from single plant was weighed and measured in grams.

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Traits for Drought Tolerance:

Observations were recorded on leaf temperature, transpiration rate and relative water content at preflowering stage to identify the genotypes for drought tolerance. The former two observations were recorded under field conditions whereas, observations on RWC recorded in laboratory. The number of plants selected for observations were same as mentioned for above characters *i.e.*, five from each plot. The values obtained were used to calculate mean for further analysis.

The equipment used for measuring was Porometer (transpiration rate and leaf temperature).

The following observations were recorded.

1. Leaf temperature and transpiration rate

Leaf temperature and transpiration rate were recorded with the help of Steady State Porometer at preflowering. Three leaves were randomly selected from upper, middle and lower portion of each plant .The time for recording data was between 11.30 am to 1.30 pm.

2. Relative water content

A sample of ten leaves was collected and relative water content was measured. The sample of leaves was put in plastic bag and transferred to laboratory on ice. Then fresh weight was measured by electronic balance. Afterward leaf samples were immerged in distilled water at room temperature and placed in dark place. After 5 - 6 h saturated weight was measured. Then the leaves samples were oven dried and finally dry weight was recorded. Relative water content was calculated according to following formula (Ritchie et al., 1990).

RWC = FW-DW/TW-DW ×100

Where FW= Fresh weight, DW = Dried weight, TW =Turgid weight,

3.5 Statistical procedures:

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 covariances, standard error, coefficient of variation and critical difference were obtained for all the fourteen traits. The significant differences between genotypes were tested for the characters under study.

ANOVA			
Source of variation	**d.f.**	**S.S.**	**M.S.**
Replication	**(r-1) 2**	**SSr**	**Mr**
Genotypes	**(g-1) 39**	**SSg**	**Mg**
Error	**(r-1) (g-1) 78**	**SSe**	**Me**

Where, r = No. of replication

g = No. of genotypes

Mr = Mean sum of square for replication

Mg = Mean sum of square for genotypes

Me = Mean sum of square for error

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

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

Enviormental Variance = Me

2. Estimation of phenotypic and genotypic coefficients of variation:

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

$$PCV\ (\%) = \frac{\sqrt{\text{Phenotypic Variance}}}{\text{Mean}} \times 100$$

$$GCV\ (\%) = \frac{\sqrt{\text{Genotypic Variation}}}{\text{Mean}} \times 100$$

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

3. Estimation of heritability and genetic advance:

Heritability:

Heritability in broad sense was estimated by the following formula:

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

Genetic advance:

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested 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 in broad sense, and

σ_p = Phenotypic standard deviation

4. Estimation of correlations:

Phenotypic and genotypic 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,

$Cov_{x,y}$ = 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 estimated values were compared with the tabulated values of Fisher and Yates (1938) at n-2 d.f. at two levels of probability *viz.,* 5% and 1%.

5. Path coefficient analysis:

The proportion of direct and indirect contributions of various characteristics to the total correlation coefficients with seed yield was estimated through path coefficient analysis as suggested by Wright (1921, 1934) and elaborated by Dewey and Lu (1959).

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

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

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots + r_{1l}P_{ly}$$

$$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots + r_{2l}P_{ly}$$

$$r_{ly} = r_{l1}P_{1y} + r_{l2}P_{2y} + r_{l3}P_{3y} + \ldots + P_{ly}$$

Where,

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

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

P_{1y} to P_{ly} = Direct effects of characters 1 to I 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}) = $\sqrt{1 - R^2}$

Where,

$$R^2 = \sum_{iy} P_i^2 Y + 2 \sum_{\substack{i \neq j \\ i > j}} P_{iy} \, P_{jy} \, R_{ij}$$

3.6 Multivariate analysis:

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

To test the significance of difference between lines, taking all the characters simultaneously, 'V' statistic was calculated 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".

To calculate the value of "Λ" following relationship was used:

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

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 was used to test the significance of "Λ" as

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

Where,

m = n - $\frac{p + q + 1}{2}$ with pq degree of freedom.

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 i^{th} character, and

δ_j = Difference between mean values of the two lines for the j^{th} 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 cumbersome. To overcome this 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.

CHAPTER-IV
RESULTS

The experimental results of the present study are presented under the following headings:

1. Analysis of variance
2. Mean performance and range
3. Phenotypic and genotypic coefficients of variation
4. Heritability
5. Genetic advance
6. Correlation coefficients estimates
7. Path analysis
8. D^2 statistic

4.1. Analysis of variance:

The data for all the fourteen traits were analyzed for different sources of variation under RBD and is presented in Table 4.1. The analysis of variance revealed that component of variance for genotypes was significant at 1% level of probability in respect to all the characters namely, days to flower initiation, days to 50% flowering, number of 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.

4.2. Mean performance and range:

The mean values of fourteen characters and their range for forty genotypes are presented in Appendix-I, Appendix-II and Table 4.2.

Table 4.1. ANOVA showing mean sum of squares for different traits in safflower

Source of variation		Replication	Treatment	Error
d.f.		2	39	78
Mean sum of square	Days to flower initiation	8.71	119.61**	0.80
	Days to 50% flowering	3.18	110.51**	2.15
	Number of branches/ plant	0.77	6.30**	0.38
	Lower branch height	0.109	242.77**	2.80
	Plant height	18.75	423.67**	3.25
	Number of capitula/ plant	0.75	23.88**	0.33
	Days to maturity	12.75	34.75**	3.04
	Number of seeds per capitulum	1.42	57.90**	0.65
	100-seed weight	0.002	0.83**	0.050
	Vegetative phase	7.90	119.12**	0.75
	Reproductive phase	6.81	69.38**	6.51
	Biological yield per plant	6.21	454.85**	2.17
	Harvest index	6.12	106.93**	3.14
	Seed yield / plant	0.45	36.87**	0.53

*** Significant at p = 0.05**

**** Significant at p = 0.01**

(i) Days to flower initiation:

The range for this character was from 81.00 (GMU- 4852) to 106.33 days (GMU- 2801) around a grand mean of 90.90 days.

(ii) Days to 50% flowering:

Days to 50% flowering ranged from 92.67(GMU- 4852) to 115.67 days (GMU-2859) and mean was 103.94 days.

(iii) Number of branches per plant:

It ranged from 5.33 (GMU- 2811) to 11.33 (GMU- 2795) around a grand mean of 6.35.

(iv) Lower branch height (cm):

Genotype GMU- 2929 had the lowest node to start branching *i.e.,* 31.67 cm and that of highest was of genotype GMU- 2812 (71.67 cm). Lower branch has mean of 57.69 cm.

(v) Plant height (cm):

The range for plant height was from 85.00 (GMU- 4852) to 132.00 cm (GMU-2812) with mean of 110.90 cm.

(vi) Number of capitula per plant:

The range for this character was from 7.33 (GMU- 5336) to 20.67(GMU-2795) with the mean of 11.73.

(vii) Days to maturity:

It ranged from 136 (GMU- 4852) to 154.33 days (GMU- 2801) with mean of 143.83 days.

(viii) Number of seeds per capitulum:

Number of seeds per capitulum ranged from 7.33 (GMU- 5391) to 24.67 (GMU- 5336) around a grand mean of 15.67.

(ix) 100-seed weight (g):

The entry GMU- 2801 recorded the maximum 100 seed weight of 6.30 g while the entry GMU- 5740 recorded the minimum 100 seed weight of 3.43 g. It had the general mean of 5.38 g.

(x) Vegetative phase:

For vegetative phase mean data ranged from 81.00 (GMU- 4545) to 106.33 days (GMU- 2801) and mean was 90.88 days.

(xi) Reproductive phase:

Reproductive phase ranged from 42.00 (GMU- 2859) to 61.67 days (GMU-5775) with a grand mean of 52.96 days.

(xii) Biological yield per plant (g):

It ranged from 15.00 (GMU- 4573) to 67.33 g (GMU- 2801) around a grand mean of 33.87 g.

(xiii) Harvest index (%):

The range for harvest index was from 19.13 (GMU- 2859) to 38.93 per cent (GMU- 2852) with a grand mean of 29.24 per cent.

(xiv) Seed yield per plant (g):

GMU- 2795 recorded the maximum seed yield (17.40 g/plant) while the minimum by GMU- 5125 (4.57 g/plant) with the grand mean of 9.77 g.

(xiii) Leaf tempreture at preflowering:

The range obtained for leaf temperature was 31.1^{0}C (GMU-4813) to 35.3 ^{0}C (GMU-4545) with a mean value of 32.9 ^{0}C.

(xiv) Transpiration rate at preflowering

The range obtained for transpiration rate was 18.93 µgcm^2 s-1 (GMU-4413) to 38.76 µgcm^2 s-1 (GMU-5741) with mean value of 28.03 µgcm^2 s-1.

(xv) Relative water content

The range obtained for this character was 27.31 to 75 per cent with a grand mean of 48.98 per cent. The Highest Relative Water Content was recorded in genotypes GMU-5336(75.00%) followed by GMU-4813(72.13), GMU-2812(63.75) and lowest relative water content GMU-5131(27.31).

4.3. Coefficient of variation:

Estimates of phenotypic coefficient of variation (PCV) and genotypic coefficients of variation (GCV) were worked out and are presented in Table 4.2

The highest PCV was recorded for biological yield per plant 36.52% followed by seed yield per plant (35.95%), number of seeds per capitula (28.34%), number of capitulum per plant (24.39%), number of branches per plant (24.18%), harvest index (21.01%), lower branch height (15.77%), plant height (10.80%), reproductive phase (9.90%) and 100-seed weight (9.86%). However, low PCV was observed for days to maturity (2.57%), days to 50% flowering (5.95%), vegetative phase (6.98) and days to flower initiation (6.99%).

The highest GCV was observed for biological yield per plant 36.26% followed by seed yield per plant (35.87%), number of seeds per capitulum (27.87%), number of capitula per plant (23.88%), number of branches per plant (22.18%), harvest index (20.11%), lower branch height (15.50%), plant height (10.67%), 100-seed weight (9.77) and reproductive phase (8.64%). However, low GCV was observed for days to maturity (2.26%), days to 50% flowering (5.78%), vegetative phase (6.91) and days to flower initiation (6.92%).

4.4. Heritability:

Heritability in broad sense was estimated for all the traits under study and are presented in table 4,2.

High heritability estimates (Table 4.2) were recorded for seed yield per plant (99.60%), biological yield per plant (98.60%), 100-seed weight (98.20%), vegetative phase (98.10), days to flower initiation (98.00%), plant height (97.70%), number of seeds per capitulum (96.70%), lower branch height (96.60%), number of capitula per plant (95.90%), days to 50% flowering (94.40%), harvest index (91.70%), number of branches per plant (83.80%) and it was moderate for days to maturity (67.60%) and reproductive phase (66.30%).

4.5. Genetic advance:

The expected genetic advance was estimated for all the traits under study and are presented in table 4,2.

The estimates of expected genetic advance expressed as percentage of mean was highest for biological yield per plant (74.17%) followed by seed yield per plant (73.69%), number of seeds per capitulum (56.48%), number of capitula per plant (48.17%), number of branches per plant (41.73%), harvest index (39.67%), lower branch height (31.39%) and plant height (21.74%) while, 100-seed weight

(19.89%), reproductive phase (15.56%), vegetative phase (14.11%), days to flower initiation (14.11%) and days to 50% flowering (11.57%) showed relatively moderate estimates of genetic advance. Days to maturity (4.10%) possessed low values for expected genetic advance.

4.6 Estimates of correlation coefficients:

Phenotypic and genotypic correlation coefficients between yield and its contributing characters and among themselves were calculated and presented in Table 4.3 and 4.4 respectively.

4.6.1 Correlation with seed yield:

(a) Phenotypic correlation coefficients:

Table 4.3 revealed that seed yield per plant showed significant positive correlation with biological yield per plant (0.539), number of capitula per plant (0.451), number of branches per plant (0.315) and 100 seed weight (0.271). However, lower branch height (-0.247), days to maturity (-0.233) and reproductive phase (-0.177) had significant negative association with seed yield per plant at phenotypic level.

(b) Genotypic correlation coefficients:

Table 4.4 showed that biological yield per plant (0.681), number of capitula per plant (0.601) number of branches per plant (0.500) and 100 seed weight (0.383) exhibited positive correlation while days to maturity (-0.278), reproductive phase (-0.270), plant height (-0.239) and days to 50% flowering (-0.181) had negative correlation with seed yield per plant at genotypic level.

Table 4.2 Parameters of genetic variation for various characters in safflower

S.No.	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability (BS) (%)	Genetic Advance	Genetic advance as % of mean
			Min.	Max.					
1	Days to flower initiation	90.90	81.00	106.33	6.99	6.92	98.00	12.83	14.11
2	Days to 50% flowering	103.94	92.67	115.67	5.95	5.78	94.40	12.03	11.57
3	No. of branches/ plant	6.35	5.33	11.33	24.18	22.18	83.80	2.65	41.73
4	Lower branch height	57.69	31.67	71.67	15.77	15.50	96.60	18.11	31.39
5	Plant height	110.90	85.00	132.00	10.80	10.67	97.70	24.11	21.74
6	No. of capitula/ plant	11.73	7.33	20.67	24.39	23.88	95.90	5.65	48.17
7	Days to maturity	143.83	136.00	154.33	2.57	2.26	67.60	5.90	4.10
8	Number of seeds per capitulum	15.67	7.33	24.67	28.34	27.87	96.70	8.85	56.48
9	100-seed weight	5.38	3.43	6.30	9.86	9.77	98.20	1.07	19.89
10	Vegetative phase	90.88	81.00	106.33	6.98	6.91	98.10	12.82	14.11
11	Reproductive phase	52.96	42.00	61.67	9.90	8.64	66.30	8.24	15.56
12	Biological yield p/plant	33.87	15.00	67.33	36.52	36.26	98.60	25.12	74.17
13	Harvest index	29.24	19.13	38.93	21.01	20.11	91.70	11.60	39.67
14	Seed yield / plant	9.77	4.57	17.40	35.95	35.87	99.60	7.20	73.69

4.6.2 Correlation among yield attributes:

Phenotypic and genotypic correlation coefficients among yield attributes were calculated and presented in Table 4.3 and 4.4 respectively

(a) Phenotypic correlation coefficients:

Days to flower initiation had significant positive correlation with vegetative phase (0.823), days to 50% flowering (0.805), days to maturity (0.676), plant height (0.647), lower branch height (0.400) and 100 seed weight (0.196) while, it was negative with number of branches per plant (-0.364), number of capitula per plant (-0.309) and reproductive phase (-0.305).

Days to 50% flowering showed significant positive correlation with vegetative phase (0.809), plant height (0.666), days to maturity (0.657), lower branch height (0.400) and 100 seed weight (0.164) while, negative with number of capitula per plant (-0.336) number of branches per plant (-0.314), reproductive phase (-0.205) and biological yield per plant (-0.171).

Number of branches per plant had significant positive correlation with number of capitula per plant (0.486) and biological yield (0.295) while negative with lower branch height (-0.581), days to maturity (-0.411), vegetative phase (-0.357) and number of seeds per capitulum (-0.221).

Number of capitula per plant exhibited significant positive correlation with biological yield per plant (0.462) and negative with lower branch height (-0.363), days to maturity (-0.344), plant height (-0.331) and vegetative phase (-0.312).

Plant height had significant positive correlation with lower branch height (0.660), vegetative phase (0.653) and days to maturity (0.627) while, it was negative with 100 – seed weight (-0.263).

Lower branch height had significant and positive correlation with days to maturity (0.501), vegetative phase (0.400), number of seeds per capitulum (0.220) reproductive phase (0.198) and 100 seed weight (0.195) while negative with biological yield per plant (-0.196).

Days to maturity showed significant and positive correlation with vegetative phase (0.686), reproductive phase (0.294) and 100-seed weight (0.201) while negative with biological yield per plant (-0.205).

Number of seeds per capitulum exhibited non-significant positive correlation with reproductive phase (0.071).

100 - seed weight had significant positive correlation with harvest index (0.291) and vegetative phase (0.198).

Biological yield per plant had negative significant correlation with harvest index (-0.518).

Harvest index exhibited non–significant negative correlation with vegetative phase (-0.091).

Vegetative phase showed negative significant association with reproductive phase (-0.311).

(b) Genotypic correlation coefficients:

Days to flowering initiation showed positive correlation with days to 50% flowering (0.924), vegetative phase (0.904), plant height (0.829), days to maturity (0.811), lower branch height (0.447) and 100 seed weight (0.290) while, negative with number of capitula per plant (-0.475), number of branches per plant (-0.388), reproductive phase (-0.253) and biological yield per plant (-0.179).

Days to 50% flowering had positive correlation with vegetative phase (0.921), days to maturity (0.844), plant height (0.832), lower branch height (0.455) and 100 seed weight (0.283) however it shows negative association with number of capitula per plant (-0.489), number of branches per plant (-0.456), reproductive phase (-0.266) and biological yield per plant (-0.205).

Number of branches per plant exhibited positive correlation with number of capitula per plant (0.750) and biological yield per plant (0.410) while negative with lower branch height (-0.711), plant height (-0.597), days to maturity (-0.485), vegetative phase (-0.393) and number of seeds per capitulum (-0.318).

Number of capitula per plant showed positive correlation with biological yield per plant (0.572) and negative with days to maturity (-0.581), plant height (-0.557), lower branch height (-0.514), vegetative phase (-0.472), number of seeds per capitulum (-0.242) and harvest index (-0.193).

Plant height showed positive correlation with days to maturity (0.840), vegetative phase (0.825), lower branch height (0.780) and 100 – seed weight (0.314).

Lower branch height had positive correlation with days to maturity (0.583), vegetative phase (0.447), reproductive phase (0.351), number of seeds per capitulum (0.301) and 100 seed weight (0.225) while negative with biological yield per plant (-0.267).

Days to maturity showed positive correlation with vegetative phase (0.803), reproductive phase (0.465) and 100–seed weight (0.235) while negative with biological yield per plant (-0.198).

Number of seeds per capitulum exhibited positive correlation with reproductive phase (0.110) and 100 – seed weight (0.153).

100 – seed weight showed positive correlation with harvest index (0.429) and vegetative phase (0.288).

Biological yield per plant had negative correlation with harvest index (-0.701) and vegetative phase (-0.179).

Table 4.3: Estimates of Phenotypic correlation coefficients for various characters in safflower

Characters	Days to 50% flowering	No. of branches/ plant	No. of capitula / plant	Plant height	Lower branch height	Days to maturity	Number of seed /capitulum	100 – seed weight	Biological yield/ plant	Harvest index	Vegetative phase	Reproductive phase	Seed yield/ plant
Days to flower initiation	**0.805****	-0.364**	-0.309**	0.647**	0.400**	0.676**	0.004	0.196*	-0.152	0.099	0.823**	-0.305	-0.104
Days to 50% flowering		**-0.314****	-0.336**	0.666**	0.400**	0.657**	-0.060	0.164*	-0.171*	0.078	0.809**	-0.205*	-0.157
No. of branch –es / plant			**0.486****	-0.444**	-0.581**	-0.411**	-0.221**	-0.006	0.295**	-0.093	-0.357**	-0.062	0.315**
No.of capitula / plant				**-0.331****	-0.363**	-0.344**	-0.108	0.035	0.462**	-0.088	-0.312**	-0.091	0.451**
Plant height					**0.660****	0.627**	-0.004	-0.263**	-0.018	-0.020	0.653**	0.097	-0.140
Lower branch height						**0.501****	0.220*	0.195*	-0.196*	0.073	0.400**	0.198*	-0.247*
Days to maturity							**0.046**	0.201*	-0.205*	0.073	0.686**	0.294**	-0.233*
Number of seeds per capitulum								**-0.087**	-0.005	-0.017	-0.012	0.071	-0.042
100-seed weight									**-0.088**	0.291**	0.198*	0.043	0.271**
Biological yield / plant										**-0.518****	-0.151	-0.094	0.539**
Harvest index											**-0.091**	-0.018	0.150
Vegetative phase												**-0.311****	-0.113
Reproductive phase													**-0.177***

***,** :** level of significance indicates

Table 4.4: Estimates of Genotypic correlation coefficients for various characters in safflower

Characters	Days to 50% flowering	No. of branches/ plant	No. of capitula/ plant	Plant height	Lower branch height	Days to maturity	Number of seed per capitula	100 seed weight	Biological yield per plant	Harvest index	Vegetative phase	Reproductive phase	Seed yield/ plant
Days to flower initiation	**0.924**	-0.388	-0.475	0.829	0.447	0.811	-0.034	0.290	-0.179	0.083	0.904	-0.253	-0.134
Days to 50% flowering		**-0.456**	-0.489	0.832	0.455	0.844	0.039	0.283	-0.205	0.114	0.921	-0.266	-0.181
No. of branches/ plant			**0.750**	-0.597	-0.711	-0.485	-0.318	-0.009	0.410	-0.018	-0.393	-0.160	0.500
No. of capitula/ plant				**-0.557**	-0.514	-0.581	-0.242	0.037	0.572	-0.193	-0.472	-0.138	0.601
Plant height					**0.780**	0.840	0.105	0.314	0.123	0.023	0.825	0.153	-0.239
Lower branch height						**0.583**	0.301	0.225	-0.267	0.131	0.447	0.351	-0.351
Days to maturity							**0.103**	0.235	-0.198	0.010	0.803	0.465	-0.278
Number of seed per capitulum								**0.153**	0.030	-0.049	-0.028	0.110	-0.052
100-seed weight									**-0.131**	0.429	0.288	0.020	0.383
Biological yield per plant										**-0.701**	-0.179	-0.057	0.681
Harvest index											**0.089**	-0.004	0.116
Vegetative phase												**-0.249**	-0.127
Reproductive phase													**-0.270**

Harvest index showed positive correlation with vegetative phase (0.089) and negative with reproductive phase (-0.004).

Vegetative phase showed negative association with reproductive phase (-0.249).

4.7 Path coefficient analysis at genotypic level:

Path coefficient analysis at genotypic level was estimated for all the characters under study and presented in table 4.5.

Days to flower initiation exhibited negative direct contribution of -0.359 and indirect positive contribution through number of capitula per plant (0.139), days to 50% flowering (0.130), number of branches per plant (0.122) and harvest index (0.104) and negative indirect contribution through plant height (-0.785) and biological yield (-0.345).

Days to 50% flowering showed positive direct contribution of 0.103 and indirect positive contribution via number of capitula per plant (0.153), harvest index (0.148) and number of branches per plant (0.143) while, negative contribution through plant height (-0.788) biological yield (-0.396), days to maturity (-0.168) and days to flower initiation (-0.368).

Number of branches per plant showed low direct negative contribution of -0.313. It had indirect positive contribution by biological yield (0.790), plant height (0.565) and days to flowering initiation (0.139) but negative contribution through days to 50% flowering (-0.502) and number of capitula per plant (-0.219).

Number of capitula per plant exhibited negative direct contribution of -0.293 on seed yield. The positive indirect contribution of number of capitula per plant was observed through plant height (0.528), days to flower initiation (0.171), days to maturity (0.116) and biological yield per plant (0.102) however, it shows negative contribution through days to 50% flowering (-0.540), harvest index (-0.243) and number of branches per plant (-0.235).

Plant height (-0.947) showed negative direct contribution of -0.947 on seed yield. It had considerable positive indirect contribution on seed yield *via* days to 50% flowering (0.917), number of branches per plant (0.187) and number of capitula per

plant (0.163) but negative indirect contribution through days to flower initiation (-0.298), biological yield per plant (-0.237) and days to maturity (-0.167).

Lower branch height showed positive direct contribution of 0.118 on seed yield. It had positive indirect contribution via days to 50% flowering (0.501), number of branches per plant (0.223), harvest index (0.165) and number of capitula per plant (0.150) and negative indirect contribution via plant height (-0.738), biological yield (-0.515) and days to flower initiation (-0.161).

Days to maturity had negative direct contribution of -0.199 on seed yield but it had considerable positive indirect effect through days to 50% flowering (0.930), number of capitula per plant (0.170) and number of branches per plant (0.152) but negative indirect contribution through plant height (-0.796) and biological yield (-0.381).

Number of seeds per capitulum showed negative direct effect of -0.177 on seed yield. It had indirect positive effect through number of branches per plant (0.100) and negative through plant height (-0.100).

100 – Seed weight showed positive direct effect of 0.198 and indirect by harvest index (0.540) and days to 50% flowering (0.312). Where as negative indirect contribution of 100 – seed weight was observed through plant height (-0.297), biological yield (-0.252) and days to flowering initiation (-0.104) on seed yield.

Biological yield per plant showed high positive direct effect of 0.927 on seed yield. It had indirect negative effect through harvest index (-0.883), days to 50% flowering (-0.226), number of capitula per plant (-0.167) and number of branches per plant (-0.128) on seed yield while it had positive indirect effect through plant height (0.116).

Harvest index (0.959) exhibited high positive direct effect of 0.959 on seed yield. It had positive indirect contribution through days to 50% flowering (0.126) and negative through biological yield (-0.351) on seed yield.

Vegetative phase showed negative direct effect but it had considerable positive indirect contribution through number of capitula per plant (0.138), days to 50% flowering (0.126), number of branches per plant (0.123) and harvest index

(0.112) it had indirect negative contribution through plant height (-0.782), days to flower initiation (-0.361), biological yield (-0.346) and days to maturity (-0.160).

Reproductive phase showed positive direct effect of 0.153 but it had considerable negative indirect contribution through days to 50% flowering (-0.293), plant height (-0.145) and biological yield (-0.109).

Residual effect was found to be 0.3031.

4.8.1 Divergence analysis:

The analysis of variance (Table 4.1) revealed highly significant differences among genotypes for all the fourteen characters under investigation. From the estimates of variances and co–variances, D^2 – statistic, which utilizes Wilk's criterion, a simultaneous test for all the fourteen characters was done, which also showed highly significant differences among genotypes. These differences suggest the existence of considerable divergence among the experimental material under study.

1. D^2 statistic:

Generalized distance was estimated through Mahalanobis' D^2 – statistic. D^2 values were calculated for 40 genotypes. The maximum divergence (D^2 = 321.84) was found between genotype 2 (GMU- 2801) and 38 (GMU-5775), minimum (D^2 = 7.68) between genotype 11(GMU- 3097) and genotype 25 (GMU-4852).

The forty safflower genotypes were grouped into eight clusters based on D^2 values. The cluster II was the largest comprising of 9 genotypes followed by cluster I and IV consisting of 7 genotypes. Cluster VIII being the smallest comprising of single genotype (Table 4.6).

Table 4.5: Genotypic path for various characters in safflower

Characters	Days to flower initiation	Days to 50% flowering	No. of branches/ plant	No. of capitula/ plant	Plant height	Lower branch height	Days to maturity	Number of seed per capitula	100 – seed weight	Biological yield per plant	Harvest index	Vegetative phase	Reproductive phase	Genotypic correlation with Seed yield/ plant
Days to flower initiation	**-0.359**	0.130	0.122	0.139	-0.785	0.053	-0.057	0.006	0.057	-0.345	0.104	-0.056	-0.039	-0.134
Days to 50% flowering	-0.368	**0.103**	0.143	0.153	-0.788	0.054	-0.168	-0.007	0.056	-0.396	0.148	-0.057	-0.041	-0.181
No. of branches/ plant	0.139	-0.502	**-0.313**	-0.219	0.565	-0.084	0.097	0.056	-0.002	0.790	-0.023	0.022	-0.025	0.500
No. of capitula/ plant	0.171	-0.540	-0.235	**-0.293**	0.528	-0.061	0.116	0.043	0.007	0.102	-0.243	0.026	-0.021	0.601
Plant height	-0.298	0.917	0.187	0.163	**-0.947**	0.092	-0.167	-0.019	0.062	-0.237	0.029	-0.046	0.023	-0.351
Lower branch height	-0.161	0.501	0.223	0.150	-0.738	**0.118**	-0.116	-0.053	0.045	-0.515	0.165	-0.025	0.054	-0.357
Days to maturity	-0.291	0.930	0.152	0.170	-0.796	0.069	**-0.199**	-0.018	0.047	-0.381	0.013	-0.044	0.071	-0.278
Number of seed per capitulum	0.012	0.043	0.100	0.071	-0.100	0.036	-0.021	**-0.177**	-0.030	0.057	-0.061	0.002	0.017	-0.052
100-seed weight	-0.104	0.312	0.003	-0.011	-0.297	0.027	-0.047	0.027	**0.198**	-0.252	0.540	-0.016	0.003	0.383
Biological yield per plant	0.064	-0.226	-0.128	-0.167	0.116	-0.032	0.039	-0.005	-0.026	**0.927**	-0.883	0.010	-0.009	0.681
Harvest index	-0.030	0.126	0.006	0.056	-0.022	0.016	-0.002	0.009	0.085	-0.351	**0.959**	-0.005	-0.001	0.116
Vegetative phase	-0.361	0.126	0.123	0.138	-0.782	0.053	-0.160	0.005	0.057	-0.346	0.112	**-0.055**	-0.038	-0.127
Reproductive phase	0.091	-0.293	0.050	0.040	-0.145	0.042	-0.93	-0.020	0.004	-0.109	-0.004	0.014	**0.153**	-0.270

Residual = 0.3031Note: Underlined values denote direct effect

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

Cluster	Genotypes	Number of genotypes
I	GMU-4485,GMU-4509,GMU-4545,GMU-4573,GMU-5391,GMU-5741,GMU-1152	**7**
II	GMU-2960,GMU-1144,GMU-4725,GMU-4787,GMU-4807,GMU-4813,GMU-5125,GMU-5411,GMU-5740	**9**
III	GMU-2795,GMU-2929	**2**
IV	GMU-2859,GMU-3036,GMU-3097,GMU-3175,GMU-4452,GMU-4490,GMU-5414	**7**
V	GMU-2852,GMU-4852,GMU-5131,GMU-5239,GMU-5336,GMU-5615	**6**
VI	GMU-2811,GMU-2812,GMU-6114	**3**
VII	GMU-2814,GMU-4413,GMU-5232,GMU-5758,GMU-5775	**5**
VIII	GMU-2801	**1**

The average distance within and between clusters and average inter and intra cluster D^2 values are presented in Table 4.7 and in Table 4.8. In these tables, the diagonal values are mean intra cluster and off the diagonal inter cluster distances.

The highest inter cluster distance of 8.645 was observed between cluster V and VIII followed by cluster III and VIII (8.510), cluster II and III (8.084), cluster I and VIII (8.062), cluster VII and VIII (7.572), cluster III and VI (7.353), cluster III and V (6.772), cluster III and IV (6.550) and cluster I and III (6.465) indicating wide diversity between genotypes in these clusters and the lowest (D = 2.850) between cluster I and V followed by cluster II and IV (3.037), cluster V and VII (3.175), cluster I and VII (3.401) and cluster IV and VI (3.591) indicating close relationship between genotypes in these clusters. The highest intra cluster distance of 2.564 was found for cluster IV and lowest for cluster V (0.000).

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

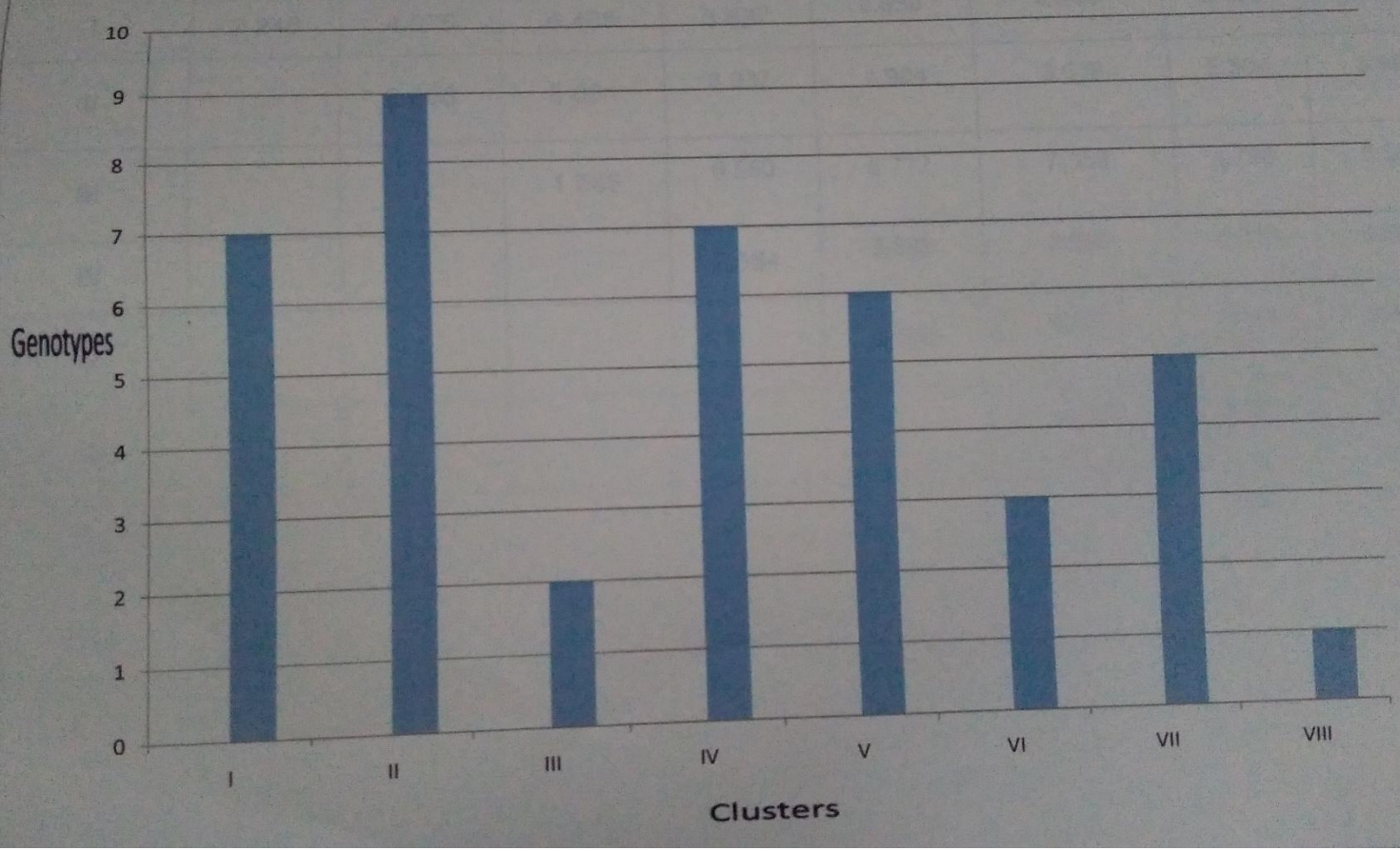

Table 4.7: Average intra and inter cluster distance ($D=\sqrt{D^2}$ values)

Cluster	I	II	III	IV	V	VI	VII	VIII
I	2.248	4.076	6.465	3.637	2.850	4.644	3.401	8.062
II		2.396	8.084	3.037	4.904	3.678	5.509	5.991
III			1.545	6.550	6.772	7.353	4.798	8.510
IV				2.564	3.898	3.591	4.310	5.396
V					0.000	4.817	3.175	8.645
VI						2.103	4.107	4.968
VII							2.062	7.572
VIII								2.260

Table 4.8: Average intra and inter cluster D^2 values

Cluster	I	II	III	IV	V	VI	VII	VIII
I	5.053	16.613	41.796	13.227	8.122	21.567	11.567	64.995
II		5.740	65.351	9.223	24.049	13.527	30.349	35.892
III			2.387	42.902	45.859	54.066	23.020	72.42
IV				6.574	15.194	12.895	18.576	29.116
V					0.000	23.203	10.080	74.736
VI						4.422	16.867	24.681
VII							4.251	57.335
VIII								5.108

Cluster mean:

Clusters means of all fourteen characters are presented in Table 4.10.

1. Days to flower initiation:

Cluster mean was highest (106.33) for cluster VIII and lowest (85.17) for cluster V.

2. Days to 50% flowering:

Cluster mean was highest (116.33) for cluster VIII and lowest (98.33) for clusterV

3. Number of branches per plant:

Cluster mean was highest (11.33) for cluster III and lowest (5.50) for cluster V.

4. Lower branch height:

Cluster mean was highest (65.44) for cluster VI and lowest (34.00) for cluster III.

5. Plant height:

Cluster mean was highest (131.33) for cluster VIII and lowest (99.44) for cluster V.

6. Number of capitula per plant:

Cluster mean was highest (19.00) for cluster III and lowest (9.06) for cluster V.

7. Days to maturity:

Cluster mean was highest (154.33) for cluster VIII and lowest (140.22) for cluster V.

8. Number of seeds per capitulum:

Cluster mean was highest (20.94) for cluster V and lowest (11.48) for cluster I.

9. 100-seed weight:

Cluster mean was highest (6.30) for cluster VIII and lowest (4.82) for cluster II.

10. Vegetative phase:

Cluster mean was highest (106.33) for cluster VIII and lowest (85.24) for cluster I.

11. Reproductive phase:

Cluster mean was highest (58.33) for cluster VII and lowest (47.19) for cluster IV.

12. Biological yield per plant:

Cluster mean was highest (58.00) for cluster VIII and lowest (24.04) for cluster I.

13. Harvest index:

Cluster mean was highest (33.49) for cluster V and lowest (19.57) for cluster VIII.

14. Seed yield per plant:

Cluster mean was highest (16.63) for cluster III and lowest (6.39) for cluster II.

Cluster characteristics:

Table 4.10 showed that cluster I had minimum vegitative phase which is a desirable character.

Cluster II showed lowest 100 seed weight and lowest seed yield per plant which is not desirable.

Cluster III was characterized by lower branch height (34.00), which had lowest mean values for these traits and for higher number of branches per plant (11.33), number of capitula per plant (19.00) and seed yield per plant (16.63) which had highest mean values for these traits.

Cluster IV showed lowest reproductive phase which is not desirable.

Cluster V was characterized for higher number of seeds per capitulum (20.94), harvest index (33.49), which had highest mean values for these traits and days to flower initiation (85.17), days to 50% flowering (98.33), dwarfness plant height (99.44), and earliness in maturity (140.22), which had lowest mean values for these traits.

Cluster VI showed higher value for lower branch height which will facilitate the mechenichal harvesting.

Cluster VII was characterized for long reproductive phase as it recorded highest reproductive phase of (58.33).

Cluster VIII was characterized for bold seed size (100 seed weight, 6.30) and higher biological yield per plant (58.00), which had highest mean values for these traits. It was characterized for long duration and tall plant types.

2. Canonical analysis:

How far divergence between the genotypes determined through D^2 values agree with those determined by canonical analysis was also examined. Canonical analysis deals with the replacement of the measurements of a number of mutually correlated characters by a relatively few measurements obtained as linear combinations of large number of such measurements. The divergence was determined by canonical analysis following the procedure given by Rao (1952). The standardized best linear functions (canonical vectors) were obtained and presented in Table 4.9. It was found that first two canonical roots accounted for about 70.09 per cent variation.

With respect to the relative importance of different characters under study, it could be apparent from the absolute size of coefficient that the lower branch height (0.8567), biological yield per plant (-0.3345), plant height (0.2487), harvest index (-0.2366) and days to flower initiation (0.2343) were important in the primary axis of differentiation, and 100 seed weight (0.8354), days to flower initiation (0.3885), harvest index (0.2646) and lower branch height (-0.2405) were important in the secondary axis of differentiation.

Study on drought tolerance in safflower-

Forty genotypes were screened for tolerance to drought stress that is moisture stress situation. For this, scrutining for earliness, canopy temperature, transpiration rate and relative water content were considered.

Earliness -

Earliness in flowering and maturity leads to escape terminal drought stress situation. Genotype GMU- 4852 exhibited earliness in flower initiation, 50% flowering days to maturity.

Canopy temperature –

Genotypes viz., GMU-4813, GMU-5741 recorded relatively low leaf temperature.

Transpiration rate -

Genotypes viz., GMU-4413, GMU-4545 recorded relatively low transpiration rate.

Relative water content –

Genotypes viz., GMU-5336, GMU-4813 recorded relatively high relative water content.

Table 4.9: Values of first two canonical vectors, which supply best linear function of varieties

Characters	Canonical roots	
	CRI	**CRII**
Days to flower initiation	0.2343	0.3885
Days to 50% flowering	0.0707	0.1382
No. of branches/ plant	0.0587	0.0894
No. of capitula/ plant	-0.1127	0.0623
Plant height	0.2487	0.1619
Lower branch height	0.8567	-0.2405
Days to maturity	-0.0675	0.1734
Number of seeds per capitulum	0.1475	-0.1629
100-seed weight	0.1264	0.8354
Biological yield per plant	-0.3345	0.0156
Harvest index	-0.2366	0.2646
Vegetative phase	0.1687	0.0346
Reproductive phase	0.1765	0.0756
Seed yield / plant (g)	0.2156	0.1774
Percentage of variation absorbed	**55.54**	**14.55**

Table 4.10. Clusters means for fourteen characters in safflower

Characters	Cluster number							
	I	II	III	IV	V	VI	VII	VIII
Days to flower initiation	85.24	95.95	86.27	96.05	85.17	93.78	86.14	106.33
Days to 50% flowering	100.14	110.04	99.50	106.95	98.33	106.33	98.61	116.33
No. of branches/ plant	6.10	6.15	11.33	6.24	5.50	5.78	6.33	7.67
Lower branch height	56.95	63.81	34.00	56.90	56.22	65.44	56.27	53.33
Plant height	107.71	113.22	113.17	110.00	99.44	127.22	111.40	131.33
No. of capitula/ plant	12.10	10.44	19.00	11.95	9.06	10.44	14.13	12.67
Days to maturity	142.19	145.48	141.50	143.24	140.22	149.22	143.93	154.33
Number of seeds per capitulum	11.48	13.26	16.33	14.81	20.94	19.11	18.80	14.00
100-seed weight	5.46	4.82	5.42	5.81	5.38	5.62	5.33	6.30
Vegetative phase	85.24	95.89	86.19	96.05	86.17	93.78	85.27	106.33
Reproductive phase	56.48	49.63	55.33	47.19	54.67	56.00	58.33	48.00
Biological yield per plant	24.04	25.48	56.50	33.90	30.22	44.06	47.13	58.00
Harvest index	31.13	25.44	30.48	30.22	33.49	25.68	30.57	19.57
Seed yield / plant (g)	7.36	6.39	16.63	10.12	10.07	11.57	14.20	11.37

CHAPTER-V
DISCUSSION

The investigation entitled “Screening of Safflower (*Carthamus tinctorius L.*) genotypes for drought tolerance” was carried out during Rabi 2013-14 at experimental area of All India Coordinated Research Project on Safflower, College of Agriculture, Indore (M.P.).

The discussion pertaining to the various relevant topics of the present investigation has been furnished *viz.,* genetic variability, heritability, genetic advance, correlation analysis, path analysis, genetic divergence analysis and drought tolerance.

Genetic Variability:

A broad spectrum of variability is a key factor for success of a crop improvment programme as it provides an opportunity to the plant breeder for making desired improvement in population by increasing the frequency of desirable individuals. Wide range of variability for traits is also necessary to isolate significantly superior genotypes for commercial cultivation as variety or to be used as parents in hybridization programme for combination breeding or to create useful genetic variability for further improvement.

Wide range of variability was observed in the experimental material for days to flower initiation, days to 50% flowering, number of 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 character under study. The values of mean and range revealed that there is wide variability among genotypes for most of the characters. The variation was uniformly distributed on the both sides of the means for each character, indicating normal distribution in the population for all characters. The value of mean sum of squares due to genotypes was significant for all the traits. Which indicating that the experimental material differed significantly amongst them.

High estimates of PCV was observed for biological yield per plant, followed by seed yield per plant, number of seeds per capitulum, number of capitula per plant,

number of branches per plant, harvest index, lower branch height, plant height, reproductive phase and 100-seed weight. Similar trend was observed at genotypic level also. Thus, the present investigation revealed that the existence of sufficient genetic variability in the population and there is a lot of scope for achieving desirable improvement.

The difference between PCV and GCV was negligible or very low for biological yield per plant, seed yield per plant, number of seeds per capitulum, number of capitula per plant, harvest index, lower branch height, plant height, reproductive phase and 100-seed weight. This suggests that the expression of these traits were least affected by the environmental factors and their phenotype is the true representative of its genotype. Further, the selection on the basis of *per se* performance will be effective.

On the other hand days to maturity, days to 50% flowering, vegetative phase, days to flower initiation was found to be consistent in its behavior at both, phenotypic and genotypic, levels having lowest coefficient of variation. It suggested that these were least influenced by non-genetic factors and hence, were quite stable. The range was also quite wide for these traits and there was ample scope for selecting parents to develop an early and dwarf genotypes.

These results were in agreement with the findings of Choulwar *et al.(*2005), Lakshyadeep *et al*. (2005) and Biradar *et al*. (2012) for seed yield per plant, lower branch height, number of capitula per plant, number of branches per plant, biological yield per plant, harvest index, seed yield per plant, number of seeds per capitulum and 100 seed weight in safflower.

Heritability:

The total variability which is present in the population will not be transmitted; only its heritable portion will be transmitted to the next generation. The knowledge of heritable proportion of genetic variability present in the population can be obtained by another genetic parameter known as heritability estimates.

Heritability estimate in broad sense is the ratio 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 offsprings. It helps the plant breeders in the

selection of superior genotypes from the genetically variable population. Robinson *et al.* (1949) had classified heritability estimate in broad sense as high (above 70%), medium (50-70%) and low (below 50%).

The estimates of heritability are influenced by various factors such as sample size, sampling methods, effects of linkage, method of estimation and population density *etc*. and other biotic and abiotic factors that effect the expression of the characters in the population. Thus, heritability estimate 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 indicating the phenotypic appearance would provides a close measure of genotypic value and thus, a breeder can make selection on the basis of *per se* performance of the individuals.

In present investigation high estimates of heritability in broad sense were observed for seed yield per plant, biological yield per plant, 100-seed weight, vegetative phase, days to flower initiation, plant height, number of seeds per capitulum, lower branch height, number of capitula per plant, days to 50% flowering, harvest index, number of branches per plant.

Estimate of heritability value was medium for days to maturity and reproductive phase. These characters may be used to construct selection indices but progress made through them would be low.

Similar results were also reported by Choulwar *et al*. (2005), Lakshyadeep *et al*. (2005), Beena *et a*l. (2006), Camas and Esendal (2006), Arslan *et al.* (2007) and Ichanal *et al*. (2010), for number of branches per plant, days to maturity, number of seeds per capitulum, harvest index, number of capitula per plant and seed yield per plant in safflower.

Expected Genetic advance:

Expected genetic advance is the product of selection intensity, heritability and phenotypic standard deviation. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.,* 1955). More genetic advance could be expected from a population with wide variability and high mean.

In the present investigation, the estimates of the expected genetic advance expressed as percentage of mean were high for biological yield per plant, seed yield

per plant, number of seeds per capitulum, number of capitula per plant, number of branches per plant, harvest index, lower branch height and plant height.

Heritability estimates along with genetic advance were more helpful than heritability alone in predicting the resultant gain under selection of best individual. In the present study, high heritability was associated with high genetic advance as percentage of mean was observed for biological yield per plant, seed yield per plant, number of seeds per capitulum, number of capitula per plant, number of branches per plant, harvest index, lower branch height and plant height.

The occurrence of high heritability with high genetic advance for these traits suggested predominance with additive gene action for the expression of these traits. Hence, these characters would be improved through direct selection procedures. While, characters *viz;* 100-seed weight, vegetative phase, days to flower initiation, and days to 50% flowering showed high heritability with moderate genetic advance as percentage of mean suggested that the predominance of non additive gene action for expression of these traits and high heritability (bs) was due to favourable influence of environment rather than genetic factor. Hence, these characters can be improved by a breeding method which can exploit the non additive gene action like heterosis breeding etc.

The present results were in agreement with the findings of Reddy *et al.* (2003), Sarang *et al*. (2004), Choulwar *et a*l. (2005) and Lande and Deshmukh (2012) found high with high genetic advance as percent of mean for 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 minus unity to plus unity. If increase in one variable results in the increase of other variable, the relationship is positive and if it results in the decrease of other variables, the association is negative. The two variable are uncorrelated if the increase or decrease of one variable does not affect the other variable.

Information about correlations is of great significance to a plant breeder because all the phenotypic traits are the result of interplay of several genetic factors

among themselves and their individual and combined interaction with the environmental factors.

Knowledge of correlation helps a plant breeder to determine the methodology to improve a particular trait which is not readily amenable to direct selection and so indirect selection becomes inevitable. It also provides information about the correlated response to directional selection to predict genetic advance and thus, can be used as selection indices for operating more efficient selection programme.

Correlation could be phenotypic, genotypic or environmental. Phenotypic correlation is the association between values directly measured on individuals and includes genetic and non–genetic effects. Genotypic correlation is the relationship between breeding values and accounts for only genetic causes which could be pleiotrophy, linkage or gene frequency disequilibrium. Environmental correlation is relationship between non – genetic values and arises due to the fact that several observations are affected by the same amount of environment. Information on all the three is, therefore, very useful to a plant breeder.

The estimates of phenotypic correlation coefficients revealed that seed yield was positively correlated with biological yield per plant, number of capitula, number of branches and 100 seed weight and improvement in any one of them through indirect selection would result in improvement in seed yield. These traits, thus, may be used for selecting high yielding genotypes. Anjani (2005), Dalvi *et al*. (2005), lakshyadeep *et al*. (2005), Nair *et al.* (2006), *Ali et al*. (2006), Alizadeh and Caraprtian (2006), Bidgoli *et al.* (2006), Diwakar *et al*. (2006), Jawanjal *et al*.(2006), Arsal *et al*. (2007), Ahmadzadeh *et al*. (2008), Mukta *et al*. (2008) and Maryam *et al.* (2012) reported similar findings for seed yield per plant, lower branch height, number of capitula per plant, number of branches per plant, biological yield per plant, harvest index, seed yield per plant, number of seeds per capitulum and 100 seed weight in safflower.

The inter–correlations of days to flower initiation with vegetative phase, days to 50% flowering, days to maturity, plant height, lower branch height and 100 seed weight; of days to 50% flowering with vegetative phase, plant height, days to maturity, lower branch height and 100 seed weight and biological yield per plant; of number of branches per plant with number of capitula per plant and biological yield;

of number of capitula per plant with biological yield per plant; of plant height with vegetative phase, lower branch height and days to maturity; of lower branch height with days to maturity, vegetative phase, number of seeds per capitulum, reproductive phase and 100 seed weight; of days to maturity with vegetative phase, reproductive phase and 100 seed weight; and of 100 seed weight with harvest index and vegetative phase were also found positive.

The estimates of genotypic correlation coefficients with yield were similar to those of phenotypic correlation coefficient in direction. However, these were higher in magnitude. It suggested that these correlations were due to breeding values and therefore, more dependable.

Path analysis:

The yield is complex polygenic trait and greatly influenced by its component characters. The inter – relationship among the component traits therefore, often limits the magnitude of yield. Correlation coefficient measures the strength and direction of relationship among different traits but it does not reveal contribution of each trait 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 magnitude and direction of each trait.

Path analysis, a technique suggested by Wright (1921), quantifies the direct and indirect contributions of different traits to the total correlation coefficients and helps to understand there inter – relationship.

The result of path analysis based on genotypic correlation coefficients indicated that the 100–seed weight, biological yield and harvest index showing positive correlation with seed yield per plant had substantial direct contribution to the seed yield.

100 – Seed weight had positive direct effect on seed yield but its strong correlation with seed yield might be ascribed to the fact that this character had positive effects via harvest index and days to 50% flowering. Biological yield exhibited positive direct effect through plant height. Traits namely, harvest index had positive direct effects via days to 50% flowering.

It could be concluded from the present investigation that the characters like 100–seed weight, biological yield and harvest index possessed strong positive association and high magnitude of positive direct effects on seed yield. Moreover the indirect effects of most of the characters via these characters were positive. Thus these traits were conceded as the most important yield attributing characters.

The results of the present investigations are also confirmed by the findings of Reddy *et al.* (2004), Sarang *et al.* (2004), Dalvi *et al.* (2005), Ali *et al.* (2006), Jawanjal *et al.* (2006), Bidgoli *et al*. (2006), Diwakar *et al.* (2006), Arsal (2007), Ahmadzadeh *et al.* (2008) and Tamoor *et al*. (2014) for seed yield per plant, lower branch height, number of capitula per plant, number of branches per plant, biological yield per plant, harvest index, seed yield per plant, number of seeds per capitulum and 100 seed weight in safflower.

Genetic divergence:

The choice of parents is of paramount importance in any breeding programme. It is rather a difficult task for a plant breeder. Selection of parents on the basis of *per se* performance is good but there is a possibility of related lines being chosen resulting in limited or no advances under selection and therefore, there is need for emphasis on a wide genetic base by the utilization of world collection on genetic criterion. Selection of the parents and this has led to success in some cases but these need to be supplemented with genetic diversity. The measures based on genetic criteria qualifying diversity have become important in classifying material for the use by the breeders. Further, the genetic divergence among parents is important because a cross-involving genetic diverse parent is likely to produce high heterotic effect and also a broad spectrum of variability could be expected in the segregating generations. The assessment of divergence for a set of genotypes using multivariate analysis like distance analysis, canonical analysis etc. has been attempted and effectively utilized in a number of crop plants with diverse breeding systems. Thus, the genetic divergence has a definite role towards efficient choice of parents for hybridization programme.

The dispersion among variables for the aggregate effect of the fourteen characters as tested by Wilk’s criterion was also highly significant indicating existence of considerable divergence in the material under study.

Genetic differences among genotypes were quantified by estimating D^2 statistic. The estimates of D^2 values varied substantially from 7.68 to 321.84. The maximum divergence (D^2= 321.84) was recorded between genotype GMU- 2801 and GMU- 5758. These two genotypes also showed significant differences between them in respect of most of the characters (Appendix-I). A cross between these two genotypes is expected to give a heterotic hybrid and wide spectrum of variability. Therefore, these genotypes may be used as parents for hybridization. On the other hand minimum divergence (D^2 = 7.68) was observed between genotypes GMU-3097 and GMU- 4852 which did not differ significantly from each other for most of the characters taken under study therefore, these may be related in their evolution.

The forty genotypes were grouped into 8 clusters. Cluster II contained maximum number of genotypes 9, followed by cluster I and IV (7), cluster V (6), cluster VII (5), cluster VI (3), cluster III (2) and cluster VIII contained only one genotype.

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

Average intra-cluster distance revealed that cluster III, which contained 2 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.

Sometimes a breeder is asked to improve a particular trait of a variety 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 traits of all the 8 clusters were worked out. Cluster I was characterized by lowest reproductive phase. Cluster III had exhibited lowest mean value for lower branch height while, highest mean value for number of branches per plant, number of capitula per plant and seed yield per plant. Cluster V had lowest mean values for days to flower initiation, days to 50% flowering, plant height; days to maturity and highest mean value for seeds per capitulum, harvest index. Cluster Highest mean value for reproductive phase was

observed in class VII. Cluster VIII was characterized for 100 seed weight, vegetative phase and biological yield per plant as they recorded highest mean values for these traits. 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	Characters	Genotypes
I	Minimum vegetative phase	GMU- 4545
III	Lower branch height	GMU- 2929
	Higher number of branches, higher number of capitula per plant and higher seed yield per plant	GMU- 2795
V	Early in days to flower initiation, early in days to 50% flowering, Dwarf and early in maturity	GMU- 4852
	Higher number of seeds per capitulum	GMU- 5336
	Higher harvest index	GMU- 2852
VII	Higher reproductive phase	GMU- 5775
VIII	Higher 100 seed weight and higher biological yield per plant	GMU- 2801

To improve number of seeds per capitulum a line from cluster V, *viz.,* genotype GMU- 5336 would be a right choice. Lines from cluster V, for example genotype GMU- 4852 having earlier initiation of flowering as well as 50% flowering could be used to develop early and dwarf varieties. Line from cluster VIII, for example genotype GMU- 2801 could be used to develop higher 100 seed weight and higher biological yield.

Earliness –

Genotype 4852 showed earliness in flower initiation, days to 50% flowering and day to maturity. This suggests that these genotypes possessed capacity to escape terminal drought situation.

Leaf temperature –

Genotypes *viz.,* GMU-4813, GMU–5741 exhibited low canopy temperature indicates that plants maintained cool environment to verify the adverse effect of high temperature on productivity.

Transpiration rate –

Genotypes *viz.,* GMU–4413, GMU-4545 showed low transpiration rate suggesting that these genotypes possessed capacity to lower down the losses of moisture from shoot system to mitigate moisture stress / drought stress condition.

Relative water content –

Genotypes *viz.,* GMU–5336, GMU–4813 showed high relative water content indicates that genotypes have capacity to maintain moisture in their shoot system which has benefit to utilize to combat under drought stress situations.

In present study, it was observed that genotypes GMU-4813,GMU-2812, GMU-5336 and GMU-5741 has lowest value for leaf temperature. Plants exposed to water stress closed their stomata to maintain their inner moisture content and consequently, their transpiration rate decreased (Gollan *et a*l.1986, Termatt *et al*. 1985, Turner 1986). The ability to maintain a lower leaf temperature may indicate high transpiration rate under drought. Lower leaf temperature with high transpiration rate may be considered useful tool to identify the genotypes, which may perform better in drought tolerance.

This variation in relative water content may be due to different ability of the genotypes in water absorption from the soil or different mechanisms in osmolyte accumulation in plant tissues to retain turgescence pressure. Interestingly, those genotypes which had high relative water content showed the lowest yield loss in compare with sensitive genotypes. Among genotypes, GMU-5336 showed the highest relative water content. Since relative water content maintenance in plants need to low leaf temperature. In general, there are so many reports stating that

drought stress decreases relative water content. This variation in relative water content in different genotypes can be used as a tool for screening of high yield genotypes under drought stress conditions.

Canonical analysis:

Generalized distance, D^2 statistic of Mahalanobis (1936) is an important parameter to ascertain the genetic divergence among genotypes. It provides degree of divergence based on multiple variables. However, it does not provide any indication about the quantum of contribution of each trait towards the total genetic divergence. Thus, it becomes difficult to discriminate through D^2 statistic, among the major or secondary traits of genetic diversity based on their relative contribution. To circumvent this problem another technique, the canonical analysis, is used to determine the contribution of each trait towards the total genetic divergence.

The divergence as determined by canonical analysis revealed that the 1^{st} two roots together accounted for 70.09% of the total variation present in the genotypes. The amount of variation explained by 1^{st} two canonical roots was satisfactory as many more traits contribute towards the variability and a higher number of canonical roots would be required to account for total variability. The coefficient of 1^{st} canonical root revealed that the primary axis rotated around lower branch height, biological yield per plant, plant height, harvest index and days to flower initiation. These traits thus, were primarily responsible for variation between genotypes. It indicated that these yield components were the major traits for genetic divergence. Therefore, greater significance needs to be attached to these traits during selection.

The estimates of coefficients of canonical root II revealed that the second axis was primarily concerned with 100 seed weight, days to flowering initiation, harvest index and lower branch height. It suggested that these traits were secondary in importance in contributing to total genetic divergence. It could be concluded that these traits contributed moderately to the genetic differences and thus be given careful attention while selecting parents to improve these traits.

CHAPTER-VI
SUMMARY, CONCLUSION AND SUGGESTIONS FOR FURTHER WORK

"Screening of Safflower (*Carthamus tinctorius L.*) genotypes for drought tolerance" was conducted using forty genotypes. The experiment was conducted during *Rabi* 2013-14 in randomized block design with three replications at experimental area of All India Coordinated Research Project on Safflower, College of Agriculture, Indore (M.P.).

The observations were recorded on days to flower initiation, days to 50% flowering, number of branches per plant, lower branch height, plant height, number of capitula per plant, days to maturity, number of seed 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, inter relationship among traits and direct and indirect contribution of traits and drought tolerance. The data on all characters were subjected to statistical analysis.

Salient findings are summarized as below-

1. Analysis of variance revealed highly significant differences among genotypes for all the characters at univariate as well as at multivariate level. Estimates of population mean were high and range was also wide for most of the traits. Trend of variability at genotypic level was similar to that of at phenotypic level for most of the characters. The genotypic co-efficient of variation was highest for biological yield per plant followed by seed yield per plant, number of seeds per capitulum, number of capitulum per plant, number of branches per plant, harvest index, lower branch height, plant height, 100-seed weight. reproductive phase, days to flower initiation and vegetative phase.

2. The estimates of heritability in broad sense was high for seed yield per plant, biological yield per plant, 100-seed weight, vegetative phase, days to flower initiation, plant height, number of seeds per capitulum, lower branch height, number of capitula per plant and days to 50% flowering. High heritability coupled with high genetic advance observed for biological yield per plant, plant height, lower branch

height, vegetative phase, days to 50 % flowering and harvest index indicated that these traits were governed by additive gene action. Hence, there are good chances of improvement of these traits through selection in the material.

3. The estimates of genotypic and phenotypic correlations were mostly in agreement in both sign and magnitude and genotypic correlation coefficients were higher than the phenotypic and environmental correlation coefficients. This indicated that there was strong inherent association between the various characters studied. Biological yield per plant, number of capitula per plant, number of branches and 100 seed weight showed positive correlation with seed yield per plant. These traits may be used for construction of index for yield improvement. The trait like days to maturity showed negative association with seed yield per plant.

4. Path analysis revealed that the yield components- namely100 seed weight, biological yield and harvest index were found to have direct contribution, should be given more weightage in selection of parents for hybridization for yield improvement.

5. . Based on D^2 statistic, all the forty genotypes were grouped into 8 clusters. Cluster II contained maximum number of genotypes 9, followed by cluster I and IV (7), cluster V (6), cluster VII (5), cluster VI (3), cluster III (2) and cluster VIII contained only one genotype. The maximum divergence was observed between cluster V and VIII followed by cluster III and VIII, cluster II and III, cluster I and VIII, cluster VII and VIII, cluster III and VI, cluster III and V, cluster III and IV and cluster I and III. The highest average intra cluster distance was recorded for cluster IV and lowest for cluster V.

6. The genotypes GMU-2929, GMU- 2795, GMU- 2801, GMU- 2852, GMU- 2859, GMU- 4545, GMU- 4852 and GMU- 5336 may serve as potential parents for hybridization programme in the improvement of potentiality of the yield contributing traits in safflower.

7. Canonical analysis revealed that lower branch height, biological yield per plant, plant height, harvest index and days to flower initiation relatively contributed more to the divergence as seen in the primary axis of differentiation. In the secondary axis of differentiation, 100 seed weight, days to flowering initiation, harvest index and lower branch height that these traits contribute moderately to the genetic divergence.

8. In present study, it was observed that genotypes GMU-4813,GMU-2812, GMU-5336 and GMU-5741 has lowest value for leaf temperature. Plants exposed to water stress closed their stomata to maintain their inner moisture content and consequently, their transpiration rate decreased (Gollan *et a*l.1986, Termatt *et al*. 1985, Turner 1986). The ability to maintain a lower leaf temperature may indicate high transpiration rate under drought. Lower leaf temperature with high transpiration rate may be considered useful tool to identify the genotypes, which may perform better in drought tolerance.

9. This variation in relative water content may be due to different ability of the genotypes in water absorption from the soil or different mechanisms in osmolyte accumulation in plant tissues to retain turgescence pressure. Interestingly, those genotypes which had high relative water content showed the lowest yield loss in compare with sensitive genotypes. Among genotypes, GMU-5336 showed the highest relative water content. Since relative water content maintenance in plants need to low leaf temperature. In general, there are so many reports stating that drought stress decreases relative water content. This variation in relative water content in different genotypes can be used as a tool for screening of high yield genotypes under drought stress conditions.

While combining above three parameters it may be concluded that lower mean value of leaf temperature and high relative water content with high transpiration rate may be considered favourable for drought tolerance and selection can be done on this basis .In present study genotypes GMU-2812, GMU-4813, GMU-5336 and GMU-5741 may be considered comparatively better performer based on these parameters.

Conclusions

- The characters namely, biological yield per plant, followed by seed yield per plant, number of seeds per capitulum, number of capitulum per plant, number of branches per plant, harvest index, lower branch height, plant height, reproductive phase and 100-seed weight exhibited wide range and high PCV and GCV offering ample scope for improvement through selection. Besides this, these characters also

had narrow differences between the values of PCV and GCV showing least influence of environment.

- High heritability coupled with high genetic advance observed for seed yield per plant, biological yield per plant, 100 seed weight, vegetative phase, days to flower initiation, plant height, number of seeds per capitulum and lower branch height indicated that these traits are governed by additive gene action. Hence, there are good chances of improvement of these traits through direct selection.

- On the basis of association and path coefficient analysis number of capitula per plant, number of seeds per capitulum, 100 seed weight, reproductive phase, biological yield per plant and harvest index were found to be major component traits that contribute towards seed yield. Hence, due weightage should be given while practicing selection for identifying high yielding strains.

- The maximum divergence (D^2 = 321.84) was recorded between genotype GMU- 2801 and GMU- 4852. These two genotypes also showed significant differences between them in respect of most of the characters. A cross between these two genotypes is expected to give a heterotic hybrid and wide spectrum of variability. Therefore, these genotypes may be used as parents for hybridization.

- The coefficient of canonical root I revealed that the primary axis rotated around lower branch height, biological yield per plant, plant height, number harvest index and days to flower initiation thus, was primarily responsible for variation between genotypes. It indicated that these characters were the major yield component for genetic divergence. Therefore, greater significance needs to be attached to these traits during selection.

- The estimates of coefficients of canonical root II revealed that the second axis was primarily concerned with 100 seed weight, days to flowering initiation, harvest index and lower branch height. Thus, these traits contributed moderately to the genetic differences and thus be given careful attention while selecting parents to improve these traits.

- The genotypes GMU-2929, GMU-2795, GMU-2801, GMU-2852, GMU- 2859, GMU-4545, GMU- 4852 and GMU- 5336 may serve as potential parents for hybridization programme in the improvement of potentiality of the yield contributing traits in safflower.

- Genotypes viz., GMU-2812, GMU-4813, GMU-5336 and GMU-5747 found better perform under drought stress.

Suggestions:

The following suggestions have been made for further study:-

❖ The genetic variability reported for different characters in relation to yield should be exploited.

❖ Characters showing high heritability with high genetic advance should be utilized in selection.

❖ A better crop ideotype should be developed using findings from association analysis.

❖ The promising stable genotypes identified can be tested for combining ability and inheritance of yield and its contributing traits for further use in breeding programme.

❖ On the basis of genetic divergence and mean performance the genotypes GMU- 2929, GMU- 2795, GMU- 2801, GMU- 2852, GMU- 2859, GMU- 4545, GMU-4852 and GMU- 5336 have been suggested for further use in breeding programme.

❖ Genotypes identified (GMU-4413, GMU-4545) low transpiration rate, (GMU-4813, GMU-5741) low canopy temperature and (GMU-5336 and GMU-4813) for higher relative water content vaues should be tested under drought tolerance for deriving valid conclusions.

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Appendix I : Mean performance for yield and its components of forty genotypes of safflower

S. No.	Genotypes	Days to flower initiation	Days to 50% flowering	No. of branches/ plant	Lower branch height	Plant height	No. of capitula/ plant	Days to maturity	Number of seeds per capitulum	100-seed weight	Vegeta-tive phase	Reproductive phase	Biological yield per plant	Harvest index	Seed yield/ plant
1	GMU 2795	87.33	95.67	11.33	36.33	122.33	20.67	141.67	14.33	5.67	87.33	54.33	58.00	25.17	17.40
2	GMU 2801	106.33	116.33	7.67	53.33	131.33	12.67	154.33	14.00	6.30	106.33	48.00	67.33	19.57	11.37
3	GMU 2811	95.00	103.33	5.33	62.00	125.33	12.00	151.00	24.00	5.73	95.00	56.00	55.50	29.93	16.63
4	GMU 2812	96.67	110.33	5.67	71.67	132.00	9.33	149.00	18.33	5.53	96.67	54.00	38.67	24.63	9.57
5	GMU 2814	86.33	97.67	6.00	51.67	101.00	14.33	144.67	18.67	5.17	86.33	56.33	34.00	37.03	13.83
6	GMU 2852	87.33	96.00	6.67	61.67	117.67	15.00	142.33	21.00	5.67	87.33	55.00	44.33	38.93	16.97
7	GMU 2859	104.67	115.67	6.33	65.33	122.33	13.00	146.67	9.00	4.87	104.67	42.00	30.00	19.13	5.77
8	GMU 2929	85.00	101.33	11.33	31.67	104.00	17.33	141.33	18.33	5.17	85.00	56.33	45.67	35.80	16.30
9	GMU 2960	95.67	102.33	7.00	66.33	130.00	10.67	139.67	16.67	5.77	95.67	44.00	30.00	34.70	10.33
10	GMU 3036	95.67	106.00	5.33	52.67	107.67	10.67	144.67	17.67	6.03	95.67	49.00	46.00	25.27	11.30
11	GMU 3097	94.33	105.67	6.00	54.33	98.00	7.67	142.67	13.33	5.70	94.33	48.33	22.67	25.27	5.83
12	GMU 3175	96.67	108.33	6.33	62.33	110.00	15.33	142.67	10.33	5.80	97.67	45.00	29.67	30.47	9.10
13	GMU 4413	97.00	100.67	5.33	64.33	100.67	8.33	141.67	17.00	5.70	86.67	55.00	27.67	29.80	8.17
14	GMU 1144	96.67	107.33	6.00	64.00	109.00	8.67	142.00	17.33	4.73	97.00	45.00	28.00	25.47	7.10
15	GMU 4452	83.67	106.33	7.33	66.33	120.00	13.67	144.00	17.67	5.77	96.67	47.33	36.33	36.40	13.27
16	GMU 4485	99.33	99.67	9.67	54.33	114.67	14.33	139.67	10.33	5.70	83.67	56.00	23.33	35.73	8.23
17	GMU 4490	85.67	115.00	6.00	43.00	107.33	11.00	144.67	13.67	5.87	99.33	45.33	40.33	21.80	8.80
18	GMU 4509	81.00	97.00	5.33	43.33	97.00	10.33	143.00	10.33	5.90	85.67	54.00	23.33	25.83	6.17
19	GMU 4545	85.67	97.00	5.67	65.00	113.33	12.00	142.00	14.33	4.83	81.00	61.00	23.67	35.33	8.30
20	GMU 4573	94.33	102.33	5.33	53.67	102.67	12.33	143.67	8.67	5.23	85.67	58.00	15.00	36.23	5.50

S. No.	Genotypes	Days to flower initiation	Days to 50% flowering	No. of branches/ plant	Lower branch height	Plant height	No. of capitula/ plant	Days to maturity	Number of seeds per capitulum	100-seed weight	Vegeta-tive phase	Reproductive phase	Biological yield per plant	Harvest index	Seed yield/ plant
21	**GMU 4725**	94.33	106.00	6.00	64.33	120.00	11.00	146.33	14.00	5.27	94.33	52.00	32.00	24.10	7.63
22	**GMU 4787**	96.33	107.67	6.67	62.33	118.33	11.33	148.67	9.67	5.10	96.33	52.33	25.00	21.97	6.10
23	**GMU 4807**	95.33	111.67	5.67	61.00	120.67	8.67	145.00	17.67	5.27	95.33	49.67	32.33	25.17	8.10
24	**GMU 4813**	90.33	112.33	5.67	69.33	102.67	8.33	143.00	18.67	4.60	90.33	52.67	19.00	37.20	7.00
25	**GMU 4852**	81.00	92.67	5.67	52.33	85.00	10.67	136.00	21.33	5.03	81.00	55.00	31.33	36.70	11.37
26	**GMU 5125**	94.00	112.33	6.00	63.00	112.67	8.67	145.33	10.67	5.00	94.00	51.67	22.00	20.63	4.57
27	**GMU 5131**	88.00	103.33	5.67	52.67	109.33	8.67	142.00	21.00	4.47	88.00	54.33	28.33	29.70	8.40
28	**GMU 5232**	83.00	95.00	7.67	42.00	100.33	14.33	141.00	16.33	5.23	83.67	57.33	45.67	28.80	13.07
29	**GMU 5239**	92.33	101.67	5.33	54.00	102.00	8.67	140.67	20.67	5.70	92.33	51.67	29.33	35.03	10.07
30	**GMU 5336**	87.67	100.33	5.33	59.67	113.00	7.33	142.00	24.67	5.57	87.67	54.33	33.33	30.63	10.17
31	**GMU 5391**	89.00	100.00	5.67	63.33	116.00	13.33	142.00	7.33	6.07	89.00	53.00	19.67	30.80	6.10
32	**GMU 5411**	96.00	111.00	7.33	64.00	118.00	14.00	145.33	9.00	5.13	95.33	50.00	25.33	25.83	6.57
33	**GMU 5414**	93.00	105.00	5.67	53.33	97.00	14.67	144.33	14.33	5.77	93.00	51.33	32.33	37.67	12.20
34	**GMU 5615**	81.33	93.00	5.67	54.33	86.67	10.67	139.00	21.00	5.80	81.33	57.67	31.33	39.10	12.27
35	**GMU 5740**	95.67	106.33	5.67	61.00	95.33	10.33	147.00	13.33	3.43	95.67	51.33	15.67	29.43	4.70
36	**GMU 5741**	85.33	104.33	5.67	66.67	117.00	11.67	143.00	16.00	5.47	85.33	57.67	35.00	28.93	10.13
37	**GMU 1152**	86.33	101.00	5.33	52.00	93.33	10.67	142.00	13.33	5.00	86.33	55.67	28.33	25.03	7.10
38	**GMU 5758**	83.33	101.00	5.33	66.33	122.67	13.00	144.33	20.00	5.17	83.33	61.33	49.67	26.27	13.13
39	**GMU 5775**	85.67	102.00	6.00	59.67	115.33	14.00	147.33	18.00	5.40	85.67	61.67	62.00	21.83	13.57
40	**GMU 6114**	89.67	105.33	6.33	62.67	124.33	10.00	147.67	15.00	5.60	89.67	58.00	38.00	22.47	8.50
	S.E.m (d) ±	0.73	1.19	0.50	1.37	1.47	0.48	1.42	0.66	0.06	0.70	2.08	1.20	1.44	0.18

APPENDIX II (a)- Mean performance for physiological characters of forty genotypes of safflower

S. No.	Genotypes	Leaf temperature	Transpiration rate	RWC
1	GMU 2795	32.4	32.19	62.50
2	GMU 2801	32.3	27.43	32.00
3	GMU 2811	33.5	25.27	40.00
4	GMU 2812	31.4	35.48	63.75
5	GMU 2814	31.7	31.78	59.50
6	GMU 2852	33.4	33.69	38.75
7	GMU 2859	34.3	26.80	43.32
8	GMU 2929	31.9	22.53	60.00
9	GMU 2960	32.2	20.67	41.17
10	GMU 3036	33.1	24.46	45.00
11	GMU 3097	31.4	32.17	57.46
12	GMU 3175	34.3	21.64	37.81
13	GMU 4413	32.2	18.93	40.00
14	GMU 1144	33.1	28.71	30.00
15	GMU 4452	34.9	30.42	57.75
16	GMU 4485	33.8	32.56	55.47
17	GMU 4490	32.6	25.71	43.32
18	GMU 4509	32.6	31.14	37.32
19	GMU 4545	35.3	19.38	41.17
20	GMU 4573	32.2	24.75	60.00

APPENDIX II (b)- Mean performance for physiological characters of forty genotypes of safflower

S. N.	Genotypes	Leaf temperature	Transpiration rate	RWC
21	GMU 4725	33.5	30.17	55.17
22	GMU 4787	33.1	36.58	40.15
23	GMU 4807	34.4	31.46	50.00
24	GMU 4813	31.1	36.58	72.13
25	GMU 4852	32.7	29.39	50.00
26	GMU 5125	31.6	26.40	60.00
27	GMU 5131	31.5	19.61	27.31
28	GMU 5232	34.9	23.55	55.17
29	GMU 5239	33.8	28.68	46.53
30	GMU 5336	31.4	37.81	75.00
31	GMU 5391	32.2	21.43	32.87
32	GMU 5411	32.1	27.29	37.81
33	GMU 5414	34.7	24.14	60.00
34	GMU 5615	33.6	25.31	50.00
35	GMU 5740	32.3	29.73	55.40
36	GMU 5741	31.3	38.76	62.50
37	GMU 1152	34.2	26.65	60.00
38	GMU 5758	33.1	34.57	41.17
39	GMU 5775	33.5	23.46	45.00
40	GMU 6114	32.6	28.18	37.32
	S.E.m.(d)+	**NS**	**NS**	**NS**
	MEAN	**32.9**	**28.03**	**48.98**