

“GENETIC ANALYSIS IN SAFFLOWER (*Carthamus tinctorius* L.)”

M.Sc.(Ag.) THESIS

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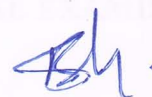
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CERTIFICATE - I

This is to certify that the thesis entitled "**GENETIC ANALYSIS IN SAFFLOWER (*Carthamus tinctorius* L.)**" submitted in partial fulfilment of the requirements for the degree of "**Master of Science in Agriculture**" of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **Sourabh Paikara** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degree or diploma (certificate awarded etc.) or has been published / published part has been fully acknowledged. All the assistance and help received during the course of the investigations have been duly acknowledged by him.

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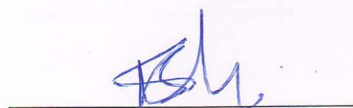


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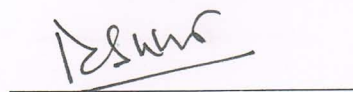
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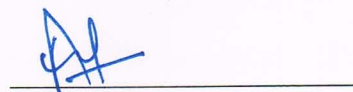
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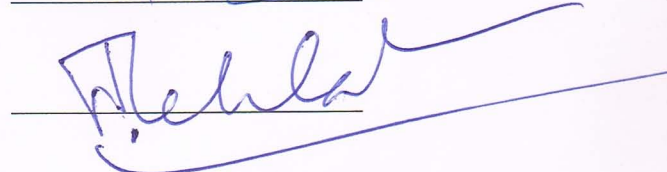
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CERTIFICATE - II

This is to certify that the thesis entitled "**GENETIC ANALYSIS IN SAFFLOWER (*Carthamus tinctorius L.*)**" submitted by **Sourabh Paikara** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur in partial fulfilment of the requirements for the degree of **M.Sc.(Ag.)** in the **Department of Genetics and Plant Breeding** has been approved by the external examiner and Student's Advisory Committee after oral examination.

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EXTERNAL EXAMINER

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LIST OF ABBREVIATIONS

Abbreviations	Full form
%	Per cent
@	at the rate
°C	Degree Celsius
CD	Critical Difference
cm	Centimeter
CV	Coefficient of Variation
DF	Days to flowering
d.f.	degree of freedom
<i>et.al.</i>	and co-workers/ and others
Fig.	Figure
FYM	Farm Yard Manures
g	Gram
GA	Genetic Advance
GCV	Genotypic Coefficient of Variation
ha	Hectare
h^2 (b)	Heritability in broad sense
Hrs	Hours
i.e.	That is
kg	kilogram
l	litre
mm	millimeter
ml	milliliter
m^2	square meter
MSS	Mean Sum of Square
No.	Number
NPK	Nitrogen, Phosphorus and Potassium
NS	Not Significant
PCV	Phenotypic Coefficient of Variation
Per se	In itself
q	Quintal
q/ha	quintal per hectare
T	Tonnes
var.	Variety
<i>via.</i>	Through
<i>viz.,</i>	Namely

Introduction

CHAPTER I

INTRODUCTION

Safflower (*Carthamus tinctorius* L.) is one of the important *Rabi* oilseed crop belongs to the family – *Asteraceae* or *Compositae*, tribe- *Tubiflorae*, sub-division- *Angiosperm* of division *Phanerogams*. Chromosome number of safflower is $2n = 2X = 24$.

Safflower is cultivated all over the world and ranks 8th among the major oil seed crops in the world. It is predominantly a self-pollinated crop with an out crossing rate exceeding 50% depending upon the genotype (Rudolphi *et al.*, 2008). The crop is mainly cultivated for its seeds which yields good quality oil (35-40%) contains (75-86%) linoleic acid content, though at one time is used to be grown for extraction of a dye from its flowers. The seeds contain 24 to 36 per cent oil. The cold pressed oil is golden yellow and is largely used for cooking purposes, or for making soap etc.

Safflower oil has good drying properties and is, therefore, used in the manufacture of paints, varnishes and linoleum. It can be mixed with white paints without any after-yellowing effects. The hot oil, if poured into cold water, becomes a plastic of thicker consistency and is then suitable for use as an adhesive for glass. The oil obtained by hot dry distillation is black and sticky and is used for greasing purposes. It is also used in the preparation of Roghan which is used in the preservation of leather and water-proof cloth.

The seeds are themselves edible and are eaten after roasting. The oil cake, particularly from decorticated seeds is used as a cattle feed. It contains 40-45% protein. The cake obtained from un-decorticated seeds is used as a manure as it contains about

5% N, 1.44% P_2O_5 and 1.23% K_2O . The green safflower crop can be used as a green fodder for cattle as it is relished by cattle.

Safflower has been grown for many centuries over a vast area from Egypt to India. It has been cultivated since ancient times in India. The cultivated forms of safflower are supposed to have originated either from *Carthamus lanatus* (saffron thistle) or from *Carthamus oxycantha* (wild safflower). India is one of the centres of origin for safflower as concluded by Vavilov (1951) based on variability and ancient culture of production. It is also referred as “*Kusumbha*” in ancient Sanskrit. Now it is commonly known as *kusum*(Hindi). According to De Candolle, probably safflower is a native of Arabia.

Wild Safflower relatives are regarded as potential genetic resources available for Safflower breeding. Genus *Carthamus* is composed of about 25 taxa (Species and Sub-Species) among which only *Carthamus tinctorius* L. is cultivated.(Asiri and Knowles,1960; Hanelt 1963). The wild relatives of Safflower viz. *Carthamus oxycantha* and *Carthamus lanatus* also occur in India.

Sabins and Pathak (1935) revised the first classification given by Howard and Khan (1915). They added 29 new types, bringing the total of Indian types to 63. In this revised classification single and distinctive characters like characters of bracts, that is , whether spinose or spineless, the shape of outer bracts, colour of inner bracts , colour of florets , growth habit of plant etc., are used.

Kupzow (1932) classified the safflower collected from different parts of the world into two groups.

- (1) The eastern types

- (2) The western types

It is highly branched, herbaceous, thistle like annual plant varying in height from 30 to 150 cm. Plant has strong and thick tap root with numerous thin laterals. The stem branch prolifically near top, thick at the base and tapering with height. The branched stems bears spirally arranged leaves. The leaves are sessile, dark green with a pronounced midrib. Leaves are toothed along their margins, with short spines scattered along the margins. The lower leaves on most varieties are spineless, but the degree of spineless, on the upper leaves is varietal characteristics, and may vary from spineless to strong spined.

Each branched terminates in a typical head type of inflorescence. The inflorescence is broad, flat or slightly curved and dense bristled owing to the presence of numerous floral bracts. The flower is generally complete and perfect. The flowers are of brilliant yellow to orange or orange- red colour, containing 20 to 100 individual florets, each of which produces seed. The fruit is a smooth, shiny white achene, very angular and nearly wedge shaped less than 1.5 centimetres in length.

It is a multipurpose crop species grown for oil, medicinal and industrial uses. It is cultivated for the vegetable oil extracted from its seeds and is known for its quality edible oil as it contains higher proportion of linoleic acid as compared to other vegetable oil .It also as high quality edible oil rich in poly saturated fatty acids extracted from seeds which is good for cardiac health. Dried petals of Safflower have therapeutic value and are being extensively used in preparation of herbal medicines.(Parmeshwar *et al.*,2009). The stems, leaves, seeds and flowers are used for different purposes. All part of the crop for the treatment of various diseases and flower of crops are used in the foods, cosmetics, paints and pharmaceutical industries.(Beyyavas *et al.*,2011.,Dajue *et al.*,1996).

The safflower seed contain 30% oil, 20% protein and 35% crude fibre. The seeds are also rich source of minerals (zinc, copper, manganese and iron), vitamins (Thiamine and beta-carotene) and tocopherols (alpha, beta and gamma)(Nagaraj,2001).

India, Mexico, USA, Ethiopia, Argentina and Australia together account for 99% and 87% of the world safflower area and production respectively. In India, Safflower is grown on 3.80 m.ha with total production of about 2.4 m.tonnes. The average productivity of Safflower in India is about 637 Kg/ ha which is much less than world average (Damodaram and Hegde, 2002). It is mainly grown in Maharashtra, Karnataka, Madhya Pradesh, Orissa and Bihar states of India.

Maharashtra and Karnataka are the two most important safflower growing states. Maharashtra accounts for about 72 per cent of area and 69 per cent of production of safflower in India (Nimbkar, 2002).

Safflower is one of the important *rabi* oil seed crop in Chhattisgarh. It is grown as a sole crop as well as mixed crop/ inter- crop with gram and wheat. Area under safflower crop is 850 ha and productivity is 294 kg / ha. production is 0.250 ton. (Anonymous, 2010)

The area under safflower has been significantly reduced in recent years in many growing countries including India. Due to low oil content of 28-30 percent and low yield of 600 kg/ha which makes safflower a poor competitor. The success of safflower as a commercial oil seed crop in traditional areas and its expansion in new areas will largely depend on the extent of improvement made in both its yield and oil content through genetic level.

The ultimate goal of any breeder is to increase the genetic potential of a crop coupled with higher yield. The estimates of different genetic parameters are important

for understanding the nature and magnitude of genetic variability. The associations of yield with its components are also important to understand their contribution.

The genetic component of variability being heritable plays an important role in the crop improvement programme. Maximum genetic improvement for quantitative traits can be achieved through a clear-cut understanding of type and magnitude of variability present in the genetic stock. Study of variability in crop is essential for selecting the desired types and knowledge of inter-relationship among various characters contributing to yield may help the breeder in simultaneous improvement of several characters in selection programme (Singh *et al.*, 1980).

Knowledge of heritability and genetic advance of character indicates the scope of improvement through selection. Seed yield is a polygenically controlled complex character and is determined by a number of character components, which may be quantitatively inherited. Knowledge of inter-relationship among these characters are necessary for evolving the high yielding genotypes by giving appropriate emphasis for each of the characters. Such information can be sorted out by correlation studies in conjunction with path coefficient analysis, which gives an insight into the cause and effect relationships between different parts of variables.

Selection of parents, based on extent of genetic divergence, has been successfully utilized in different crop species by earlier worker viz., Moll *et al.* (1962), Bhatt (1970), Anand and Rawat (1984), Pradhan and Roy (1990) and Mishra *et al.* (1994) etc. To get the actual picture of the genetic divergence, multivariate analysis with the aid of Mahalanobis's D^2 statistics has been successfully used by several workers.

However, the earlier studies indicate that these two traits are inversely related besides several other yield components (Ramachandram, 1985; Parmeshwarappa *et al.*,

1984). In addition, safflower crop is not amenable for simple breeding procedures due to complexity in inheritance of various yield and yield components, which appeared to be governed by both additive as well as nonadditive genes (Ramachandram and Goud, 1981; Parmeshwarappa *et al.*, 1990; Narkhede *et al.*, 1992; Patil 1998).

The creation of new genotypes is based on the identification, collection, assembly multiplication, evaluation and conservation of genetic resources which are available for breeding of desirable genotypes of safflower. There is need to identify the genetic accessions for better utilization in crop breeding programmes. Keeping in this view 150 Safflower germplasm were evaluated with the objective to identify the genotypes for further exploitation in Safflower improvement programme aimed to enhanced seed yield, oil content and hull content.

Objectives :-

1. To assess the genetic variability for various quantitative character in safflower.
2. To estimate correlation between yield and its component along with direct and indirect effect.
3. To study the genetic divergence D^2 .
4. Characterization of safflower germplasm for morphological and quantitative traits.

Review of Literature

CHAPTER-II

REVIEW OF LITERATURE

Safflower is one of the major *rabi* oil-seed crops as well as important source of industrial oil in country. It has not only good oil properties but it also source for dye, paints and other medicinal purposes.

Since, yield is a complex quantitative character and is influenced by a number of other characters, it was therefore, necessary to estimate the genetic parameter to understand the possibility of improvement in these traits.

The literature cited on various aspects of the present investigation has been reviewed under the following heads:

- 2.1 Genetic variability
- 2.2 Heritability and genetic advance
- 2.3 Correlation analysis
- 2.4 Path analysis
- 2.5 Divergence analysis

2.1 Genetic Variability

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. Genetic variability in a population is important for biodiversity because without variability, it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction.

Variability is an important factor in evolution as it affects an individual's response to environmental stress and thus can lead to differential survival of organisms within a population due to natural selection of the most fit variants.

The knowledge on the nature and extent of genetic variability in any crop species play an important role in framing a successful breeding programme. The genetic variability is the raw material of the plant breeding industry on which selection work to evolve superior genotypes, therefore, its thorough understanding is very important for efficient utilization in crop improvement.

Reviews in respect of genetic variability in safflower have been presented below:

Ashri *et al.* (1974) observed significant difference among 903 world collections of safflower for yield components viz., number of capitula per plant, number of seeds per capitulum and 100 seed weight but non significant difference for mean yield per plant. Khidir (1974) Observed appreciable variation for 14 quantitative characters was observed in a study involving 18 varieties. He reported high variation was observed for yield and head number per plant. Broad sense heritability estimate ranged from 65 to 98 per cent for number of heads and oil content, respectively also observed by him.

Ramesh *et al.* (1980) in a study involving ten varieties of safflower, observed higher phenotypic coefficient of variation and genotypic coefficient of variation in case of number of capitula per plant, 100 seed weight and seed yield per plant. Heritability estimates were higher for number of seeds per capitulum, days to 50 per cent flowering and 100 seed weight. However, seed yield per plant showed moderate heritability with high genetic advance.

From a study of 40 genotypes, Patil *et al.* (1984) observed wide variation for seed yield related characters viz., number of primary and secondary branches per plant, number of capitula per plant, capitulum diameter, number of seeds per capitulum, 100 seed weight and oil percentage.

Patil *et al.* (1992) noticed highest PCV and GCV for plant height and lowest for the number of branches per plant, in 34 cultivars. A high degree of heritability was observed for days to maturity, days to 50 per cent flowering, plant height and seed yield. They also observed high degree of genetic advance for seed yield per plant, secondary branches per plant and capitula per plant.

Ghongade *et al.*, (1993) noticed the highest magnitude of phenotypic and genotypic coefficient of variations for number of primary branches per plant whereas lowest for days to maturity. The broad sense heritability ranged between 32.80 to 90.36 per cent for oil content and secondary branches per plant, respectively. They observed highest genetic advance for number of primary branches per plant (71.68%) followed by secondary branches per plant (67.93%). Moderate genetic advance for seed yield per plant (47.46%) and capitula number per plant (42.48%) was also observed by him.

Aslam and Hazara (1993) and Mehthre *et al.* (1995) have observed wide range of variation for days to maturity, plant height, duration of the rosette stage, primary branches, capitula per plant, growth habit and spinelessness which are potential traits for safflower breeding programme.

High GCV, PCV and heritability estimates were observed for seed yield, number of capitula per plant, number of seeds per capitulum and 100 seed weight in a study involving 100 germplasm lines (Pandya *et al.*, 1996).

Patil and Deshmukh (1998) and Patil (1998) in a study involving germplasm collection of 150 genotypes and five released varieties as checks, reported higher variability and genetic advance for seed yield per plant, days to maturity, number of seeds per capitulum and capitula per plant.

Chavan *et al* (1999) reported the highest phenotypic coefficients of variation for seeds per capsule and number of secondary branches and all characters showed more than 75% heritability.

Mane *et al.* (1999) in a study involving germplasm collection of 30 genotypes reported the highest heritability for seed yield per capitulum and the highest phenotypic coefficient of variation for seeds per capitulum.

Sarang *et al.*, (2004) investigated that in F₂ progenies of 25 safflower hybrids for 11 different characters. A wide range of variation was observed for plant height, number of primary branches, number of secondary branches, and number of effective capitula per plant. The high genotypic and phenotypic variances were observed for plant height followed by height of first primary branch and yield per plant. Yield per plant and number of secondary branches showed high GCV and PCV.

Choulwar *et al.*, (2005) studied 11 characters and estimated that (PCV) was higher in comparison with the genotypic coefficient of variation (GCV) for all the characters. An appreciable range of variation was observed for majority of the characters viz. days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of capitula per plant, number of seeds per capitulum, test weight, seed setting, hull content and oil content in safflower.

Lakshyadeep *et al.*, (2005) recorded that 12 traits were assessed in 150 germplasm lines of safflower. The germplasm were significant for all traits except for number of leaves on main axis after branching, 100-seed weight and oil content, indicating the occurrence of considerable variability. The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all traits, thus the germplasm lines showed high GCV, PCV, heritability and genetic advance for number of capitula per plant and seed yield per plant.

Patil *et al.*, (2006) indicated that significant differences in all the populations for plant height, number of secondary branches per plant, number of effective capitula per plant, number of seeds per capitula and seed yield per plant, except 200301(Bhima x GMU-2055) and 200302 (PBNS-12 x GMU-2055) for plant height and 200313(GMU-6957 x A-1)for number of effective capitula per plant. The estimates of phenotypic coefficient of variation were higher than genotypic coefficient of variation. High magnitude of heritability estimates were exhibited by seed yield per plant and number of seeds per capitula in all populations.

Mahajan *et al.*, (2009) observed that maximum range was existing in plant height followed by number of seeds per capitulum, seed yield per plant and number of capitula per plant, primary branches per plant, oil content and 100 seed weight. PCV was greater than GCV for all the characters indicated apparent variation. GCV and PCV were low for days to maturity and seed yield per plant. Number of branches, number of seed per capitulum and number of capitula per plant exhibited high GCV and PCV.

Biradar *et al.*, (2012) noticed that high GCV and PCV for number of capitulum per plant, number of seeds per capitulum, 100 seed weight and oil content. They also

reported that all the yield components showed high heritability and high genetic advance.

Deshmukh *et al.*, (2012) observed significant and large genetic variation among progenies are prerequisite for recurrent selection programmes. Genotypic and Phenotypic variation (CV) ranged from 1.55 to 55.93 and 3.88 to 59.12 for days to maturity and seed yield per plant. Highest genotypic and phenotypic coefficient of variation were recorded to seed yield per plant, number of capitula per plant, number of primary branches per plant, number of seed per capitulum and plant height.

Dikshit *et al.* (2012) observed wide range of variation to all 10 quantitative characters from 0.212 to 1.164. Yield per plant expressed high CV followed by number of capitula per plant, 100 seed weight and plant height. Days to 50% flowering exhibited least CV.

Mukta (2012) studied that among the 12 traits evaluated, wide variability was present for number of capitula, number and location of branches, number of seeds per capitulum and seed yield per plant with a coefficient of variation (CV) above 25 per cent.

Pandey and Singh (2012) observed wider differences between genotypic and phenotypic variance expressed in days to 50% flowering, plant height and number of productive capitulum per plant.

2.2 Heritability and genetic advance:

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. However it is not necessary that a character showing high heritability also exhibit high genetic advance (Johnson *et al.*, 1955).

Channeshappa (1980) reported that high heritability and genetic advance in F_1 , F_2 and four back crosses of safflower for hull percentage but high broad sense heritability and low genetic advance for oil content, 100 seed weight and plant height.

Rao (1982) estimated High narrow sense heritability for oil content and seed size, moderately high for capitulum diameter and low for seed yield per plant, number and weight of capitulum were observed in 8 x 8 and 11 x 11 diallel experiments.

Shitole *et al.*, (1986) revealed high estimates of heritability were found in F_3 for seed yield, oil percent and other six yield components. In F_4 generations, the number of days to 50 per cent flowering and maturity were found to be more heritable but recorded relatively low values of expected genetic advance.

Meghannavar *et al.*, (1998) reported high heritability for 100 seed weight and hull content, moderate to high heritability for seed yield and oil content and low heritability for number of capitulum per plant and number of branches in F_3 populations. They also reported high genetic advance for number of capitulum per plant and capitulum weight.

Senapati *et al.*, (1999) reported high heritability and genetic advance for number of capitulum per plant, yield per plant and 100 seed weight and thus indicated additive gene effects.

Sarang *et al.*, (2004) studied that medium to high heritability showed for all the characters. Test weight (99.05%), yield per plant (95.03%) and height of first primary branch (87.78%) showed high heritability estimates. High heritability estimates coupled with high expected genetic advance were observed for the characters yield per plant followed by number of secondary branches and number of capitulum per plant.

Choulwar *et al.*, (2005) estimated that 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 capitulum per plant and plant height, which indicated presence of additive gene effect.

Lakshyadeep *et al.*, (2005) revealed that the germplasm lines showed high heritability and genetic advance for number of capitulum per plant and seed yield per plant.

Mahajan *et al.*, (2009) reported that broad sense heritability was low for oil content and it was high for seed yield per plant and expected genetic advance as mean population.

Biradar *et al.*, (2012) reported that high heritability and high genetic advance estimates for capitulum per plant, seeds per capitulum, 100-seed weight, oil content and hull content in F_3 segregating population.

Lande and Deshmukh (2012) reported that the broad sense heritability estimates were high for days to 50 % flowering, followed by seed yield per plant, number of seed per capitulum, number of capitulum per plant, and number of primary branches per plant. The expected genetic advance was high for seed yield per plant.

Pandey and Singh (2012) reported that the characters with high and moderate heritability (h^2)_{bs} ranging from 94.51% to 40.41%. highest heritability in broad sense along with high genetic advance was observed for test weight followed by primary branches per plant, seed yield, number of filled seed per capitulum, high heritability in days to maturity and plant height whereas moderate for days to 50% flowering and number of productive capitulum per plant.

Rudranaik *et al.*, (2012) estimates high heritability for all the characters viz., days to 50% flowering, number of branches per plant, number of capsule per plant and oil content. High heritability coupled with genetic advance viz. number of branches per plant, number of capsule per plant, number of seeds per capsule and seed yield.

Swarup *et al.*, (2012) revealed that high heritability was observed in seed yield per plant, number of branches per plant, number of seeds per capitulum, lower branch height and number of capitulum per plant. Heritability coupled with genetic advance observed for harvest index and seed yield.

2.3 Correlation analysis:

Coefficient of correlation is a measure of the association between two or more than two variables (Galton, 1888) or a statistical measure which is used to find out the degree and direction of relationship between two or more variables. This concept of correlation was later on elaborate and discussed by Fisher (1918) and Wright (1921) for plant breeding programmes. A brief review of correlation of seed yield and its component in safflower is summarized below:

Khidir (1974) working with eighteen varieties of safflower noticed significant positive association between seed yield with number of seeds per capitulum, capitulum width, bract width, while 100 seed weight was significantly and negatively correlated with seed number per capitulum and plant height.

Ranga Rao *et al.* (1977) analyzed inter-relationship of various component characters with yield and oil content using 215 entries of safflower from India and USA. The correlation of capsule number per plant and capsule weight with yield per plant was positive and pronounced. Seed size had little effect on yield while seed number exerted

a positive influence, whereas, a highly significant and negative association was found between oil and hull content.

Ramachandram and Goud (1982) and Ramachandram (1983) observed in F_1 and F_2 populations, significant positive correlation of seed yield with yield per capitulum, stem girth, plant height, branch length and diameter of capitulum. The number of capitula had significant . negative correlation values with diameter of capitulum, yield per capitulum and seed number. The seed weight showed significant negative correlation with oil content.

Chavan *et al.* (1999) indicated that plant height was positively and significantly correlated with number of seeds per capsule and number of primary and secondary branches showed significant and positive correlation with number of capsules per plant.

Senapati *et al* (1999) observed in a study involving 17 genotypes including two checks, high positive correlations with capitula per plant, biological yield and 100 seed weight.

Kubsad *et al.* (2000) noticed that the highest association was observed between seed yield and 100 seed weight.

Bagheri *et al.* (2001) revealed that plant yield was highly and positively correlated with capsule diameter, days to first flowering, number of seeds per capsule, number of capsules per plant and seed weight of capsule. Correlation between 1000 seed weight and seed oil content was negative.

Lakshyadeep *et al.*, (2005) revealed 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.

Anjani (2005) observed that oil content, capitula per plant and 100-seed weight showed positive association with seed yield. The negative association between seed yield and days to maturity in wild safflower *Carthamus oxyacantha*.

Diwakar *et al.*, (2006) revealed that number of effective capitula per plant, number of filled seeds in main capitulum, diameter of main capitulum and 100 seed weight were significantly and positively associated with seed yield, while plant height, days to 50% flowering and oil content exhibited negative association with seed yield.

Correlation studies by Khoshnoud and Carapetian (2006) indicated that only the average number of seeds per head has a significant positive correlation with grain yield. there was a negative significant correlation between grain yield and days to flowering.

Mahasi *et al.*, (2006) noticed that yield per plot was positively associated with number of primary branches, secondary branches, capitula per plant, effective capitula per plant and seeds per capitulum in both years and only significant with seed yield per plant and 100 seed weight in second year. Seed weight recorded the highest positive correlation with yield per plant, while the number of capitula per plant and effective capitula per plant had high positive effect on yield per plot in 2003.

Correlation studies by Sreenivasa *et al.*, (2011) revealed positive significant relationship between seed yield and number of filled seeds in main capitulum , diameter of main capitulum , oil content and days to 50 % flowering . Diameter of main capitulum exhibited highly significant and positive correlation with number of filled seeds in main capitulum and oil content.

Hassanpour rad *et al.*, (2012) observed seed yield had showed positive correlation with seed per head (0.53). There was a positive correlation between head and

branch number (0.46). and also there was negative correlation between 1000 seed weight and head diameter (-0.65).

Jagtap *et al.*, (2012) observed highest positive and significant association with number of capitulum per plant, which is followed by the association with number of seeds per capitulum , volume weight , plant height and number of primary branch per plant . oil content showed negative correlation with all the yield contributing characters.

Sirisha *et al.*, (2012) studies association analysis in 64 genotypes and revealed that biological yield per plant had significant positive association with seed yield per plant.

2.4 Path Analysis

Yield is a complex character which is influenced by many yield contributing characters both through direct and indirect effects. Generally, direct selection for yield is not sufficiently effective due to its low heritability and it is desirable to select indirectly through component traits for yield improvement. Here path analysis helps to resolve the correlation indicating direct and indirect effects of various component characters on seed yield. The biometrical technique of path analysis was first developed by Sewall Wright (1921) and subsequently extended for crop experiments by Dewey and Lu (1959).

Khidir (1974) and Mehrotra and Jain (1976) in their studies involving 18 and 24 varieties, respectively noticed that plant height was the only character to exert highest direct positive effect on seed yield although it had a negative influence on seed yield via capitulum width. Mehrotra and Jain (1976) also observed the highest direct effects of number of capitula per plant on yield.

Mathur *et al.* (1976) observed the greater direct effect of capitulum width on seed yield by seed weight, plant height, height of branch, branch length and days to flowering.

Ranga Rao *et al.* (1977) opined that seed number and seed weight are the most important characters influencing the seed yield per plant directly. The hull per cent influenced seed yield both directly and through indirect paths. The indirect effect was through capitulum weight and oil per cent. The combined negative indirect effects of oil content through hull per cent and capitula weight outweighed its positive direct contribution, thereby resulting in a negative phenotypic association of oil content with seed yield.

Thombre and Joshi (1981) found that number of seeds per capitulum had a direct positive effect on seed yield followed by days to first flower and 1000 seed weight. The negative direct effects of branches per plant, 1000 seed weight and capitula per plant was masked by positive indirect effects of seeds per capitulum.

Channeshwarappa *et al.* (1984) concluded that direct selection for oil content is not effective but it could be achieved indirectly through selection for reduced hull content. The yield per capitulum, plant height and capitula per plant exhibits greater direct contribution towards yield (Malleshappa *et al.*, 1989).

Patil *et al.* (1990) observed that the capitula weight per plant was responsible for greatest direct contribution towards yield per plant. Jadhav *et al.* (1992), Reddy *et al.* (1992) and Ghongade *et al.* (1993) observed that the number of seeds per plant, number of capitula per plant, 100 seed weight and number of seeds per capitulum had the highest positive direct influence on seed yield.

The number of capitula per plant, 100 seed weight and number of seeds per capitulum were the direct contributors to the seed yield (Pandya *et al.*, 1996, Patil *et al.*, 1997 and Meghannavar *et al.*, 1998). They also observed the indirect positive effect of plant height and number of branches throughout number of capitula per plant on seed yield.

Patil and Deshmukh (1998) and Patil (1998) revealed highest direct effect of 100 seed weight followed by number of capitula per plant, number of primary and secondary branches per plant and seeds per capitulum towards seed yield.

Chavan *et al.* (1999) revealed that plant height, number of secondary branches, number of capsules and number of seeds/capsule showed highest positive direct effects on seed yield.

Kubsad (2000) indicated that the dry matter per plant had maximum contribution towards seed yield and was closely followed by seeds per main capitulum.

Bagheri *et al.* (2001) indicated that number of capsules per plant had the highest direct effect on plant yield. It exerted a large indirect effect by increasing seed weight of a capsule.

Diwakar *et al.* (2006) revealed that number of effective capitula per plant had maximum positive direct effect followed by number of filled seeds in main capitulum in seed yield. Days to 50 % flowering and plant height exhibited negative direct effect in seed yield.

Mahasi *et al.* (2006) revealed that component with the highest correlation to yield also had the direct effect to yield i.e. primary branches, capitula per plant, effective capitula, seed per capitula and 100 seed weight as this has a high significant positive association with seed yield.

Topal *et al.* (2010) reported in respect of parametric and nonparametric coefficient measure in both years. shows that the larger path coefficients on seed yield found oil content and plant height respectively. Number of heads/plant has the large negative direct effect on seed yield. Number of seed/head has positive little direct effect on seed yield and lesser negative indirect effect *via* 1000- seed weight, but has positive indirect effect *via* oil content on seed yield.

Sreenivasa *et al.* (2011) reported that number of filled seed in main capitulum showed the highest direct effect on seed yield, which was followed by 100 seed weight and oil content. Number of filled seed in main capitulum also showed the highest direct effect on seed yield.

Jagtap *et al.* (2012) indicated that path analysis for seed yield and various component characters *viz.* volume weight, number of capitula per plant, days to 50 % flowering, number of secondary branches per plant showed the highest direct effect.

Sirisha *et al.* (2012) revealed that biological yield per plant had highest positive direct effect on seed yield per plant followed by 100 seed weight. Days to 50 % flowering, plant height and oil content exhibited negative direct effect on seed yield.

2.5 Divergence analysis:

It has been well established that greater the genetic variability in the plant population, greater will be the chance of obtaining the desirable gene recombinants with high heterotic effect. In this context, Mahalanobis's D^2 statistics is an effective tool in quantifying the degree of divergence at genetic level and it also provides a quantitative measure of association between geographic and genetic diversity based on genotype distance (Mahalanobis, 1936). A brief review of divergence analysis in safflower based on D^2 statistic is summarized below.

Pawar *et al.*, (2006) revealed that genotypes of D^2 statistics differ significantly for all characters. The maximum inter-cluster distance between cluster XV and XIII, while the closest proximity was noticed between cluster IX and VI. The genetic diversity indicated that oil content, plant height, days to 50% flowering and number of branches per plant contributed maximum to the total genetic divergence.

Shivani *et al.*, (2010) studied D^2 in 4 x 6 line x tester crosses in safflower and seven parameters, i.e., D^2_7 based on 7 characters and D^2_4 based on yield and its 3 direct components there is significant difference among parental varietal and among the F_1 hybrids for all seven characters thus the parental varieties ranged from 12.56 to 47.31 and D^2_4 ranged from 10.84 to 38.67. With D^2_7 that the 10 varieties grouped into 3 clusters and D^2_4 they grouped into 4 clusters. The D^2 values and number of clusters to which the varieties grouped indicated substantial genetic diversity.

Sreenivasa *et al.*, (2010) Studied diversity analysis and revealed that maximum inter-cluster was observed between cluster VIII and cluster II (2761.41), while the closest between cluster I and cluster II (273.13). Among the 8 characters studied, days to 50% flowering, number of effective capitulum per plant, plant height and number of filled seed in main capitulum together contributed for more than 90% of the total divergence.

Murkute and Deshmukh (2011) Studied diversity analysis and genotypes were grouped into 9 clusters. They also reported maximum inter-cluster distance between cluster II and cluster IX (77.55) and the minimum inter-cluster distance was observed between cluster V and cluster VI (15.79). Among the 11 characters studied height of insertion of first primary branch contributed maximum towards genetic divergence (33.49%) followed by plant height (19.46%) and seeds per capitulum (16.38%).

Shailaja *et al.*, (2011) Studied D^2 statistics and grouped genotypes into 8 clusters. They also reported maximum inter-cluster distance between cluster II and cluster VIII (712.48), while least distance between cluster V and cluster VI (101.89).

Harish babu *et al.*, (2012) Studied D^2 statistics of 154 genotypes and genotypes were grouped into 9 clusters. The cluster I was the largest containing 42 genotypes followed by cluster II 28 genotypes and cluster IV 26 genotypes. The inter-cluster distance was higher than inter-cluster indicating wider genetic diversity among the genotypes of safflower. The inter-cluster was maximum between cluster VI and cluster IX followed by cluster V and cluster IX. The number of capitulum per plant contributed maximum towards genetic divergence followed by 100 seed weight and number of seeds per capitulum.

Mukta (2012) Studies diversity analysis and revealed that the highest inter-cluster distance between cluster III and VIII (214.83), while it was least for cluster I and II(40.18).

Sirisha *et al.*, (2012) studies that genotypes exhibited wide divergence and they were grouped into 9 cluster. Maximum genetic divergence was found between cluster VI and cluster IX followed by cluster II and cluster IX. Seed yield per plant contributed maximum towards genetic divergence while oil content and diameter of main capitulum contributed the least.

Tirkey *et al.*, (2012) Studies diversity analysis and revealed that GMU 3494, GMU 3482, GMU 3514 and GMU 3443 are the highest yielder.

Materials and Methods

CHAPTER-III

MATERIALS AND METHODS

3.1 Experimental Location

The present study was conducted at the Research and Instructional farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishawavidalaya, Raipur (C.G.)

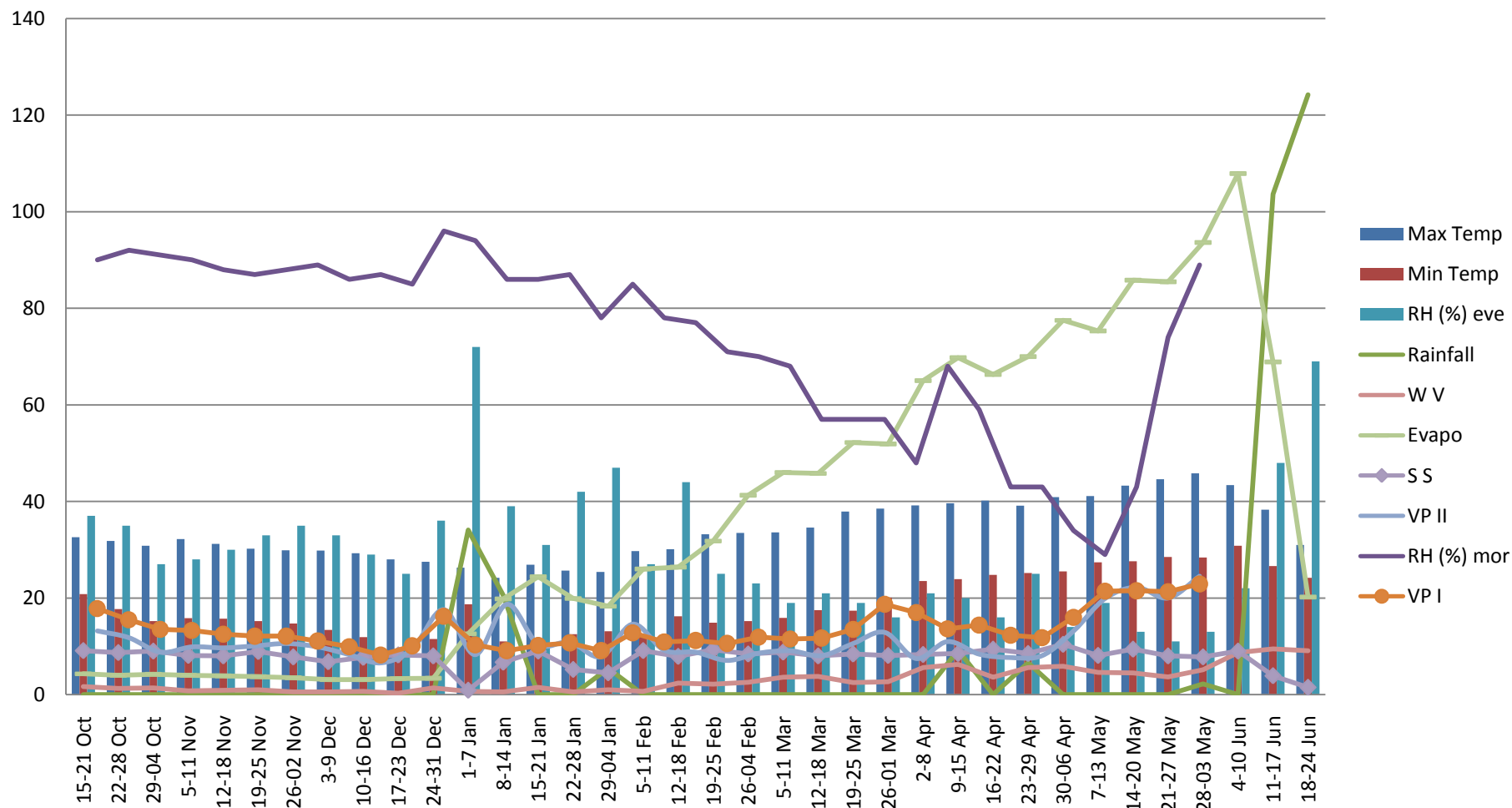
3.2 Experimental Material

The present investigation “Genetic analysis in Safflower” was carried out during *Rabi* season of 2011-12 at Raipur. Raipur is situated in the southern part of Chhattisgarh of 21° 16' N latitude and 81° 31' E longitude with an altitude of 289.56 meter above the mean sea level. The climatic condition of Raipur is sub-tropical. The maximum and minimum temperature, monthly rainfall, relative humidity, wind velocity and sunshine hours for entire crop growing period have been given in figure-

Agro-climatic conditions especially temperature and cool climate plays an important role for seed yield in safflower. In the present investigation meteorological data figure 3.1 showed the maximum temperature 45.8°C and minimum of 9.1°C over the entire crop growth period and received 34.1 mm of rainfall during January.

The Experimental Material used in the present study consisted of 150 Safflower provided by Directorate of Oilseeds Research, Hyderabad including 5 Checks varieties of Safflower viz. A-1, Manjira, PBNS-12, PBNS-40 and JSF-1. The details are as follows:

Fig. 3.1 Meteorological weeks during crop period in rabi 2011-12



S. No.	Experimental Materials	Sources
1	GMU (Appendix)	Directorate of Oilseeds Research, Hyderabad (Andhra Pradesh)
2	A-1 (Check)	University of Agricultural sciences, Dharwad (Karnatka)
3	PBNS-12 (Check)	Marthawada Agriculture University, Parbhani (Maharashtra)
4	PBNS-40 (Check)	Marthawada Agriculture University, Parbhani (Maharashtra)
5	Manjira (Check)	Directorate of Oilseeds Research, Hyderabad (Andhra Pradesh)
6	JSF-1 (Check)	AICRP Safflower Centre, Indore, JNKV, Jabalpur(M.P)

3.3 Experimental design

The experiment was laid out in Randomize Complete Block Design (RCBD) with two replications. Each genotype was grown in 3.0 m length and 0.9 m width size of plot. The row to row distance was 45 cm. All the recommended packages and practices were followed to facilitate good crop growth and development.

3.4 Observations recorded

Within each treatment, observations are recorded on five randomly selected plants in both the replication for following traits. The mean value was considered as statistical analysis.

(A) Quantitative Characters-

3.4.1 Days to 50% of flowering:

The time of 50% flowering is reached when 50% of the plants have at least one flower open in the main capitulum.

3.4.2 Plant height (cm):

The height of the plant was measured at maturity from the ground level to the apex of the main capitulum in (cm).

3.4.3 Number of primary branches:

The number of primary branches was counted emerging from the plant base at the time of maturity.

3.4.4 Length of leaf blade (cm):

The measurement of leaf from tip to base position in (cm).

3.4.5 Width of leaf blade (cm):

The measurement of leaf upper, middle and lower lamella in (cm).

3.4.6 Plant population:

Total number of plants present in per m² area.

3.4.7 Number of capitula per plant:

Total number of capitulum per plant was counted at the time of harvest.

3.4.8 Diameter of main capitulum:

It was recorded in centimeters at the maximum width of the capitula at maturity.

3.4.9 Number of seeds per capitulum:

Total number of seeds obtained from the main capitulum were counted and recorded.

3.4.10 100-Seed weight (g):

Weight of 100 seeds selected at random from each plants were counted and weighted in gram (g) on electronic balance.

3.4.11 Hull content (%):

Soak 5 g seeds in water for 24 hours. Separate the hull, dry, weigh and express as percent.

$$\text{Hull content (\%)} = \frac{\text{Weight of oven/sun dried hull}}{\text{Weight of seeds}} \times 100$$

3.4.12 Oil content (%):

Oil content of dry seeds was determined using Nuclear Magnetic Resonance (NMR) machine in terms of per cent.

3.4.13 Seed yield (kg/ha):

The total seed yield harvested from each plot was recorded in kilograms.

(B) Morphological Characters-

3.4.1 Petal colour:

The colour of petal may be white, pale-yellow and yellow, orange was recorded after flowering.

3.4.2 Leaf shape:

The shape of leaf may be fusiform, ovate, elliptic and obovate was recorded after flowering.

3.4.3 Number of spines in a leaf:

The spines in a leaf may be absent, very few, few, medium, many and very many was recorded before maturity.

3.4.4 Leaf dentation:

The leaf may be absent, weak, medium, strong and very strong was recorded before maturity.

3.4.5 Seed colour:

The colour of seed may be white, white yellowish, brown yellowish and brown was recorded after harvesting.

3.5 Statistical Analysis:

The data was finally subjected to various analyses as per the objectives.

3.5.1 Analysis of variance (ANOVA):

The mean values of above mentioned characters in replication were taken for analysis of variance. The analysis of variance was carried out as per Singh and Chaudhary (1985).

Source of Variation	Degree of freedom	Mean Sum of Square
Replication	r-1	M_r
Treatment	t-1	M_t
Error	(r-1)(t-1)	M_e

Where,

r = Number of replications

t = Number of treatments

M_r = Replication mean sum of square

M_t = Treatment mean sum of square

M_e = Error mean sum of square

3.5.2 Range and Mean

Range= maximum- minimum.

Mean = This mean was calculated by summing up all the observations and dividing the sum by the number of observations.

$$\bar{X} = \frac{\sum x}{N}$$

Where,

$\bar{X}$ = Mean of the respondents

$\sum x$ = Sum of total number of respondents

N = Number of observations

3.5.3 Genotype and phenotype coefficient of variation

The Genotype and Phenotype coefficient of variation was computed by Burton and Devane (1953).

$$GCV (\%) = \frac{\sqrt{\text{Genotypic variance}}}{\bar{X}} \times 100$$

$$PCV (\%) = \frac{\sqrt{\text{Phenotypic variance}}}{\bar{X}} \times 100$$

Where,

GCV = Genotypic co-efficient of variation.

PCV= Phenotypic co-efficient of variation.

$\bar{X}$ = Mean of the character.

GCV and PCV values were categorized as low, moderate and high values as suggested by Shivasubramanian and Menon (1973) which is as follows.

0-10%	: Low
10-20%	: Moderate
20% and above	: High

3.5.4 Heritability (h^2)

Heritability in broad sense was computed to know the extent of variation due to genotype in the phenotype expressed in percentage by using the following formulae suggested by Hanson *et al.* (1956).

$$\text{Broad sense heritability } (h^2)_{bs} = \frac{V_g}{V_p} \times 100$$

Where,

V_g = Genotypic variance

V_p = Phenotypic variance

The heritability percentage was categorized as suggested by Robinson *et al.* (1949) and mentioned below,

0-50%	: Low
50-70%	: Medium/ Moderate
70% and above	: High

3.5.5 Genetic Advance (GA)

The extent of genetic advance expected from selecting five per cent of the superior progeny as calculated by using the following formula given by Robinson *et al.* (1949).

$$\text{Genetic Advance (GA)} = ih^2 \sigma_p \text{ or } GA = \frac{\sigma_g^2}{\sigma_p} \times k$$

Where,

i = Intensity of selection

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation

σ_g^2 = Genotypic variance

k = Selection differential, the value of which is 0.80 at 30% selection intensity .

$$GA \text{ (as \% of mean)} = \frac{GA}{\bar{X}} \times 100$$

The value of 'i' was taken as 2.06 assuming five per cent selection intensity.

Genetic advance as per cent mean was categorized as low, moderate and high as given by Johnson *et al.* (1955). It is as follows,

0-10%	: Low
10-20%	: Moderate
20% and above	: High

3.5.6 Path Co-efficient Analysis

Path coefficient analysis is a standardized partial regression coefficient and as such a measure of direct and indirect effects on seed yields of any one variable through another. Direct and indirect effects on seed yield by other variable was computed using appropriate correlation coefficient analysis as suggested by Wright (1921) and Dewey and Lu (1959). The following set of simultaneous equations were formed and solved for estimating direct and indirect effects as described by Goulden (1959).

$$r_1y = a + r_{12}b + r_{13}c + \dots + r_{1i}i$$

$$r_2y = a + r_{21}b + r_{23}c + \dots + r_{2i}i$$

$$r_3y = a + r_{31}b + r_{32}c + \dots + r_{3i}i$$

$$\dots$$

$$\dots$$

$$r_1y = r_{11}a + r_{12}b + r_{13}c + \dots + i$$

Where,

r_{1y} to r_{iy} = Coefficient of correlations between causal factors 1 to I and dependent character Y

r_{12} to r_i = Coefficient of correlation among causal factors a,b,c ... i = Direct effects of characters a to i on the dependent character Y.

$$\text{Residual effect (R)} = 1 - \sqrt{a^2 + b^2 + c^2 + \dots + i^2 + 2abr_{12} + 2acr_{13} + \dots}$$

The results of path coefficient analysis were interpreted as per following scale suggested by Lenka and Mishra (1973).

Value of direct / indirect effects	Rate / scale
0.00-0.09	Negligible
0.10-0.19	Low
0.20-0.29	Moderate
0.30-0.99	High
>1.00	Very high

3.5.7 Genetic divergence analysis

The genetic divergence among the genotypes was carried out using Mahalanobis's D^2 statistic (Rao, 1952). The difference in the means of two populations, Mahalanobis's D^2 statistics is defined as follows:

$$_pD^2 = b_1d_1 + b_2d_2 + \dots + b_pd_p$$

In term of variances and covariances, the D^2 value is obtained as follows:

$$_pD^2 = W^{ij} (x^1_i - x^2_i) (x^1_j - x^2_j)$$

3.5.8 Character association (Correlation Co-efficient)

Correlation coefficient (r) were calculated for all possible combination of yield and its component parameters by using the standard procedure given by Searle *et al.*, (1961).

$$r_{(x,y)} = \frac{\text{Cov. (x,y)}}{\sqrt{\text{Var(x)} \cdot \text{Var(y)}}}$$

where, $r_{(x,y)}$ = Correlation coefficient between character x and y
 var(x) = Variance of x character
 Var(y) = Variance of y character

3.5.9 Test of Significance

Phenotypic and genotypic coefficients were tested for their significance 't' test as follows

$$t_c = r \sqrt{\frac{n-2}{1-r^2}} \quad \text{Where, } n = \text{Number of genotype}$$

If 't' calculated (t_c) is greater than 't' tabulated (t_t) at (n -2) degree of freedom at given probability level the phenotypic correlation is taken as significant. The calculated (r) is then compared with table value of 'r' at 5% and 1% level of significance (Snedecor and Cochran, 1967).

Results and Discussion

CHAPTER- IV

RESULTS AND DISCUSSION

The genetic information has been obtained through analysis of genetic variability, heritability, genetic advance, association analysis, existing among characters at genotypic and phenotypic levels, path and divergence analysis. The results obtained from present investigation are presented and discussed under the following heads:-

4.1 Analysis of variance

4.2 Genetic variability, heritability and genetic advance

4.3 Characterization of safflower germplasm

4.4 Estimation of correlation coefficient

4.5 Path coefficient analysis

4.6 Divergence analysis

4.1 Analysis of variance

The analysis of variance presented in Table 4.1 revealed that mean sum of square due to genotypes were highly significant for all the characters except for plant height, number of primary branches, length of leaf blade, plant population and number of seeds per capitulum which showed non-significant performance.

4.2 Genetic variability, heritability and genetic advance

The genetic variability was estimated for 150 diverse genotypes under following heads:

4.2.1 Mean and Range

Mean and range for different characters are presented in Table 4.2 and 4.3. The results of mean and ranges are as follows:

Table 4.1: Analysis of variance of thirteen characters in Safflower

Characters	Mean sum of square		
	Replication df 01	Genotypes df 149	Error df 149
Days to 50% flowering	0.50	0.77**	0.13
Plant height(cm)	0.01	0.017	0.43
Number of primary branches per plant	0.75	0.28	0.35
Length of leaf blade(cm)	0.39	0.30	0.29
Width of leaf blade(cm)	0.58	0.83**	0.51
Plant population	0.73	0.77	0.70
Number of capitula per plant	0.20	0.46**	0.12
Diameter of capitulum(cm)	0.24	0.98**	0.13
Number of seeds per capitulum	0.20	0.15	0.15
100-seed weight(g)	0.19	0.81**	0.13
Hull content(%)	0.12	0.61**	0.15
Oil content(%)	0.24	0.54**	0.13
Seed yield (kg/ha)	0.24	0.74**	0.29

*, ** Significant at 5% and 1 % levels, respectively.

4.2.1.1 Days to 50% flowering:

The mean for days to 50 per cent flowering was 101.35 days and it ranged from 94.00 (GMU- 3735) to 107.00 (GMU- 3653) days. Among all genotypes, GMU- 3637, GMU- 3672, GMU- 3702, GMU- 3708, GMU- 3725 exhibited early flowering (94.5 days to 98.5 days) and GMU- 3768, GMU- 3684, GMU -3792, GMU- 3793, GMU- 3800 showed late flowering (102 days to 105.5 days).

4.2.1.2 Plant height:

Plant height in centimetre showed the mean of 85.49 cm with a minimum of 70.00 cm in GMU- 3636 and maximum 112.5 cm in GMU- 3684. Following genotypes recorded short plant height viz. GMU-3670 (74 cm), GMU-3667 (78 cm), GMU- 3641 (76 cm), GMU- 3637 (74 cm) and GMU- 3628 (72.5 cm).

4.2.1.3 Number of primary branches per plant:

The number of primary branches per plant ranged from 6.0 (GMU- 3718) to 24.0 (GMU- 3633) with a mean of 13.89. Among all genotypes, the genotypes namely GMU- 3645 (24), GMU-3663 (22), GMU-3668 (24), GMU-3686 (24) and GMU-3771 (20) showed more number of primary branches.

4.2.1.4 Length of Leaf Blade:

The mean of length of leaf blade was 8.15 cm ranged from 5.5 cm (GMU- 3716) to 11 cm (GMU- 3783). Among all genotypes, the genotypes possessed large length of leaf blade namely, GMU-3740, GMU-3741, GMU-3766, GMU-3775 and GMU-3786.

4.2.1.5 Width of Leaf Blade:

The mean of width of leaf blade was 3.82 cm, ranged from minimum 2.25 cm (GMU- 3796) to 5.10 cm (GMU- 3711). Among all genotypes, the genotypes possessed

Table 4.2 : Mean performance of 13 yield and yield parameters in 150 Safflower genotypes

Characters	DF	PH	PB	LLB	WLB	PP	CP	DMC	NSC	HSW	HC (%)	OC (%)	SY
GMU- 3621	99.5	74.5	17.5	6.0	4.00	13.0	31.5	1.45	16	4.42	19.0	32.21	1077.76
GMU- 3623	99.0	96.0	20.5	10.0	5.00	12.0	31.0	1.75	18	4.50	20.0	33.29	787.00
GMU- 3624	102.0	82.0	12.0	9.0	4.00	13.0	22.0	1.60	18	4.58	19.0	30.99	735.20
GMU- 3625	100.5	83.0	16.0	9.0	3.50	12.5	17.0	2.00	18	4.58	20.0	30.87	696.30
GMU- 3626	105.0	109.0	18.5	7.0	4.00	14.0	19.5	2.20	16	5.23	19.5	30.21	1013.00
GMU- 3628	103.0	72.5	17.5	6.0	3.00	13.0	23.0	1.60	16	4.52	20.5	31.55	772.20
GMU- 3631	102.0	75.0	12.0	10.0	5.00	15.0	31.0	1.65	20	5.23	19.5	29.62	651.85
GMU- 3632	101.0	80.0	14.0	8.0	4.00	13.5	23.5	1.90	23	5.16	21.5	30.19	522.25
GMU- 3633	102.0	90.0	24.0	10.0	4.65	11.5	17.5	1.80	21	4.89	17.0	28.93	496.30
GMU- 3634	99.5	82.0	8.0	10.5	3.05	12.0	17.5	1.60	20	3.89	20.0	30.94	733.30
GMU- 3635	100.0	82.0	17.0	7.0	3.50	12.5	11.5	2.15	18	5.31	19.5	30.83	859.30
GMU- 3636	100.5	70.0	13.5	8.5	4.75	12.0	22.5	1.90	23	3.52	15.0	27.32	553.70
GMU- 3637	94.5	74.0	9.5	11.0	3.05	13.5	25.5	1.95	19	4.80	18.0	31.04	1144.45
GMU- 3638	102.0	85.0	15.0	10.0	5.00	10.5	33.0	1.65	21	5.19	12.0	27.44	529.60
GMU- 3639	101.5	85.0	14.5	6.5	3.50	15.0	26.5	1.60	15	4.08	21.0	32.57	681.45
GMU- 3640	104.0	80.5	12.0	8.0	4.00	14.5	22.0	2.05	17	4.69	16.0	27.19	898.10
GMU- 3641	101.0	76.0	11.0	9.0	4.00	13.5	19.5	1.55	16	4.94	18.0	31.63	811.10
GMU- 3642	102.5	89.0	17.5	9.5	5.00	15.5	26.0	1.65	17	5.65	19.0	30.57	722.20
GMU- 3643	104.5	89.0	14.0	8.5	5.20	18.0	30.5	1.50	17	6.45	20.0	31.43	944.40
GMU- 3644	102.5	81.5	16.5	7.5	4.90	17.0	28.5	2.10	17	4.12	19.5	32.41	738.85
GMU- 3645	102.0	84.0	24.0	7.5	2.95	14.0	28.5	1.95	18	4.41	20.0	32.45	548.15
GMU- 3646	99.5	86.5	16.0	9.0	4.05	14.0	24.0	1.80	19	5.17	20.5	32.08	890.75
GMU- 3647	100.5	86.5	12.5	11.0	5.00	15.5	18.0	1.45	23	4.17	21.0	32.68	722.20
GMU- 3648	101.0	88.0	15.0	9.0	3.50	13.0	21.5	2.20	20	4.24	22.5	33.90	977.75

GMU- 3649	103.0	80.0	18.0	7.5	3.10	13.0	16.5	2.05	22	4.11	20.5	29.58	833.30
GMU- 3651	103.5	87.0	10.0	6.5	3.10	14.5	19.5	1.50	21	4.52	20.5	32.18	1255.55
GMU- 3652	105.0	83.5	8.0	6.5	3.05	14.5	24.5	1.45	20	5.00	21.0	29.93	409.25
GMU- 3653	107.0	88.5	7.0	10.0	4.75	14.5	24.0	1.95	23	5.57	20.5	29.71	994.45
GMU- 3654	103.5	81.0	13.5	7.0	4.15	14.5	27.0	2.20	17	4.74	21.5	34.38	622.25
GMU- 3656	104.0	80.0	17.0	8.5	4.95	15.5	25.5	2.00	16	4.62	20.5	33.11	511.10
GMU- 3658	101.5	91.0	11.0	10.0	4.75	16.0	31.5	2.15	16	4.01	19.5	30.45	792.55
GMU- 3659	100.5	79.5	9.5	7.5	4.10	13.5	22.0	2.20	19	4.64	20.5	31.11	644.40
GMU- 3660	101.0	79.5	15.5	7.0	4.20	11.0	19.0	1.95	18	4.43	21.0	32.90	729.65
GMU- 3661	102.5	82.0	12.0	9.0	3.50	14.0	17.5	1.55	17	4.29	19.5	31.58	753.75
GMU- 3662	106.0	86.0	12.0	9.0	4.00	15.5	39.0	1.95	16	3.86	20.5	32.63	731.45
GMU- 3663	105.5	78.5	21.5	9.5	5.00	13.0	28.0	1.45	17	3.79	22.5	32.35	566.70
GMU- 3664	106.5	109.5	16.0	7.0	3.75	11.5	21.0	1.75	24	4.11	20.5	33.90	474.05
GMU- 3666	100.0	104.0	12.0	6.0	3.50	14.0	18.0	2.05	23	3.56	21.0	31.24	731.50
GMU- 3667	100.0	78.0	15.5	6.5	3.75	16.0	17.5	2.30	20	6.11	20.5	29.38	846.30
GMU- 3668	100.5	79.0	24.0	12.5	5.05	11.5	18.0	1.95	19	5.92	20.5	30.20	879.65
GMU- 3670	100.5	74.0	15.5	9.0	4.40	14.0	26.0	2.15	25	4.70	19.5	30.87	592.55
GMU- 3671	99.5	79.5	15.0	9.0	5.00	13.0	30.5	1.80	22	5.44	22.0	32.17	831.50
GMU- 3672	98.5	90.5	17.0	12.5	3.15	11.0	30.5	2.15	20	4.45	21.0	33.73	557.45
GMU- 3673	101.5	87.5	12.5	7.0	3.05	13.0	27.5	1.80	19	4.59	18.5	30.66	712.95
GMU- 3674	102.5	91.0	21.5	7.5	3.50	12.0	19.0	1.85	23	4.29	20.0	31.47	551.85
GMU- 3675	99.5	85.5	16.0	8.0	4.00	12.5	23.5	1.80	22	4.80	20.5	29.43	844.45
GMU- 3676	101.5	78.0	15.0	9.0	5.00	10.0	30.0	1.40	19	3.73	15.0	30.63	296.30
GMU- 3677	101.0	82.0	13.5	11.0	3.50	10.0	22.0	1.75	21	4.58	21.0	32.07	444.45
GMU- 3678	102.5	77.5	19.5	8.5	2.85	7.0	25.0	1.65	19	4.14	19.0	32.68	629.65
GMU- 3679	104.0	81.0	17.5	9.0	3.75	11.0	26.5	1.85	21	4.80	19.5	28.21	661.15
GMU- 3680	102.5	85.5	13.5	9.0	3.05	10.0	27.0	2.15	18	3.88	18.5	32.42	613.00

GMU- 3681	101.0	99.0	13.5	8.5	4.65	13.5	22.5	1.80	20	4.34	19.5	30.93	625.90
GMU- 3682	100.5	85.0	7.5	9.0	4.00	13.5	26.5	1.90	17	5.07	18.0	30.22	720.40
GMU- 3683	100.5	83.5	10.0	8.5	5.10	12.5	26.0	1.95	19	4.66	19.5	32.64	822.25
GMU- 3684	106.0	112.5	14.0	6.5	3.75	15.5	18.5	1.95	16	5.50	20.5	30.07	672.25
GMU- 3686	105.0	83.0	23.5	6.0	3.50	20.0	18.0	1.60	19	3.49	21.0	32.92	325.90
GMU- 3687	103.0	82.0	14.0	8.0	3.50	15.0	16.0	1.75	18	4.12	21.0	32.92	668.50
GMU- 3690	103.5	94.5	9.0	6.5	3.00	12.5	24.0	1.55	17	3.88	20.5	31.62	281.45
GMU- 3691	103.5	96.5	15.0	6.5	3.25	14.0	31.0	1.95	26	5.32	21.5	29.79	685.15
GMU- 3692	103.0	87.5	9.5	9.5	3.15	12.5	33.0	2.20	24	4.98	22.0	32.29	605.55
GMU- 3693	103.5	86.5	11.0	11.0	4.65	14.0	20.0	2.30	20	5.02	20.5	30.07	677.80
GMU- 3694	103.5	77.5	11.0	10.0	4.15	15.0	24.5	1.95	23	5.39	20.5	29.77	792.60
GMU- 3696	99.5	77.0	8.5	8.5	4.55	12.0	13.0	1.55	21	5.18	21.0	31.94	572.20
GMU- 3698	100.0	81.5	19.5	8.0	3.15	15.0	19.0	1.65	23	4.70	17.0	28.49	524.05
GMU- 3699	100.5	84.0	13.5	8.5	3.50	12.0	23.0	1.55	19	5.89	17.5	30.65	555.55
GMU- 3700	99.5	86.5	14.0	8.5	3.25	13.5	20.0	2.10	21	5.55	18.5	30.72	946.30
GMU- 3701	100.0	90.0	12.0	8.5	4.65	12.0	21.0	1.95	20	4.18	21.0	29.50	446.30
GMU- 3702	99.0	76.0	17.0	7.0	4.75	12.5	25.5	2.00	21	5.09	22.0	31.27	557.40
GMU- 3703	100.5	90.0	9.0	7.5	4.25	11.0	24.0	1.60	14	4.78	17.5	31.75	788.90
GMU- 3704	103.0	85.0	17.5	6.5	3.05	12.5	24.0	2.10	16	4.61	16.5	31.76	672.25
GMU- 3705	102.0	82.0	17.0	10.0	3.10	14.0	16.5	1.95	15	4.77	20.5	33.42	587.05
GMU- 3706	100.5	105.5	19.0	8.5	4.95	14.5	22.0	1.45	16	4.29	22.5	32.02	738.90
GMU- 3708	98.5	73.0	9.0	6.0	3.00	13.5	18.0	1.45	16	5.07	20.5	31.71	883.30
GMU- 3709	99.0	73.5	13.0	10.0	2.25	14.0	19.0	1.95	18	4.54	21.0	30.81	424.05
GMU- 3711	101.0	82.5	16.0	8.0	5.10	12.5	14.5	2.20	17	4.70	20.5	30.53	977.75
GMU- 3713	100.5	84.0	16.0	8.5	3.50	12.0	17.0	1.95	18	5.39	18.0	32.11	1457.40
GMU- 3715	101.0	85.0	15.5	6.5	3.25	13.5	18.0	2.10	18	5.52	20.5	30.21	762.95
GMU- 3716	99.5	97.5	21.0	5.5	3.10	10.0	21.0	2.15	19	6.32	18.5	29.09	931.45

GMU- 3718	98.5	84.0	6.0	9.5	2.75	12.0	22.5	1.80	20	3.87	15.5	28.29	414.85
GMU- 3719	100.0	89.5	12.5	9.0	5.05	13.0	19.0	2.00	21	5.79	20.5	28.46	796.30
GMU- 3720	101.0	83.0	11.5	8.5	3.50	10.5	22.0	2.05	22	5.24	18.0	28.66	729.60
GMU- 3721	100.0	86.0	20.0	7.5	3.25	12.5	25.5	1.55	23	4.67	14.0	27.39	596.30
GMU- 3722	99.0	86.5	10.0	6.0	3.50	12.0	26.5	1.50	26	3.81	21.5	29.45	613.00
GMU- 3723	98.5	87.5	8.5	9.5	2.75	14.0	22.0	1.65	24	5.71	19.5	30.47	816.65
GMU- 3725	97.5	84.5	13.5	8.0	4.55	17.5	32.0	2.10	16	5.03	18.0	29.65	690.75
GMU- 3726	99.5	79.0	10.0	8.0	3.50	16.5	27.5	2.05	18	5.64	20.5	31.14	1059.30
GMU- 3727	98.0	83.0	10.5	6.5	3.00	11.5	17.0	2.10	17	5.26	21.0	27.94	629.65
GMU- 3729	100.5	80.5	14.5	8.5	2.75	16.0	25.0	1.70	18	4.75	20.5	32.49	637.05
GMU- 3730	100.0	76.5	9.0	7.0	4.65	16.5	18.5	2.25	20	4.22	20.5	23.64	120.35
GMU- 3731	98.5	83.5	16.5	8.5	3.25	11.5	23.0	1.95	21	4.46	18.5	32.92	561.15
GMU- 3733	100.5	92.5	13.5	6.5	3.15	13.5	26.5	2.00	19	4.18	20.0	31.20	687.05
GMU- 3734	100.0	81.5	11.5	8.5	4.65	13.0	21.5	1.60	21	4.75	21.0	29.22	975.95
GMU- 3735	97.0	82.0	9.5	9.0	5.05	15.5	21.0	2.20	21	4.42	20.5	29.74	546.25
GMU- 3736	98.0	78.5	11.5	7.5	2.75	14.0	15.5	1.65	20	4.72	21.5	30.52	816.70
GMU- 3737	99.5	79.5	9.0	6.0	2.75	17.5	18.0	1.60	19	4.54	20.5	32.78	675.95
GMU- 3738	101.5	83.0	17.5	7.0	3.25	7.0	21.0	1.45	20	4.58	20.0	32.77	724.05
GMU- 3740	99.5	78.5	16.5	10.0	4.75	12.0	22.5	1.90	18	5.02	21.5	32.61	562.95
GMU- 3741	100.0	86.0	19.0	10.0	4.75	13.5	24.5	2.00	19	4.76	21.0	31.60	725.95
GMU- 3743	98.5	82.5	12.0	9.0	4.75	13.0	17.5	1.75	19	5.21	20.0	33.04	670.35
GMU- 3744	99.0	80.5	14.5	6.5	3.15	15.0	21.0	2.15	21	4.27	20.5	31.11	714.85
GMU- 3745	100.5	89.5	15.0	7.5	3.25	12.0	22.5	2.05	20	4.97	18.0	28.47	733.30
GMU- 3746	102.5	93.0	14.5	8.5	3.00	12.0	25.0	2.05	21	4.74	21.5	30.89	598.15
GMU- 3747	100.5	73.0	9.5	9.0	4.10	15.0	26.0	1.95	23	4.46	23.5	34.06	618.50
GMU- 3748	99.5	90.5	10.0	8.5	4.55	13.0	20.0	1.85	23	4.83	20.5	33.32	920.35
GMU- 3749	100.0	83.0	8.0	8.0	4.50	15.5	30.5	1.75	24	5.10	21.0	30.33	659.25

GMU- 3750	101.5	81.5	15.5	6.5	4.00	13.5	16.5	1.80	23	5.80	18.0	30.43	490.75
GMU- 3752	102.0	77.5	14.5	8.0	2.75	14.5	20.5	1.65	20	4.57	18.0	30.92	581.50
GMU- 3753	99.0	86.5	12.5	9.0	4.50	13.5	25.5	2.10	21	4.12	17.0	31.92	900.00
GMU- 3754	99.0	90.5	9.0	7.5	3.75	11.5	24.5	2.15	21	4.44	17.0	31.12	801.85
GMU- 3756	98.5	78.5	16.0	9.5	4.95	16.5	21.0	2.20	20	5.34	18.0	30.65	731.50
GMU- 3757	99.0	83.0	13.5	7.0	4.05	16.0	20.0	1.95	23	4.43	20.5	31.49	490.75
GMU- 3759	99.5	97.5	17.0	9.5	3.25	13.5	18.0	1.65	20	5.25	21.0	31.21	674.05
GMU- 3760	101.0	94.0	10.0	7.5	3.25	15.5	22.5	1.70	24	4.11	20.5	32.90	559.30
GMU- 3761	100.5	91.5	14.5	6.0	2.75	10.5	21.5	1.55	22	3.86	20.5	31.05	707.40
GMU- 3762	102.0	90.5	11.0	6.5	3.10	10.0	17.5	1.95	20	4.06	22.5	31.72	542.60
GMU- 3764	102.5	107.5	8.0	7.0	3.15	16.0	14.0	1.90	20	3.97	21.0	31.86	677.75
GMU- 3765	102.0	83.5	11.5	8.0	3.25	16.5	17.5	2.05	22	5.61	18.0	29.24	668.50
GMU- 3766	101.0	103.5	12.5	10.0	4.55	15.5	24.0	1.80	20	3.72	15.5	32.25	759.25
GMU- 3768	106.0	86.5	10.0	7.5	3.55	14.0	24.0	2.15	23	4.43	18.5	30.71	472.25
GMU- 3769	101.5	77.0	13.5	8.5	3.75	12.5	19.0	1.95	20	4.18	20.5	33.85	748.15
GMU- 3770	101.0	85.0	12.0	8.0	4.05	12.5	23.0	1.70	20	4.10	21.5	34.02	692.55
GMU- 3771	98.5	105.0	20.0	9.0	5.10	14.0	27.0	1.85	22	4.96	22.5	32.19	509.25
GMU- 3772	104.0	85.5	15.5	7.5	4.25	11.5	31.0	2.05	21	4.61	21.0	32.46	611.15
GMU- 3773	104.5	93.5	8.5	7.5	2.60	13.5	27.0	1.70	20	4.64	21.0	30.24	627.80
GMU- 3774	104.0	90.5	11.0	8.0	3.05	16.0	24.0	1.95	19	4.58	22.0	30.15	574.05
GMU- 3775	102.5	86.0	12.0	10.0	4.65	16.5	18.0	1.80	21	3.48	21.0	32.60	903.70
GMU- 3776	102.0	87.0	9.0	7.5	3.25	13.0	19.5	1.85	18	5.28	21.0	32.05	596.30
GMU- 3777	101.0	95.0	15.5	6.5	3.00	13.0	30.5	1.90	18	4.33	18.5	33.06	950.00
GMU- 3778	101.0	96.5	15.5	7.0	3.75	12.5	26.0	2.20	17	4.18	17.5	30.97	970.35
GMU- 3780	100.5	91.5	12.0	7.0	3.05	10.5	30.0	2.05	19	4.62	19.0	33.14	618.55
GMU- 3781	103.0	76.0	7.0	8.0	3.75	14.0	19.0	1.80	16	4.18	19.0	34.37	725.90
GMU- 3782	101.5	97.5	15.0	9.0	4.15	13.5	27.0	2.10	19	5.55	21.0	30.37	590.75

GMU- 3783	102.0	100.5	17.0	11.0	4.75	14.5	30.0	1.85	17	5.00	21.5	33.37	711.10
GMU- 3786	104.0	95.0	13.0	11.0	5.00	12.5	22.5	1.95	19	4.13	20.5	29.78	720.40
GMU- 3787	104.0	89.5	12.5	8.0	3.50	14.0	23.5	1.75	18	3.66	20.0	31.19	627.75
GMU- 3789	102.0	80.5	9.0	8.0	3.50	15.5	18.0	1.85	20	3.73	23.0	33.84	651.85
GMU- 3790	102.5	88.0	7.0	7.5	3.00	9.5	26.0	1.80	19	3.83	21.5	32.60	596.30
GMU- 3791	103.0	91.0	10.0	6.5	3.00	12.0	23.0	1.65	19	3.08	18.5	33.20	433.15
GMU- 3792	106.0	86.5	11.5	5.5	2.75	12.5	19.0	1.90	20	4.00	19.5	34.63	598.15
GMU- 3793	105.5	94.5	16.0	6.0	3.50	14.0	23.5	1.95	21	4.96	19.0	31.59	522.25
GMU- 3794	101.0	90.5	17.0	5.5	2.75	13.5	20.5	1.75	21	4.64	18.0	30.97	835.20
GMU- 3796	100.5	100.0	13.0	6.0	2.25	13.0	22.0	1.85	20	5.49	21.5	30.16	896.30
GMU- 3798	102.0	77.5	11.5	6.5	3.15	14.5	23.0	2.05	23	4.42	23.0	33.86	616.65
GMU- 3799	104.0	86.5	16.0	5.5	2.75	15.0	19.0	1.90	24	5.92	21.0	26.74	57.45
GMU- 3800	105.5	93.0	14.5	9.5	4.75	14.0	17.5	1.80	20	4.56	22.5	33.16	875.90
A-1(C)	102.5	84.0	17.0	8.0	4.15	14.5	27.0	2.20	18	6.19	21.0	30.71	700.00
Manjira(C)	99.5	86.5	14.0	10.0	4.25	11.0	27.5	1.80	17	5.53	19.0	30.53	679.60
PBNS-12(C)	101.5	92.5	20.0	10.0	4.15	13.5	32.0	1.80	15	5.80	17.0	29.08	774.10
PBNS-40(C)	102.0	93.5	17.0	7.5	4.05	13.0	25.0	1.90	18	5.64	17.0	27.81	933.35
JSF-1(C)	101.0	71.0	19.0	7.0	4.15	13.5	28.0	1.75	16	6.06	20.0	31.70	1085.2
Grand mean	101.35	85.49	13.89	8.15	3.82	13.42	23.01	1.87	19.67	4.68	19.83	31.01	697.52
CV (%)	5.14	6.42	13.57	19.19	18.70	19.80	15.40	6.23	6.27	7.99	6.37	5.74	20.66

maximum widths of leaf blade were GMU- 3683(5.10 cm), GMU-3711(5.10 cm), GMU- 3719 (5.05 cm) and GMU-3735 (5.05 cm).

4.2.1.6 Plant Population:

The mean for Plant population was 13.42 plants per square metre and ranged from 7.00 plants (GMU- 3678) to 20.00 (GMU- 3686). Among all genotypes only GMU-3686 (20) possessed maximum number of plant population.

4.2.1.7 Number of Capitula per plant:

The number of capitula per plant showed ranged from 14 (GMU- 3764) to 39 (GMU- 3662) with a mean of 23. Genotypes GMU-3621, GMU-3623, GMU-3631, GMU-3638, GMU-3658 and GMU- 3671, recorded more number of capitula per plant.

4.2.1.8 Diameter of Main Capitulum:

The mean of diameter of main capitulum was 1.87 ranged from 1.40 cm (GMU-3676) to 2.30 cm (GMU- 3693). The genotypes showed large diameter of main Capitulum are- GMU- 3667 and GMU- 3693.

4.2.1.9 Number of seeds per capitulum:

The number of seeds per capitulum ranged from 14 (GMU- 3703) to 26 (GMU- 3691) with a mean of 19.67. In this trait, genotype GMU- 3692, GMU-3723 and GMU- 3799 showed maximum number of seeds per capitulum.

4.2.1.10 100-seed weight:

The 100-seed weight had meant of 4.68 g with a minimum 3.08 g (GMU- 3791) and maximum 6.45 g (GMU-3643). Among all genotypes, some genotypes exhibited high 100- seed weight viz. GMU- 3667(6.11g), GMU- 3716 (6.32g), GMU- 3750 (5.80g), JSF-1 (6.06g) and A-1 (6.19g).

4.2.1.11 Hull Content:

The hull content had a mean 19.83 per cent with minimum 12.00 per cent (GMU-3638) and maximum 24 per cent (GMU- 3747). Genotype GMU-3747 showed highest hull content per cent.

4.2.1.12 Oil content:

The oil content had a mean 31.01 per cent with minimum 23.64 per cent (GMU-3730) and maximum 34.63 per cent (GMU- 3792). Among genotypes only one genotypes possessed high oil content namely, GMU-3792 (34.63%).

4.2.1.13 Seed yield:

The seed yield ranges from 57.45 Kg (GMU-3799) to 1144.45 Kg (GMU-3637). Maximum seed yield was recorded in genotype GMU- 3713 (1457.40 kg/ha), GMU-3651 (1255.55 kg/ha), GMU-3637 (1144.45 kg/ha), GMU-3621 (1077.78 kg/ha) and GMU-3726 (1059.30 kg/ha).

4.2.2 Coefficient of variation (PCV and GCV)

The genetic variability is a methodology on which selection acts to developed superior genotypes. Thus, higher the amount of variation present for a character in the breeding materials is the scope for its improvement through selection. The phenotypic and genotypic coefficients of variation were computed to assess the existing variability in the material (Table 4.3).

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are categorized as low (less than 10%), Moderate (10-20%) and high (more than 20%) as suggested by Sivasubramanian and Madhavamenon (1973). The estimated GCV and PCV helped in getting a clear understanding of the variability present among the various genotypes. The graph of PCV and GCV in figure 4.1 and figure 4.2.

Table 4.3 Genetic parameters of different traits in Safflower

Characters	Mean ($\bar{X}$)	Range		PCV (%)	GCV (%)	h^2 (bs) (%)	GA	GA % mean
		Min.	Max.					
Days to 50% flowering	101.35	94	107	2.10	1.76	70.30	3.08	3.03
Plant height (cm)	85.49	70	112.5	10.96	10.69	95.10	18.35	21.46
Number of primary branches per plant	13.89	06	24	28.65	25.23	77.50	6.36	45.78
Length of leaf blade (cm)	8.15	5.5	11	21.40	12.95	19.3	0.70	0.85
Width of leaf blade (cm)	3.82	2.25	5.10	21.48	10.55	24.10	0.41	0.10
Plant population	13.42	07	20	20.25	14.21	43.5	0.24	1.78
Number of capitula per plant	23.01	14	39	23.55	17.81	57.20	6.38	0.27
Diameter of capitulum (cm)	1.87	1.4	2.3	12.65	11.01	75.70	0.37	19.78
Number of seeds per capitulum	19.67	13	28	14.69	13.29	81.80	4.87	24.75
100-seed weight (g)	4.68	3.08	6.45	14.78	12.43	70.70	1.01	21.58
Hull content (%)	19.83	12	24	9.95	7.64	58.90	2.40	12.10
Oil content (%)	31.01	23.64	34.63	5.94	4.61	60.30	2.29	7.38
Seed yield (kg/ha)	697.52	57.4	1144.4	32.77	21.58	43.40	204.24	29.28

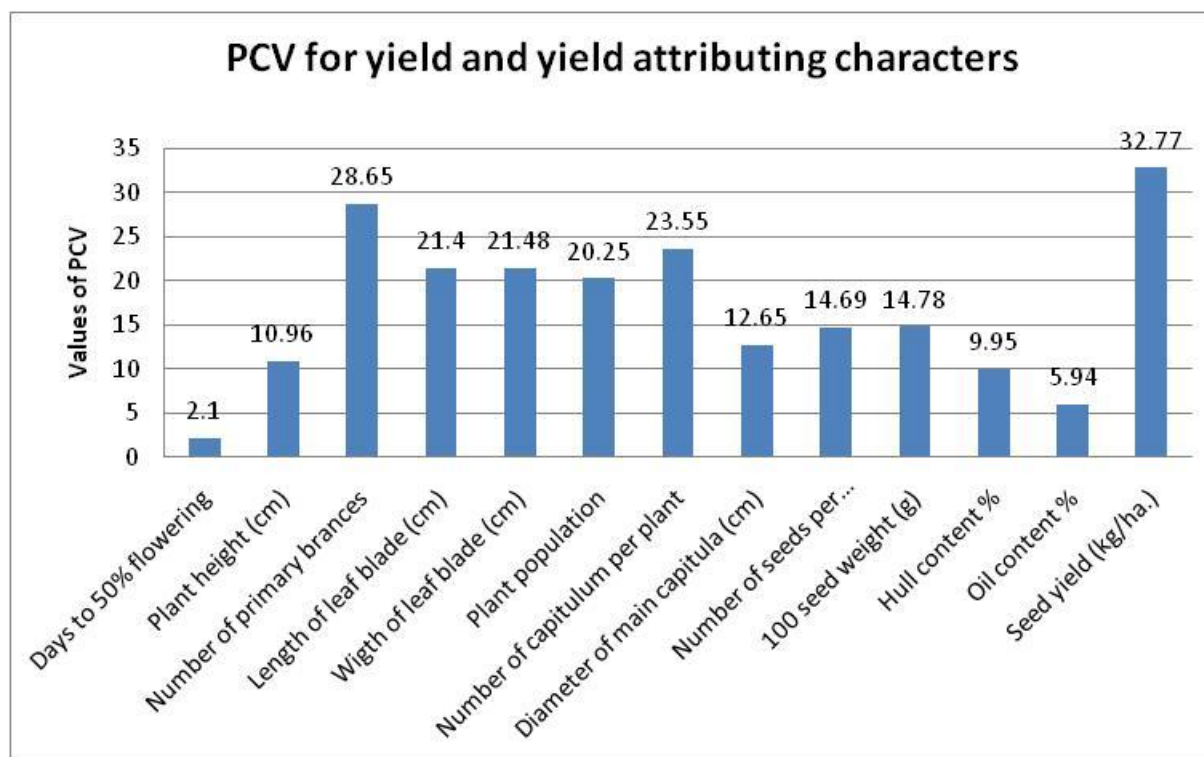


Fig.- 4.1 Phenotypic coefficient of variation for yield and yield attributing characters.

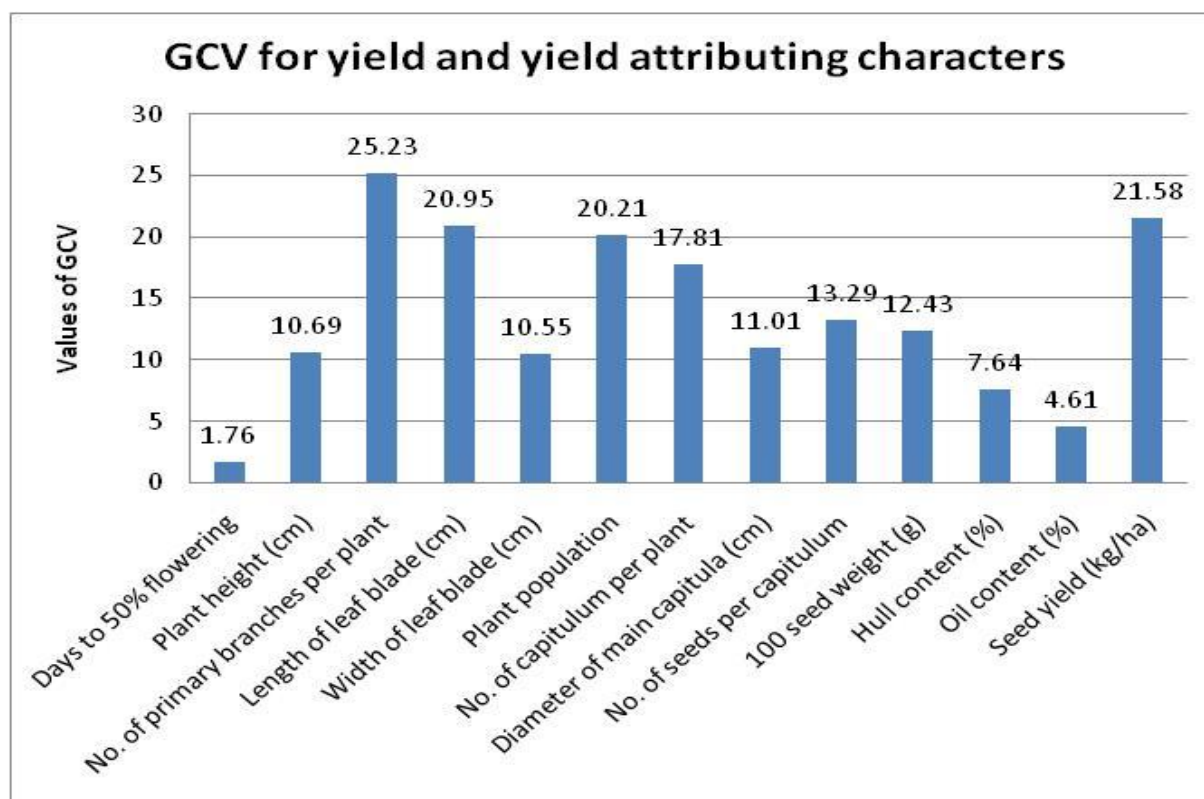


Fig.- 4.2 Genotypic coefficient of variation for yield and yield attributing characters.

The phenotypic and genotypic coefficient of variation was recorded higher for seed yield (PCV= 32.77; GCV= 21.58%), number of primary branches per plant (PCV= 28.65%; GCV= 25.23%), length of leaf blade (PCV= 21.40%; GCV= 20.95%) and plant population (PCV= 20.25%; GCV= 20.21%). This indicated possibility of obtaining higher selection response in respects of these traits.

The PCV and GCV moderate was observed for the traits namely, plant height (PCV= 10.96%; GCV= 10.69%), diameter of capitulum per plant (PCV=12.65%; GCV= 11.01%), number of seeds per capitulum (PCV=14.69%; GCV= 13.29%) and 100-seed weight (PCV= 14.78%; GCV= 12.43%). Whereas width of leaf blade and capitulum per plant exhibited high PCV and moderate GCV. The rest of the characters exhibited low magnitude of PCV and GCV viz., days to 50% flowering; oil content indicating that selection directly based on these traits could not be beneficial.

The estimation of phenotypic and genotypic components of variation is of primary importance to get an idea of relative extent of heritable and non-heritable variation. For most of the characters studied, the magnitude coefficient of variation was little higher than the genotypic coefficient of variation. It indicates that there was little influence of environment in the expression of traits.

Characters seed yield and number of primary branches per plant exhibited high PCV and GCV. The above results are in agreement of findings of Ramesh *et al.* (1980); Pandya *et al.* (1996); Sarang *et al.*(2004); Lakshyadeep *et al.* (2005); Patil *et al.*(2006) ; Deshmukh *et al.*(2012); Mukta (2012) for seed yield ; Ghongade *et al.* (1993); Choulwar *et al.* (2005); Mahajan *et al.* (2009); Deshmukh *et al.*(2012) for number of primary branches.

In the present findings, low magnitude of coefficient of variation for Days to 50% flowering is in agreement with the finding of Dikshit *et al.* (2012).

4.2.3 Heritability and Genetic advance as per cent of mean:

Heritability governs the resemblance between parents and their progeny whereas; the genetic advance provides the knowledge about expected gain for a particular character after selection. Heritability suggests the relative role of genetic factors in expression of phenotypes and also acts as an index of transmissibility of a particular trait to its offspring. However, the knowledge of heritability alone does not help in formulating concrete breeding programme, genetic advance along with heritability helps to ascertain the possible genetic control for any particular trait. The nature and extent of the inherent ability of a genotype for a character is an important parameter determining the extent of improvement of any crop species. The parameter, genetic advance as per cent of mean (GA) % as mean is more reliable index for understanding the effectiveness of selection in improving the traits because its estimates is derived by involvement of heritability, phenotypic standard deviation and intensity of selection. The graph of heritability and genetic advance as per cent mean in figure 4.3 and figure 4.4

Heritability and genetic advance as per cent of mean were estimated for 150 genotypes. The results are presented below:-

An attempt has been made in the present investigation to estimate heritability in broad sense and categorized as low (<50%), moderate (50%-70%) and high (>70%) as suggested by Robinson (1966).

High magnitude of heritability (>70%) was obtained for most of the characters. The highest heritability was recorded for plant height (95.10%) followed by number of

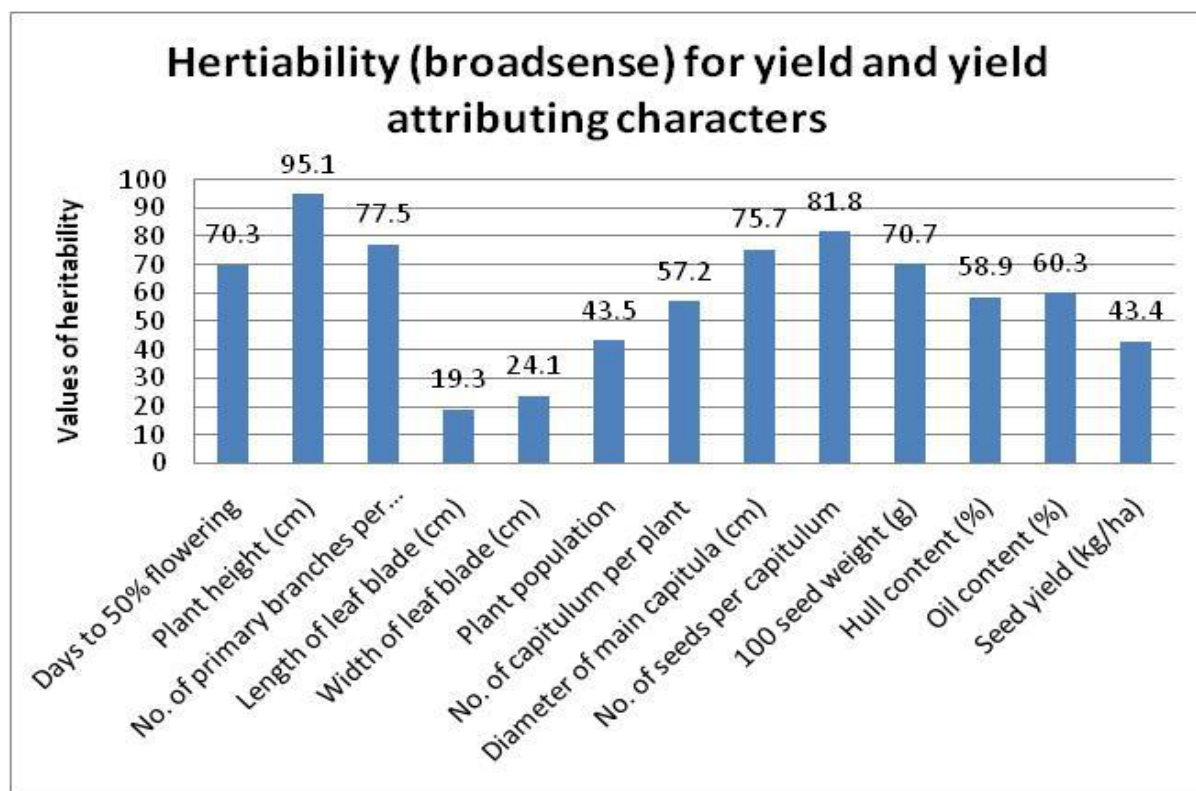


Fig.- 4.3 Heritability (broad sense) for yield and yield attributing characters

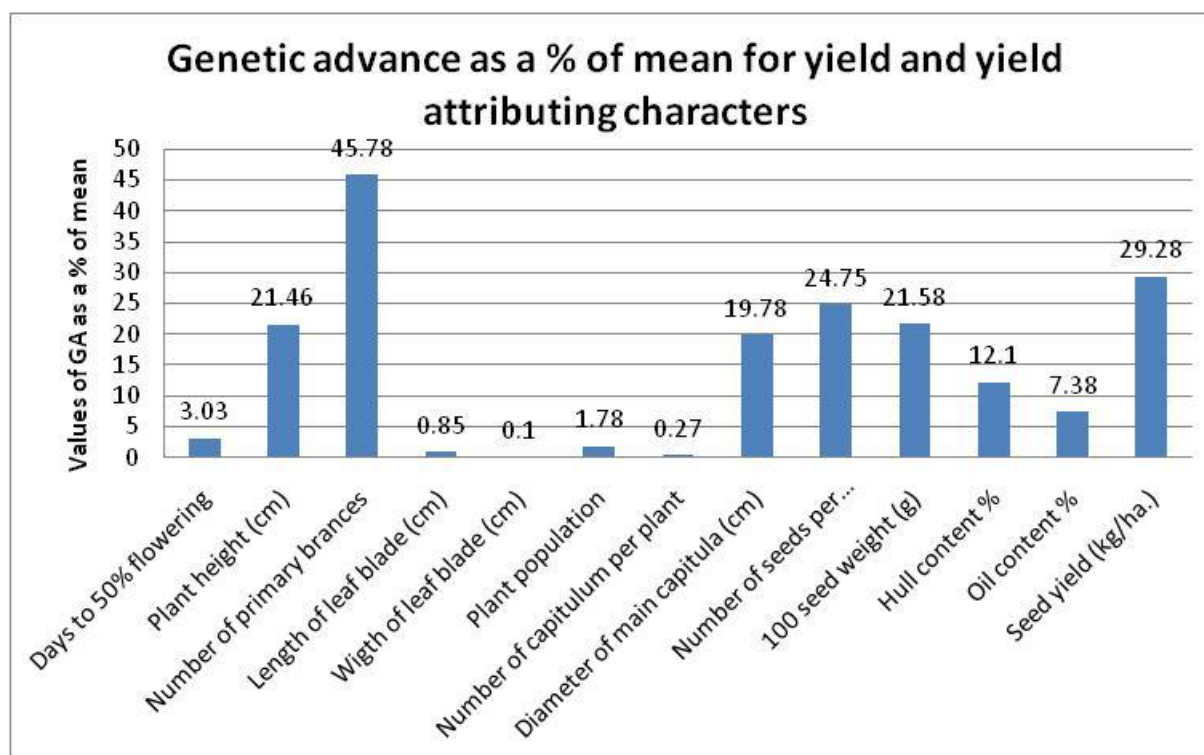


Fig.- 4.4 Genetic advance as a % of mean for yield and yield attributing characters.

seeds per capitula (81.80%), number of primary branches per plant (77.50%), diameter of capitulum (75.70%), 100-seed weight (70.70%) and days to 50% flowering (70.30%) also exhibited high heritability. The findings of present study agreed with the earlier finding of Choulwar *et al.* (2005) for plant height; for number of seeds per capitulum by Choulwar *et al.* (2005), Biradar *et al.*, (2012), Lande and Deshmukh (2012) and Swarup *et al.*, (2012); number of primary branches per plant Sarang *et al.*, (2004), Lande and Deshmukh (2012), Swarup *et al.*, (2012); for 100-seed weight, Meghannavar *et al.*, (1998), Senapati *et al.*, (1999), Sarang *et al.*, (2004) and Biradar *et al.*, (2012) ; for days to 50% flowering Shitole *et al.*, (1986) and Lande and Deshmukh (2012), Whereas, number of capitulum per plant (57.20), hull content (58.90), oil content (60.30%) exhibited moderate (50%-70%) heritability. Similiar results were obtained by Pandey and Singh (2012) for number of capitula per plant and Meghannavar *et al.*, (1998) for oil content. However, seed yield (43.40%) length of leaf blade (19.3%), width of leaf blade (24.1%), plant population (43.5%) exhibited low (< 50%) heritability. Similar results were reported by Rao (1982) for seed yield. On the other hand; few workers reported different findings as Lakshyadeep *et al.*, (2005), Mahajan *et al.*, (2009), Swarup *et al.*, (2012) and Pandey and Singh (2012) showed high heritability for seed yield.

The magnitude of genetic advance as percentage of mean was categorized as high (> 30%), moderate (30% - 10%) and low (< 10%). The highest genetic advance as percentage of mean was found in number of primary branches per plant (45.78%). This indicates that the character primary branches per plant are governed by additive gene and selection will be rewarded. Moderate magnitude of genetic advance was obtained for seed yield (29.28%), followed by number of seeds per capitulum (24.75%), 100-

seed weight (21.58%), plant height (21.46%), diameter of capitulum (19.78) and hull content (12.10%). This showed the existence of additive as well as non-additive gene action for seed yield, number of seeds per capitulum, 100-seed weight, plant height, diameter of main capitulum and hull content. Whereas, low magnitude of genetic advance was obtained for days to 50 % flowering (3.03%), length of leaf blade (0.85%), width of leaf blade (0.10%), plant population (1.78%), number of capitulum per plant (0.27%) and oil content (7.38%), suggesting that the character is governed by non-additive genes and heterosis breeding may be exploited for the above traits.

Heritability and genetic advance are the important parameters for selecting genotypes that permits greater effectiveness of selection by separating out environmental influence from the total variability. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will exhibit high genetic advance (Johnson *et al.*, 1955). Estimates of heritability also give some idea about the gene action involved in the expression of various polygenic traits.

Results indicated that high heritability coupled with high genetic advance was observed for character like number of primary branches per plant indicating that heritability is due to additive gene action and selection based on this character may be effective. These results are in agreement with the findings of Pandey and Singh (2012).

The characters representing high values of heritability and genetic advance emerge as ideal traits for improvement through selection due to high variability and transmissibility. Thus, the characters mentioned above are likely to show very high response to selection practiced in breeding population.

4.3 Characterization of safflower germplasm:

4.3.1 Petal colour:

All the 150 germplasm under studies were classified into different classes of petal colour. The graphical representation is shown in figure 4.5. The petal colour may be white, red, pale yellow, yellow and orange, out of which seven genotypes were grouped into white petal colour named as GMU- 3643, GMU- 3699, GMU- 3700, GMU- 3713, GMU- 3770, GMU- 3771 and JSF-1. Seven were grouped into red colour named as GMU-3636, GMU-3692, GMU-3719, GMU-3729, GMU-3731, GMU-3760 and GMU-3774. Eleven genotypes were grouped into pale yellow they were colour GMU- 3625, GMU- 3631, GMU- 3668, GMU- 3671, GMU- 3675, GMU- 3706, GMU- 3723, GMU- 3725, GMU- 3741, GMU- 3750 and GMU- 3752. Twenty seven were grouped into yellow petal colour named as GMU- 3644, GMU- 3646, GMU- 3647, GMU- 3652, GMU- 3654, GMU- 3656, GMU- 3667, GMU- 3678, GMU- 3687, GMU- 3690, GMU- 3691, GMU- 3715, GMU- 3716, GMU- 3718, GMU- 3730, GMU- 3738, GMU- 3740, GMU- 3743, GMU- 3744, GMU- 3746, GMU- 3747, GMU- 3764, GMU- 3776, GMU- 3777, GMU- 3778, GMU- 3783, GMU- 3799. Ninety eight were grouped into orange petal colour they were GMU- 3621, GMU- 3623, GMU- 3624, GMU- 3626, GMU- 3628, GMU- 3632, GMU- 3633, GMU- 3634, GMU- 3635, GMU- 3637, GMU- 3638, GMU- 3639, GMU- 3640, GMU- 3641, GMU- 3642, GMU- 3645, GMU- 3648, GMU- 3649, GMU- 3651, GMU- 3653, GMU- 3658, GMU- 3659, GMU- 3660, GMU- 3661, GMU- 3662, GMU- 3663, GMU- 3664, GMU- 3666, GMU- 3670, GMU- 3672, GMU- 3673, GMU- 3674, GMU- 3676, GMU- 3677, GMU- 3679, GMU- 3680, GMU- 3681, GMU- 3682, GMU- 3683, GMU- 3684, GMU- 3686, GMU- 3693, GMU- 3694, GMU- 3696, GMU- 3698, GMU- 3701, GMU- 3702, GMU- 3703, GMU- 3704, GMU- 3705,

Characterization of safflower germplasm on petal colour

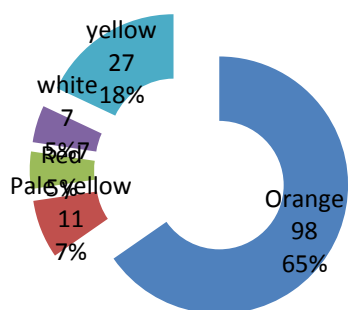


Fig.- 4.5 Safflower germplasm classified in to different classes of petal colour.

Characterization of safflower germplasm on leaf shape

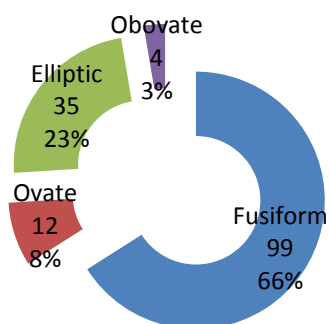


Fig.- 4.6 Safflower germplasm classified in to different classes of leaf shape.

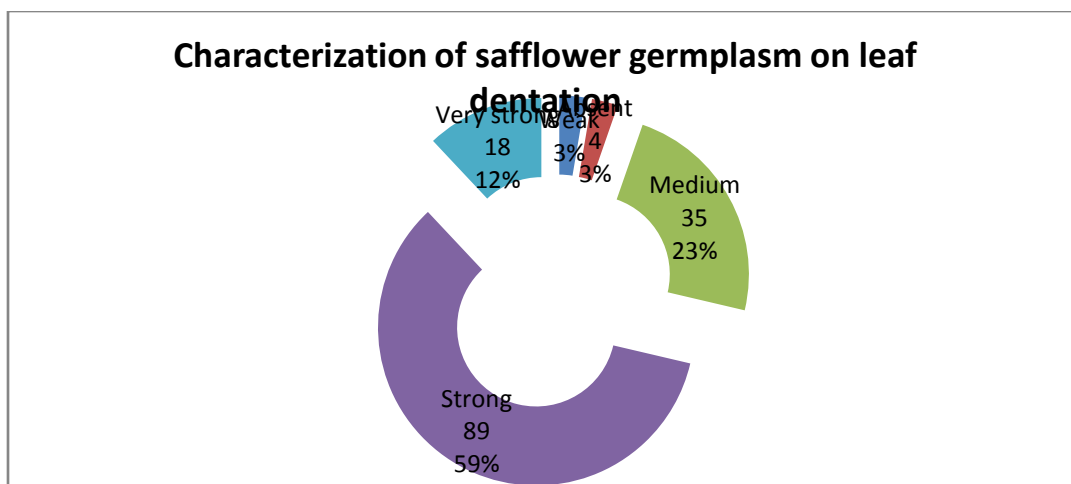


Fig.- 4.7 Safflower germplasm classified in to different classes of leaf dentation.

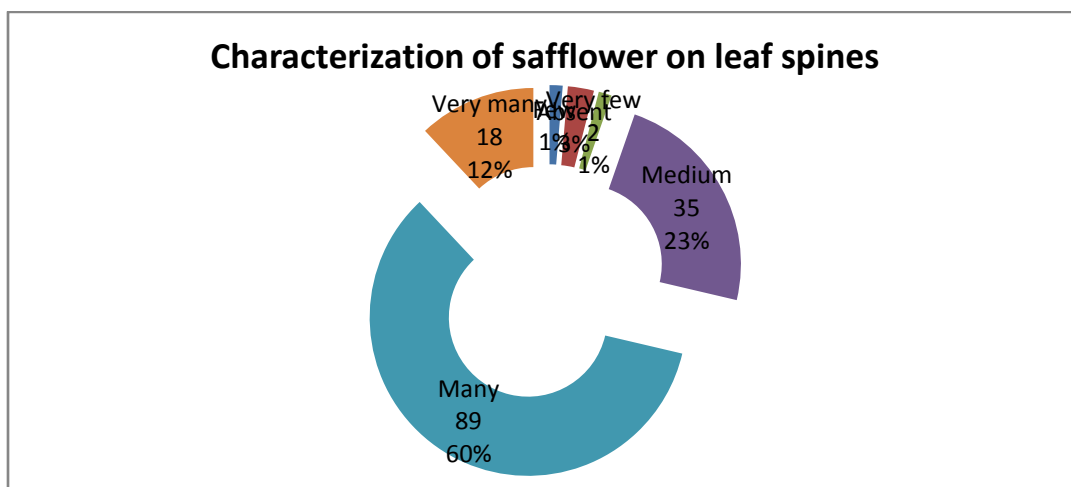


Fig.- 4.8 Safflower germplasm classified in to different classes of leaf spines.

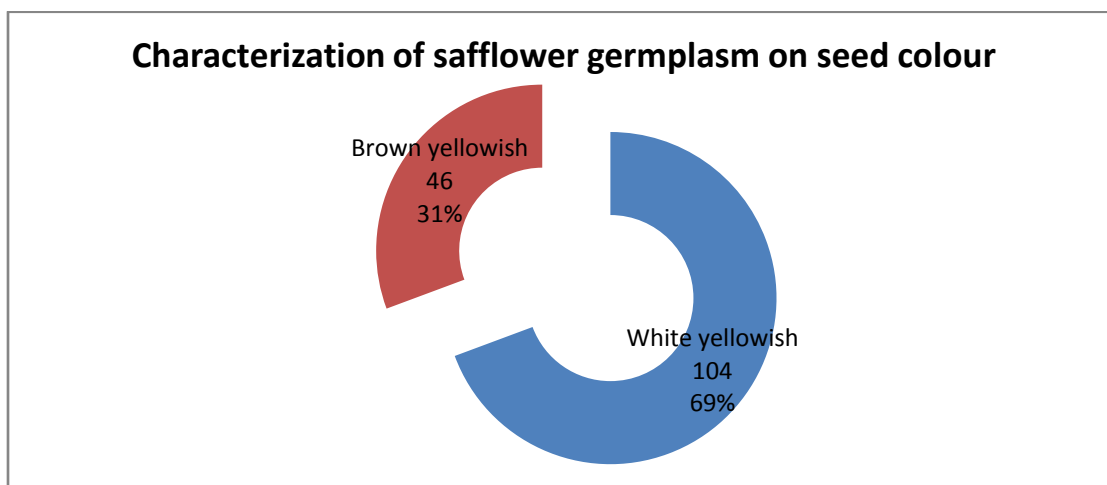


Fig.-4.9 Safflower germplasm classified in to different classes of seed colour.

Table 4.4 : Characterization of Safflower germplasm

Genotypes	Petal colour	Leaf shape	No. of spines	Dentation leaf	Seed colour
GMU- 3621	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3623	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3624	Orange	Fusiform	Very Many	Very Strong	Brown yellowish
GMU- 3625	Pale yellow	Fusiform	Very Many	Very Strong	Brown yellowish
GMU- 3626	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3628	Orange	Fusiform	Very Many	Very Strong	Brown yellowish
GMU- 3631	Pale yellow	Obovate	Many	Strong	Brown yellowish
GMU- 3632	Orange	Fusiform	Very Many	Very Strong	Brown yellowish
GMU- 3633	Orange	Fusiform	Very Many	Very Strong	White yellowish
GMU- 3634	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3635	Orange	Obovate	Few	Weak	White yellowish
GMU- 3636	Red	Ovate	Absent	Absent	White yellowish
GMU- 3637	Orange	Ovate	Absent	Absent	White yellowish
GMU- 3638	Orange	Ovate	Absent	Absent	White yellowish
GMU- 3639	Orange	Obovate	Medium	Medium	White yellowish
GMU- 3640	Orange	Obovate	Medium	Medium	White yellowish
GMU- 3641	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3642	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3643	White	Fusiform	Many	Strong	White yellowish
GMU- 3644	Yellow	Ovate	Absent	Absent	White yellowish
GMU- 3645	Orange	Elliptic	Very Few	Weak	Brown yellowish
GMU- 3646	Yellow	Ovate	Few	Weak	Brown yellowish
GMU- 3647	Yellow	Ovate	Very Few	Weak	White yellowish
GMU- 3648	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3649	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3651	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3652	Yellow	Fusiform	Very Many	Very Strong	Brown yellowish
GMU- 3653	Orange	Fusiform	Very Many	Very Strong	White yellowish
GMU- 3654	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3656	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3658	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3659	Orange	Elliptic	Medium	Medium	Brown yellowish
GMU- 3660	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3661	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3662	Orange	Fusiform	Very Many	Very Strong	White yellowish
GMU- 3663	Orange	Fusiform	Very Many	Very Strong	White yellowish
GMU- 3664	Orange	Elliptic	Medium	Medium	White yellowish

GMU- 3666	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3667	Yellow	Fusiform	Many	Strong	Brown yellowish
GMU- 3668	Pale yellow	Fusiform	Many	Strong	White yellowish
GMU- 3670	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3671	Pale yellow	Ovate	Medium	Medium	White yellowish
GMU- 3672	Orange	Ovate	Medium	Medium	White yellowish
GMU- 3673	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3674	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3675	Pale yellow	Fusiform	Many	Strong	White yellowish
GMU- 3676	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3677	Orange	Fusiform	Very Many	Very Strong	White yellowish
GMU- 3678	Yellow	Elliptic	Very Many	Very Strong	Brown yellowish
GMU- 3679	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3680	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3681	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3682	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3683	Orange	Elliptic	Very Many	Very strong	White yellowish
GMU- 3684	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3686	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3687	Yellow	Fusiform	Many	Strong	Brown yellowish
GMU- 3690	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3691	Yellow	Fusiform	Many	Strong	Brown yellowish
GMU- 3692	Red	Elliptic	Medium	Medium	White yellowish
GMU- 3693	Orange	Elliptic	Medium	Medium	White yellowish
GMU- 3694	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3696	Orange	Elliptic	Very Many	Very Strong	White yellowish
GMU- 3698	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3699	White	Fusiform	Many	Strong	Brown yellowish
GMU- 3700	White	Fusiform	Many	Strong	White yellowish
GMU- 3701	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3702	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3703	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3704	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3705	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3706	Pale yellow	Fusiform	Many	Strong	Brown yellowish
GMU- 3708	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3709	Orange	Elliptic	Medium	Medium	White yellowish
GMU- 3711	Orange	Elliptic	Medium	Medium	White yellowish
GMU- 3713	White	Elliptic	Medium	Medium	Brown yellowish
GMU- 3715	Yellow	Elliptic	Medium	Medium	Brown yellowish
GMU- 3716	Yellow	Fusiform	Many	Strong	White yellowish

GMU- 3718	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3719	Red	Fusiform	Many	Strong	White yellowish
GMU- 3720	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3721	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3722	Orange	Elliptic	Very Many	Very Strong	White yellowish
GMU- 3723	Pale yellow	Fusiform	Many	Strong	Brown yellowish
GMU- 3725	Pale yellow	Elliptic	Medium	Medium	White yellowish
GMU- 3726	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3727	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3729	Red	Fusiform	Many	Strong	White yellowish
GMU- 3730	Yellow	Fusiform	Many	Strong	Brown yellowish
GMU- 3731	Red	Elliptic	Medium	Medium	White yellowish
GMU- 3733	Orange	Elliptic	Medium	Medium	Brown yellowish
GMU- 3734	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3735	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3736	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3737	Orange	Elliptic	Medium	Medium	White yellowish
GMU- 3738	Yellow	Elliptic	Medium	Medium	White yellowish
GMU- 3740	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3741	Pale yellow	Fusiform	Many	Strong	White yellowish
GMU- 3743	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3744	Yellow	Elliptic	Very Many	Very strong	White yellowish
GMU- 3745	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3746	Yellow	Elliptic	Very Many	Very Strong	White yellowish
GMU- 3747	Yellow	Elliptic	Very Many	Very Strong	White yellowish
GMU- 3748	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3749	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3750	Pale yellow	Elliptic	Medium	Medium	White yellowish
GMU- 3752	Pale yellow	Elliptic	Medium	Medium	White yellowish
GMU- 3753	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3754	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3756	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3757	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3759	Orange	Elliptic	Medium	Medium	White yellowish
GMU- 3760	Red	Fusiform	Many	Strong	White yellowish
GMU- 3761	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3762	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3764	Yellow	Elliptic	Medium	Medium	White yellowish
GMU- 3765	Orange	Elliptic	Medium	Medium	Brown yellowish
GMU- 3766	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3768	Orange	Fusiform	Many	Strong	White yellowish

GMU- 3769	Orange	Elliptic	Medium	Medium	Brown yellowish
GMU- 3770	White	Elliptic	Medium	Medium	White yellowish
GMU- 3771	White	Elliptic	Medium	Medium	White yellowish
GMU- 3772	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3773	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3774	Red	Fusiform	Many	Strong	White yellowish
GMU- 3775	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3776	Yellow	Elliptic	Very Many	Very Strong	White yellowish
GMU- 3777	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3778	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3780	Orange	Elliptic	Medium	Medium	White yellowish
GMU- 3781	Orange	Elliptic	Medium	Medium	White yellowish
GMU- 3782	Orange	Elliptic	Medium	Medium	White yellowish
GMU- 3783	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3786	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3787	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3789	Orange	Elliptic	Medium	Medium	Brown yellowish
GMU- 3790	Orange	Elliptic	Medium	Medium	Brown yellowish
GMU- 3791	Orange	Elliptic	Medium	Medium	Brown yellowish
GMU- 3792	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3793	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3794	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3796	Orange	Fusiform	Many	Strong	White yellowish
GMU- 3798	Orange	Fusiform	Many	Strong	Brown yellowish
GMU- 3799	Yellow	Fusiform	Many	Strong	White yellowish
GMU- 3800	Orange	Fusiform	Many	Strong	White yellowish
A-1	Orange	Obovate	Many	Strong	Brown yellowish
Manjira	Orange	Ovate	Medium	Medium	Brown yellowish
PBNS-12	Orange	Ovate	Medium	Medium	Brown yellowish
PBNS-40	Orange	Ovate	Medium	Medium	White yellowish
JSF-1	White	Ovate	Medium	Medium	Brown yellowish

GMU- 3708, GMU- 3709, GMU- 3711, GMU- 3720, GMU- 3721, GMU- 3722, GMU- 3726, GMU- 3727, GMU- 3733, GMU- 3734, GMU- 3735, GMU- 3736, GMU- 3737, GMU- 3745, GMU- 3748, GMU- 3749, GMU- 3753, GMU- 3754, GMU- 3756, GMU- 3758, GMU- 3759, GMU- 3761, GMU- 3762, GMU- 3765, GMU- 3766, GMU- 3768, GMU- 3769, GMU- 3772, GMU- 3773, GMU- 3775, GMU- 3780, GMU- 3781, GMU- 3782, GMU- 3786, GMU- 3787, GMU- 3789, GMU- 3790, GMU- 3791, GMU- 3792, GMU-3793, GMU- 3794, GMU- 3796, GMU- 3798, GMU- 3800, A-1, Manjira, PBNS-12 and PBNS-40.

4.3.2 Leaf shape:

Out of one fifty genotypes under studied, leaf shape are categorized into fusiform, ovate, elliptic and obovate. The graphical representation is shown in figure 4.6

Ninety nine germplasm showed named as fusiform leaf shape GMU- 3621, GMU- 3623, GMU- 3624, GMU- 3625, GMU- 3626, GMU- 3628, GMU- 3632, GMU- 3633, GMU- 3634, GMU- 3641, GMU- 3642, GMU- 3643, GMU- 3648, GMU- 3649, GMU- 3651, GMU- 3652, GMU- 3653, GMU- 3654, GMU- 3656, GMU- 3658, GMU- 3660, GMU- 3661, GMU- 3662, GMU- 3663, GMU- 3664, GMU- 3666, GMU- 3667, GMU- 3668, GMU- 3670, GMU- 3673, GMU- 3674, GMU- 3675, GMU- 3676, GMU- 3677, GMU- 3679, GMU- 3680, GMU- 3681, GMU- 3682, GMU- 3684, GMU- 3686, GMU- 3687, GMU- 3690, GMU- 3691, GMU- 3694, GMU- 3698, GMU- 3699, GMU- 3700, GMU- 3701, GMU- 3702, GMU- 3703, GMU- 3704, GMU- 3705, GMU- 3706, GMU- 3708, GMU- 3716, GMU- 3718, GMU- 3719, GMU- 3720, GMU- 3721, GMU- 3723, GMU- 3725, GMU- 3726, GMU- 3727, GMU- 3723, GMU- 3730, GMU- 3734, GMU- 3735, GMU- 3736, GMU- 3740, GMU- 3741, GMU- 3743, GMU- 3745, GMU- 3748, GMU- 3749, GMU- 3753, GMU- 3754, GMU- 3756, GMU- 3757, GMU- 3760, GMU-

3761, GMU- 3762, GMU- 3766, GMU- 3768, GMU- 3772, GMU- 3773, GMU- 3774, GMU- 3775, GMU- 3777, GMU- 3778, GMU- 3783, GMU- 3786, GMU- 3787, GMU- 3792, GMU- 3793, GMU- 3794, GMU- 3796, GMU- 3798, GMU- 3799 and GMU- 3800. Twelve germplasm recorded ovate shape leaf named as GMU- 3644, GMU- 3646, GMU- 3644, GMU- 3638, GMU- 3636, GMU- 3637 GMU-3671, GMU-3672, Manjira, PBNS-12, PBNS-40 and JSF-1. Thirty five were grouped into elliptic leaf shape they were GMU- 3659, GMU- 3664, GMU- 3678, GMU- 3683, GMU- 3692, GMU- 3693, GMU- 3696, GMU- 3709, GMU- 3711, GMU- 3713, GMU- 3715, GMU- 3722, GMU- 3725, GMU- 3731, GMU- 3733, GMU- 3737, GMU- 3738, GMU- 3744, GMU- 3746, GMU- 3747, GMU- 3750, GMU- 3752, GMU- 3659, GMU- 3764, GMU- 3765, GMU- 3776, GMU- 3769, GMU- 3770, GMU- 3771, GMU- 3780, GMU- 3781, GMU- 3782 , GMU- 3789, GMU- 3790 and GMU- 3791. Four were grouped into obovate leaf shape named as GMU- 3639, GMU- 3640, GMU- 3631 and GMU- 3635.

4.3.3 Dentation of leaf :

The dentation of leaf was categorized into absent, weak, medium, strong and very strong. The graphical representation is shown in figure 4.7. Out of one fifty germplasm, four germplasm recorded absent dentation named as GMU- 3636, GMU- 3637, GMU- 3638 and GMU- 3644. Weak dentation was recorded into four germplasm GMU- 3635, GMU- 3645, GMU- 3646 and GMU- 3647. Thirty five medium dentation were grouped into GMU- 3639, GMU- 3640, GMU- 3659, GMU- 3664, GMU- 3671, GMU- 3672, GMU- 3692, GMU- 3693, GMU- 3709, GMU- 3711, GMU- 3713, GMU- 3715, GMU- 3725, GMU- 3731, GMU- 3733, GMU- 3737, GMU- 3738, GMU- 3750, GMU- 3752, GMU- 3759, GMU- 3764, GMU- 3765, GMU- 3769, GMU- 3770, GMU- 3771, GMU- 3780, GMU- 3781, GMU- 3782, GMU- 3789, GMU- 3790, GMU- 3791,

Manjira, PBNS-12, PBNS-40 and JSF-1. Eighty nine germplasm recorded strong dentation GMU- 3621, GMU- 3623, GMU- 3626, GMU- 3631,GMU- 3634, GMU- 3641, GMU- 3642, GMU- 3643, GMU- 3648, GMU- 3649, GMU- 3651, GMU- 3654, GMU- 3656, GMU- 3658, GMU- 3660, GMU- 3661, GMU- 3666, GMU- 3667, GMU- 3668, GMU- 3670, GMU- 3673, GMU- 3674, GMU- 3675, GMU- 3676, GMU- 3679, GMU- 3680, GMU- 3681, GMU- 3682, GMU- 3684, GMU- 3686, GMU- 3690, GMU- 3691, GMU-3694, GMU-3698, GMU-3699, GMU- 3700, GMU- 3701, GMU- 3702, GMU- 3703, GMU- 3704, GMU- 3705, GMU- 3706, GMU- 3708, GMU- 3716, GMU- 3718, GMU- 3719, GMU- 3720, GMU- 3721, GMU- 3723, GMU- 3726, GMU- 3727, GMU- 3729, GMU- 3730, GMU- 3734, GMU- 3735, GMU- 3736, GMU- 3740, GMU- 3741, GMU- 3743, GMU- 3743, GMU- 3745, GMU- 3748, GMU- 3749, GMU- 3753, GMU- 3754, GMU- 3756, GMU- 3757, GMU- 3760, GMU- 3761, GMU- 3762, GMU- 3766, GMU- 3768, GMU- 3772, GMU- 3773, GMU- 3774, GMU- 3775, GMU- 3777, GMU- 3778, GMU- 3783, GMU- 3786, GMU- 3787, GMU- 3792, GMU- 3793,GMU- 3794, GMU- 3796, GMU- 3798, GMU- 3799, GMU- 3800, A-1. Very strong dentation of leaf recorded eighteen germplasm named as GMU- 3624, GMU- 3625, GMU- 3628, GMU- 3632, GMU- 3633, GMU- 3652, GMU- 3653, GMU- 3662, GMU- 3663, GMU- 3677, GMU- 3678, GMU- 3683, GMU- 3696, GMU- 3722, GMU- 3744, GMU- 3746, GMU- 3747 and GMU- 3776.

4.3.4 Number of spines in a leaf :

Numbers of spines in a leaf were grouped into six classes absent, very few, few, medium, many and very many. The graphical representation is shown in figure 4.8. Out of one fifty germplasm, four germplasm recorded number of spines viz., GMU- 3636, GMU- 3637, GMU- 3638 and GMU- 3644. Very few numbers of spines in a leaf

showed two germplasm viz., GMU- 3645, GMU- 3647. Few numbers of spines in a leaf recorded in two germplasm named as GMU- 3635, GMU- 3646. Medium number of spines in a leaf showed by thirty five germplasm named as GMU- 3639, GMU- 3640, GMU- 3659, GMU- 3664, GMU- 3671, GMU- 3672, GMU- 3692, GMU- 3693, GMU- 3709, GMU- 3711, GMU- 3713, GMU- 3715, GMU- 3725, GMU- 3731, GMU- 3733, GMU- 3737, GMU- 3738, GMU- 3750, GMU- 3752, GMU- 3759, GMU- 3764, GMU- 3765, GMU- 3769, GMU- 3770, GMU- 3771, GMU- 3780, GMU- 3781, GMU- 3782, GMU- 3789, GMU- 3790, GMU- 3791, Manjira, PBNS-12, PBNS-40 and JSF-1. Many number of spines in a leaf showed by eighty nine classes named as GMU- 3621, GMU- 3623, GMU- 3626, GMU- 3631, GMU- 3634, GMU- 3641, GMU- 3642, GMU- 3643, GMU- 3649, GMU- 3651, GMU- 3654, GMU- 3656, GMU- 3658, GMU- 3660, GMU- 3661, GMU- 3667, GMU- 3668, GMU- 3670, GMU- 3673, GMU- 3674, GMU- 3675, GMU- 3676, GMU- 3679, GMU- 3680, GMU- 3681, GMU- 3682, GMU- 3684, GMU- 3686, GMU- 3687, GMU- 3690, GMU- 3691, GMU- 3694, GMU- 3698, GMU- 3699, GMU- 3700, GMU- 3701, GMU- 3702, GMU- 3703, GMU- 3704, GMU- 3705, GMU- 3706, GMU- 3708, GMU- 3716, GMU- 3718, GMU- 3719, GMU- 3720, GMU- 3721, GMU- 3723, GMU- 3726, GMU- 3727, GMU- 3729, GMU- 3730, GMU- 3734, GMU- 3735, GMU- 3736, GMU- 3740, GMU- 3741, GMU- 3743, GMU- 3745, GMU- 3748, GMU- 3749, GMU- 3753, GMU- 3754, GMU- 3756, GMU- 3757, GMU- 3760, GMU- 3761, GMU- 3762, GMU- 3766, GMU- 3768, GMU- 3773, GMU- 3774, GMU- 3775, GMU- 3777, GMU- 3778, GMU- 3783, GMU- 3786, GMU- 3787, GMU- 3792, GMU- 3793, GMU- 3794, GMU- 3796, GMU- 3798, GMU- 3799, GMU- 3800 and A-1. Very numbers of leaf spines were recorded in eighteen germplasm GMU- 3624, GMU- 3625, GMU- 3628, GMU- 3632, GMU- 3633, GMU- 3652, GMU- 3653, GMU- 3662, GMU-

3663, GMU- 3677, GMU- 3678, GMU- 3683, GMU- 3696, GMU- 3722, GMU- 3744, GMU- 3746, GMU- 3747 and GMU- 3776.

4.3.5 Seed colour:

Seed colour may be classified into white, white yellowish, brown yellowish and brown. The graphical representation is shown in figure 4.9. Out of one hundred fifty, there was no white seed colour or white colour germplasm and brown seed colour germplasm was found. White yellowish seed colour was recorded in one hundred four named as GMU- 3621, GMU- 3623, GMU- 3626, GMU- 3633, GMU- 3635, GMU- 3636, GMU- 3637, GMU- 3638, GMU-3639, GMU- 3640, GMU- 3641, GMU- 3642, GMU- 3643, GMU- 3644, GMU- 3647, GMU- 3651, GMU- 3653, GMU- 3654, GMU- 3656, GMU- 3658, GMU- 3660, GMU- 3661, GMU- 3662, GMU- 3663, GMU- 3664, GMU- 3666, GMU- 3668, GMU- 3670, GMU- 3671, GMU- 3672, GMU- 3673, GMU- 3674, GMU- 3675, GMU- 3677, GMU- 3679, GMU- 3680, GMU- 3681, GMU- 3682, GMU- 3683, GMU- 3684, GMU- 3690, GMU- 3692, GMU- 3693, GMU- 3694, GMU- 3696, GMU- 3700, GMU- 3702, GMU- 3703, GMU- 3705, GMU- 3708, GMU- 3709 and GMU- 3711, GMU- 3716, GMU- 3718, GMU- 3719, GMU- 3720, GMU- 3721, GMU- 3722, GMU- 3725, GMU- 3726, GMU- 3727, GMU- 3729, GMU- 3731, GMU- 3736, GMU- 3737, GMU- 3738, GMU- 3740, GMU- 3741, GMU- 3743, GMU- 3744, GMU- 3745, GMU- 3746, GMU- 3747, GMU- 3748, GMU- 3749, GMU- 3750, GMU- 3752, GMU- 3753, GMU- 3754, GMU- 3757, GMU- 3759, GMU- 3760, GMU- 3761, GMU- 3762, GMU- 3764, GMU- 3766, GMU- 3768, GMU- 3770, GMU- 3771, GMU- 3774, GMU- 3776, GMU- 3777, GMU- 3778, GMU- 3780, GMU- 3781, GMU- 3782, GMU- 3783, GMU- 3792, GMU- 3793, GMU- 3794, GMU- 3796, GMU- 3799, GMU- 3800 and PBNS-40. Forty six germplasm recorded brown yellowish seed viz., GMU-

3624, GMU- 3625, GMU- 3628, GMU- 3631, GMU- 3632, GMU- 3634, GMU- 3645, GMU- 3646, GMU- 3648, GMU- 3649, GMU- 3652, GMU- 3659, GMU- 3667, GMU- 3676, GMU- 3678, GMU- 3686, GMU- 3687, GMU- 3691, GMU- 3698, GMU- 3699, GMU- 3701, GMU- 3704, GMU- 3706, GMU- 3713, GMU- 3715, GMU- 3723, GMU- 3730, GMU- 3733, GMU- 3734, GMU- 3735, GMU- 3756, GMU- 3765, GMU- 3769, GMU- 3772, GMU- 3773, GMU- 3775, GMU- 3786, GMU- 3787, GMU- 3789, GMU- 3790, GMU- 3791, GMU- 3798, A-1, Manjira, PBNS-12 and JSF-1.

4.4 Estimation of coefficient of correlation

The major objective of crop breeding programme is to achieve higher yield. Yield is regarded as an end product of a set of physiological processes which are related to each other. It is also a complex character with low heritability and therefore, direct selection for yield to improve it is often not so successful. Therefore, it is advantageous to find out the closely related component traits of yield, so that, suitable selection strategies can be devised to improve yield. Correlation analysis provides measures of relationship among the traits and serves to assess the opportunity of mutual improvement of two desirable traits by common selection programme.

Knowledge about interrelationship between yield and yield contributing characters facilitates the choice of efficient breeding method to be adopted and selection of parents for crop improvement. Phenotypic correlation coefficient helps in determining selection index, where as genotypic correlation coefficient provides a close measure of association between characters which may be useful for overall improvement of crops.

Galton, (1888) was first to suggest the use of correlation index to describe the degree of association between two variables. The degree of association effects the

Table 4.5: Phenotypic and genotypic correlation coefficient of seed yield components in safflower

Characters		DF	PH	PB	LLB	WLB	PP	CP	DMC	NSC	HSW	HC (%)	OC (%)	SY
DF	P	1.000	0.189**	0.021	-0.025	0.063	0.109	0.122	-0.021	0.132	-0.217**	0.248**	0.105	-0.135*
	G	1.000	0.225**	0.021	-0.475**	0.199**	0.452**	0.148*	-0.017	0.176**	-0.336**	0.391**	0.218**	-0.310**
PH	P		1.000	0.087	0.086	-0.045	0.016	0.023	0.099	0.019	-0.170*	0.025	0.090	-0.080
	G		1.000	0.096	0.983**	-0.058	0.103	0.006	0.118	0.039	-0.224**	0.043	0.119	-0.158*
PB	P			1.000	0.058	0.100	-0.072	0.058	0.024	0.093	0.056	-0.073	0.026	-0.008
	G			1.000	0.151*	0.159*	-0.549**	0.076	0.088	0.140*	0.081	-0.095	0.048	0.053
LLB	P				1.000	0.138*	-0.003	-0.012	-0.075	-0.135*	-0.120	-0.050	-0.045	0.025
	G				1.000	0.052	-0.467**	0.155*	-0.409**	-1.045	-0.356**	0.054	0.046	-0.126
WLB	P					1.000	0.005	0.225**	-0.025	0.023	0.125	-0.006	-0.052	-0.017
	G					1.000	0.305**	0.418**	-0.027	0.133*	0.381**	-0.006	-0.099	0.215**
PP	P						1.000	-0.014	0.020	0.007	0.016	0.010	-0.002	0.026
	G						1.000	0.262**	-0.086	-0.057	0.211**	0.183*	0.277**	0.181**
CP	P							1.000	-0.017	-0.054	0.047	-0.060	0.019	0.014
	G							1.000	0.028	-0.028	-0.020	-0.157*	0.011	-0.056
DMC	P								1.000	0.044	0.135*	0.030	-0.134*	0.055
	G								1.000	0.067	0.146*	0.032	-0.199**	0.077
NSC	P									1.000	0.034	0.107	0.092	-0.007
	G									1.000	0.062	0.130	0.133*	0.015
HSW	P										1.000	-0.009	-0.091	0.272**
	G										1.000	0.009	-0.131	0.452**
HC(%)	P											1.000	0.281**	-0.095
	G											1.000	0.371**	-0.110
OC(%)	P												1.000	0.088
	G												1.000	0.150*
SY	P													1.000
	G													1.000

DF= Days to 50% flowering; PH= Plant height; PB = Number of primary branches / plant; LLB = Length of leaf blade / plant; WLB = Width of leaf blade / plant ; PP = Number of plant / m² ; CP = Number of capitula / plant; DMC= Diameter of main capitulum / plant; NSC = Number of seeds / capitulum; HSW= 100-seed weight; HC = Hull content; OC= Oil content; SY= seed yield (kg/ha).

effectiveness of selection processes. The phenotypic and genotypic coefficients of correlation are presented in Table 4.5. For most of the characters genotypic correlation was higher in magnitude than the corresponding phenotypic correlation values and the result are presented below:

Seed yield had positive significant correlation with 100-seed weight ($r_p = 0.272$; $r_g = 0.452$) at both level, whereas, with days to 50 % flowering noted significant negative correlation ($r_p = -0.135$; $r_g = -0.310$) at both the levels. The association between width of leaf blade ($r_p = -0.017$; $r_g = 0.215$), plant population ($r_p = 0.026$; $r_g = 0.181$) and oil content ($r_p = 0.088$; $r_g = 0.150$) with seed yield was positively significant at genotypic level and with plant height, negatively significant ($r_p = -0.080$; $r_g = -0.158$) at genotypic level.

Days to 50 % flowering had a significant positive correlation with plant height ($r_p = 0.189$; $r_g = 0.225$) and hull content ($r_p = 0.281$; $r_g = 0.371$), however, days to 50% flowering had significant positive correlation with width of leaf blade ($r_g = 0.199$), plant population ($r_g = 0.452$), number of capitula per plant ($r_g = 0.148$), number of seeds per capitulum ($r_g = 0.176$) and oil content ($r_g = 0.218$) at genotypic level only. On the other hand; it had negative significant correlation with length of leaf blade ($r_p = -0.475$; $r_g = -0.025$) and 100-seed weight ($r_p = -0.217$; $r_g = -0.336$).

Plant height had significant positive association with length of leaf blade ($r_p = 0.086$; $r_g = 0.983$) at genotypic level only. However, it had significant negative correlation with 100-seed weight ($r_p = -0.224$; $r_g = -0.170$).

Number of primary branches was significant positive correlation with length of leaf blade ($r_g = 0.151$), width of leaf blade ($r_g = 0.159$) and number of seeds per

capitulum ($r_g = 0.140$) at genotypic level only and significant negative correlation with plant population ($r_g = -0.549$) at genotypic level only.

Length of leaf blade had showed significant negative correlation with number of seeds per capitulum ($r_p = -0.135$; $r_g = -1.045$) at both levels. However it had significant negative correlation at genotypic level with 100-seed weight ($r_p = -0.120$; $r_g = -0.356$), diameter of main capitulum ($r_p = -0.075$; $r_g = -0.409$) and plant population ($r_p = -0.003$; $r_g = -0.467$). On the other hand, it had significant positive correlation with number of capitula per plant ($r_p = -0.012$; $r_g = -0.155$) at genotypic level only.

Width of leaf blade had significant positive correlation with number of capitulum per plant ($r_p = 0.225$; $r_g = 0.418$) at both phenotypic and genotypic levels. However, it had positive and significant correlation with plant population ($r_g = 0.305$), number of seeds per capitulum ($r_g = 0.133$) and 100-seed weight ($r_g = 0.381$),

Plant population recorded significant positive correlation with number of capitula per plant ($r_g = 0.262$), 100-seed weight ($r_g = 0.211$), hull content ($r_g = 0.183$) and oil content ($r_g = 0.277$) at genotypic levels only.

Number of capitula per plant had significant negative correlation with hull content ($r_g = -0.157$) at genotypic level only.

Diameter of main capitulum had positive significant correlation with 100-seed weight ($r_p = 0.135$; $r_g = 0.146$) and negative significant correlation with oil content ($r_p = -0.134$; $r_g = -0.199$) at both levels.

Number of seeds per capitulum had positive significant correlation with oil content ($r_g = 0.133$) at genotypic level only.

Hull content had positive significant correlation with oil content ($r_p = 0.281$; $r_g = 0.371$) at both levels.

In this study seed yield had significant positive correlation with width of leaf blade, plant population, 100-seed weight and oil content. Same finding were also revealed by Kubsad *et al.* (2000), Anjani (2005), Diwakar *et al.*, (2006) and Mahasi *et al.*, (2006) for 100-seed weight.

Seed yield was significant and positive association with oil content was also noted by Anjani (2005).

Seed yield had negatively correlated with plant height and days to 50% flowering, negative correlation was reported by Diwakar *et al.*, (2006) and Khoshnoud and Carapetian (2006).

4.5 Path coefficient analysis

Path- coefficient analysis is a tool to partition the observed correlation coefficient into direct and indirect effects of yield components on yield. Path analysis differ from simple correlation in that it point out the cause and their relative importance whereas, the latter measure simply the mutual association ignoring the causation.

To measure the direct and indirect effects, Lenka and Mishra (1973) used the following scale in rice. The same scale given below is used in the present investigation too.

Rating scale based on path coefficient

Value of direct and indirect effect	Rate of scale
0.00 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Moderate
0.30 to 0.99	High
> 1.00	Very high

Table 4.6 : Genotypic path coefficient of seed yield contributing characters in Safflower

Characters	DF	PH	PB	LLB	WLB	PP	CP	DMC	NSC	HSW	HC (%)	OC (%)
DF	-0.336	-0.013	0.001	0.014	0.059	0.053	-0.028	-0.002	-0.009	-0.067	-0.059	0.007
PH	-0.076	-0.056	0.005	-0.029	-0.017	0.012	-0.001	0.016	-0.002	-0.045	-0.006	0.042
PB	-0.007	-0.005	0.048	-0.005	0.047	-0.064	-0.014	0.012	-0.007	0.016	0.014	0.017
LLB	0.160	-0.055	0.007	-0.030	0.165	-0.404	-0.029	-0.055	0.050	-0.071	-0.008	0.144
WLB	-0.067	0.003	0.008	-0.016	0.298	0.036	-0.079	-0.004	-0.006	0.076	0.001	-0.035
PP	-0.152	-0.006	-0.026	0.104	0.091	0.116	-0.049	-0.012	0.003	0.042	-0.028	0.098
CP	-0.050	0.000	0.004	-0.005	0.125	0.031	-0.188	0.004	0.001	-0.004	0.024	0.004
DMC	0.006	-0.007	0.004	0.012	-0.008	-0.010	-0.005	0.134	-0.003	0.029	-0.005	-0.071
NSC	-0.059	-0.002	0.007	0.031	0.040	-0.007	0.005	0.009	-0.048	0.012	-0.020	0.047
HSW	0.113	0.013	0.004	0.011	0.114	0.025	0.004	0.020	-0.003	0.201	-0.001	-0.046
HC(%)	-0.132	-0.002	-0.005	-0.002	-0.002	0.021	0.030	0.004	-0.006	0.002	-0.150	0.131
OC(%)	-0.073	-0.007	0.002	-0.012	-0.030	0.032	-0.002	-0.027	-0.006	-0.026	-0.056	0.354

Residual effect = 0.6150

Note: Bold figure are the direct effect and the off diagonals are indirect effects.

DF= Days to 50% flowering; PH= Plant height; PB = Number of primary branches / plant; LLB = Length of leaf blade / plant; WLB = Width of leaf blade / plant ; PP = Number of plant / m² ; CP = Number of capitula / plant; DMC= Diameter of main capitulum / plant; NSC = Number of seeds / capitulum; HSW= 100-seed weight; HC = Hull content; OC= Oil content.

The direct and indirect effects of different traits on yield are given in Table 4.6.

At genotypic level, oil content exhibited the highest positive direct effect (0.354), followed by width of leaf blade (0.298) and 100-seed weight (0.201). Characters, diameter of main capitulum (0.134) and plant population (0.116) exhibited low direct effects on seed yield per plant. However, highest negative direct effects were obtained by days to 50% flowering (-0.336). Followed by number of capitula per plant (-0.188), hull content (-0.150), plant height (-0.056), number of seeds per capitulum (-0.048) and length of leaf blade (-0.030).

The results of positive direct effect indicated that characters namely, oil content had a significant and positive association with seed yield. Whereas, in case of the negative direct effects days to 50% flowering also exhibited negative association with seed yield.

The indirect effects on seed yield per plant at genotypic level assessed by different characters through different traits are presented below in Table 4.6

4.5.1 Days to 50 per cent flowering:

The character days to 50 per cent flowering showed positive indirect effect on seed yield through width of leaf blade (0.059), plant population (0.053), length of leaf blade (0.014), oil content (0.007) and number of primary branches per plant (0.001) and negative indirect effect *via.*, followed by 100-seed weight (-0.067), hull content (-0.059), number of seed per capitulum (-0.009), oil content (-0.007) and diameter of main capitulum (-0.002).

4.5.2 Plant height (cm):

Plant height showed positive indirect effect on seed yield *via.*, oil content (0.042) followed by diameter of main capitulum (0.016), plant population (0.012) and primary branches (0.005). It showed negative indirect effect through days 100-seed weight (-0.045) followed by length of leaf blade (-0.029), width of leaf blade (-0.017), hull content (-0.006), number of seeds per capitulum (-0.002), number of capitula per plant (-0.001).

4.5.3 Number of primary branches per plant:

Number of primary branches showed positive indirect effect on seed yield *via.*, width of leaf blade (0.047) followed by oil content (0.017), 100-seed weight (0.016), hull content (0.014), diameter of main capitulum (0.012). It showed negative indirect effect through plant population (-0.064) followed by number of capitula per plant (-0.014), number of seeds per capitulum (-0.007), plant height (-0.005) and length of leaf blade (-0.005).

4.5.4 Length of leaf blade:

Length of leaf blade showed positive indirect effect on seed yield *via.*, width of leaf blade (0.165) followed by oil content (0.144), number of seed per capitulum (0.050) and number of primary branches (0.007). It showed negative indirect effect through plant population (-0.404), 100-seed weight (-0.071), diameter of main capitulum (-0.055) and plant height (-0.055), number of capitula per plant (-0.029) and hull content (-0.008).

4.5.5 Width of leaf blade:

Width of leaf blade showed positive indirect effect on seed yield *via.*, 100-seed weight (0.076) followed by plant population (0.036), number of primary

branches (0.008), plant height (0.003), hull content (0.001). It showed negative indirect effect through number of capitula per plant (-0.079), oil content (-0.035), length of leaf blade (-0.016), number of seed per capitulum (-0.006), diameter of main capitulum (-0.004).

4.5.6 Plant population:

Plant population showed positive indirect effect on seed yield *via.*, length of leaf blade (0.104) followed by oil content (0.098), width of leaf blade (0.091), 100-seed weight (0.042), number of seed per capitulum (0.003). It showed negative indirect effect through number of capitula per plant (-0.049) hull content (-0.028), number of primary branches (-0.026), diameter of main capitulum (-0.012) and plant height (-0.006).

4.5.7 Number of capitula per plant:

Number of capitula per plant showed positive indirect effect on seed yield *via.*, Width of leaf blade (0.125), plant population (0.031), hull content (0.024), number of primary branches (0.004), diameter of main capitulum (0.004),oil content and number of seeds per capitulum (0.001). It recorded negative indirect effect through days to 50% flowering (-0.050), length of leaf blade (-0.005) and 100-seed weight (-0.004).

4.5.8 Diameter of main capitulum:

Diameter of main capitulum recorded positive indirect effect on seed yield *via.* 100-seed weight (0.029), length of leaf blade (0.012), days to 50% flowering (0.006) and number of primary branches (0.004). It recorded negative indirect effect through oil content (-0.071), plant population (-0.010), width of leaf blade (-0.008), plant height (-0.007), number of capitula per plant (-0.005), hull content (-0.005) and number of seeds per capitulum (-0.003).

4.5.9 Number of seeds per capitulum:

Number of seed per capitulum showed positive indirect effect on seed yield *via.*, oil content (0.047) followed by width of leaf blade (0.040) and length of leaf blade (0.031), 100-seed weight (0.012), diameter of main capitulum (0.009), number of primary branches per plant (0.007) and number of capitula per plant (0.005). It recorded negative indirect effect through number of seeds per capitulum (-0.059), hull content (-0.020), plant population (-0.007) and plant height (-0.002).

4.5.10 100-seed weight:

The character 100-seed weight showed positive indirect effect on seed yield *via.*, width of leaf blade (0.114), days to 50% flowering plant (0.113), plant population (0.025), diameter of main capitulum (0.020), plant height (0.013), number of primary branches (0.004) and number of capitula per plant (0.004). It showed negative indirect effect through oil content (-0.046), number of seeds per capitulum (-0.003) and hull content (-0.001).

4.5.11 Hull content (%):

Hull content showed positive indirect effect on seed yield *via.* Oil content (0.131), number of capitula per plant (0.030), plant population (0.021), diameter of main capitulum (0.004) and 100-seed weight (0.001). It showed negative indirect effect through days to 50% flowering, number of seed per capitulum (-0.006), number of primary branches per plant (-0.005), plant height (-0.002), length of leaf blade (-0.002) and width of leaf blade (-0.002).

4.5.12 Oil content (%):

The character oil content showed positive indirect effect on seed yield *via.*, Plant population (0.032) and number of primary branches per plant (0.002). It recorded *via.*,

days to 50% flowering (-0.073), hull content (-0.056), width of leaf blade (-0.030), diameter of main capitulum (-0.027), 100-seed weight (-0.026), length of leaf blade (-0.012), plant height (-0.007), number of seeds per capitulum (-0.006) and number of capitula per plant (-0.002).

In the present study path coefficient analysis was carried out by using genotypic correlation coefficient and taking the seed yield as the dependent variable and the rest of the yield attributing characters as the independent variables.

Path coefficient analysis of different characters contributing towards seed yield revealed that oil content had highest positive direct relationship with seed yield followed by width of leaf blade, 100-seed weight, diameter of main capitulum, plant population and number of primary branches per plant.

Characters, oil content, width of leaf blade, 100-seed weight and plant population exhibited significant positive correlation with seed yield indicating the true relationship among these traits. Which indicate that the direct selection for these characters is likely to be effective in increasing seed yield. The present investigation confirmed with result obtained by Topal *et al.* (2010), Sreenivasa *et al.* (2011) and Jagtap *et al.* (2012) for direct effect of oil content on seed yield. Direct effect of 100-seed weight on seed yield was also reported by Mathur *et al.* (1976), Thombre and Joshi (1981), Jadhav *et al.* (1992), Reddy *et al.* (1992), Patil and Deshmukh (1998), Mahasi *et al.* (2006) and Sreenivasa *et al.* (2011).

4.6 Genetic divergence

Careful selection of parents for hybridization programme will decide the extent of possible improvement in the genotypes under consideration. Improvement is

primarily depends on the diversity of the parents. Hence an attempt was made to classify the genotypes into different clusters by D^2 analysis.

The existence of genetic divergence among the 150 safflower genotypes was examined by employing Mahalanobi's D^2 statistic. The clustering pattern of 150 genotypes on the basis of D^2 analysis has been presented in Table 4.7. The entries are grouped into sixteen clusters. The highest number of clusters appeared in cluster IX, which possessed 17 genotypes, namely, GMU-3624, GMU-3631, GMU-3632, GMU-3653, GMU-3682, GMU-3683, GMU-3693, GMU-3694, GMU-3699, GMU-3703, GMU-3720, GMU-3722, GMU-3726, GMU-3749, GMU-3754, GMU-3781 and Manjira. The second highest number of entries were found in cluster V, which was comprised of 16 genotypes.viz.,GMU-3625,GMU-3628,GMU-3635,GMU-3649,GMU-3660,GMU-3667,GMU-3678,GMU-3711,GMU-3715,GMU-3716,GMU-3719,GMU-3738,GMU- 3750,GMU-3769,GMU-3792,GMU-3796. Cluster X comprised of 15 genotypes, namely, GMU-3641, GMU-3646, GMU-3647, GMU-3651, GMU-3661, GMU-3696, GMU-3706, GMU-3708, GMU-3734, GMU-3736, GMU-3743, GMU-3748, GMU-3764, GMU-3775 and GMU-3800. Cluster II had 14 genotypes viz ., GMU-3644,GMU-3654,GMU-3656,GMU-3659,GMU-3670,GMU-3691,GMU-3692,GMU-3702,GMU-3744,GMU-3746, GMU-3768,GMU-3780,GMU-3798, A-1. Cluster VIII comprised of 11 genotypes, namely, GMU-3626, GMU-3658, GMU-3666, GMU-3684, GMU-3757, GMU-3765, GMU-3770, GMU-3772, GMU-3773, GMU-3782 and GMU-3793. Cluster III comprised of 10 genotypes, namely, GMU-3639, GMU-3673, GMU-3723, GMU-3725, GMU-3729, GMU-3733, GMU-3737, GMU-3745, GMU-3747 and GMU-3756. Cluster VII consisted of 9 genotypes, GMU-3637, GMU-3700, GMU-3704, GMU-3713, GMU-3753, GMU-3766, GMU-3777, GMU-

Table 4.8 : Average intra-and inter-cluster distances between five cluster in Safflower

Cluster NO.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	6.315 (2.513)	14.077	13.778	16.974	11.916	30.980	22.353	18.447	13.410	20.016	19.123	18.096	18.147	24.700	24.039	28.206
II	3.752	6.895 (2.626)	11.431	8.856	8.231	12.131	11.628	7.252	7.728	11.710	22.924	15.031	15.233	12.766	11.943	11.235
III	3.712	3.381	6.943 (2.635)	14.025	8.497	15.968	7.382	10.407	6.620	8.242	15.405	14.258	15.944	15.936	12.489	16.451
IV	4.120	2.976	3.745	7.317 (2.705)	14.025	24.059	17.994	7.064	13.278	12.383	16.564	10.246	21.068	10.634	17.598	8.265
V	3.452	2.869	2.915	3.745	7.038 (2.653)	16.337	6.630	12.730	8.708	7.958	17.131	9.834	11.971	20.079	9.941	13.853
VI	5.566	3.483	3.996	4.905	4.042	7.650 (2.766)	15.069	16.548	9.535	11.397	27.541	26.512	14.561	20.793	17.313	21.622
VII	4.728	3.410	2.717	4.242	2.575	3.882	6.553 (2.560)	11.269	8.696	11.669	14.478	15.397	12.837	22.080	11.539	16.265
VIII	4.295	2.693	3.226	2.658	3.568	4.068	3.357	6.661 (2.581)	10.588	13.373	18.352	13.184	16.321	8.934	9.696	8.862
IX	3.662	2.780	2.573	3.644	2.951	3.088	2.949	3.254	6.775 (2.603)	6.563	14.348	10.233	8.538	13.905	10.426	17.808
X	4.474	3.422	2.871	3.519	2.821	3.376	3.416	3.657	2.562	6.744 (2.597)	22.335	11.764	16.719	16.499	12.623	12.027
XI	4.373	4.788	3.925	4.070	4.319	5.248	3.805	4.284	3.788	4.726	8.317 (2.884)	16.630	10.588	22.155	20.358	21.762
XII	4.254	3.877	3.776	3.201	3.136	5.149	3.924	3.631	3.199	3.430	4.078	7.349 (2.711)	15.000	9.535	8.988	11.648
XIII	4.260	3.903	3.993	4.590	3.460	3.816	3.583	4.040	2.922	4.089	3.254	3.873	7.935 (2.817)	18.593	15.108	17.330
XIV	4.970	3.573	3.992	3.261	4.481	4.560	4.699	2.989	3.729	4.062	4.707	3.088	4.312	7.144 (2.673)	12.531	9.229
XV	4.903	3.456	3.534	4.195	3.153	4.161	3.397	3.114	3.229	3.553	4.512	2.998	3.887	3.540	7.840 (2.800)	10.608
XVI	5.311	3.352	4.056	2.875	3.722	4.650	4.033	2.977	4.220	3.468	4.665	3.413	4.163	3.038	3.257	7.300 (2.702)

Main diagonal (bold)= intra-cluster D and D² value; upper diagonal = inter-cluster D² value; lower diagonal = inter-cluster D value.

3778 and GMU-3794. Cluster IV comprised of 8 genotypes viz., GMU-3652, GMU-3681, GMU-3690, GMU-3760, GMU-3762, GMU-3776 and GMU-3791, GMU-3799. Cluster XII consisted of 7 genotypes, namely, GMU-3634, GMU-3675, GMU-3677, GMU-3709, GMU-3761, GMU-3786 and GMU-3789. Cluster XIII comprised of 7 genotypes viz., GMU-3633, GMU-3638, GMU-3640, GMU-3679, GMU-3698, PBNS-12 and PBNS-40. Cluster XIV consisted of 7 genotypes, namely, GMU-3662, GMU-3663, GMU-3664, GMU-3771, GMU-3774, GMU-3783 and GMU-3790. Cluster XVI consisted of 6 genotypes viz., GMU-3645, GMU-3680, GMU-3686, GMU-3687, GMU-3759 and GMU-3787. Cluster XI comprised of 5 genotypes, namely, GMU-3636, GMU-3676, GMU-3718, GMU-3721 and GMU-3750. Cluster VI also consisted of 5 genotypes, namely, GMU-3621, GMU-3642, GMU-3643, GMU-3671 and JSF-1. Cluster I comprised of 4 genotypes viz., GMU-3701, GMU-3727, GMU-3730, GMU-3735.

4.6.1 Intra and inter cluster distances

The estimates of intra and inter cluster distances represented by D^2 values have been presented in Table 4.8. The maximum intra-cluster distance was obtained for cluster XI (8.317) followed by cluster XIII (7.935), cluster XV (7.840), cluster VI (7.650). The lowest intra-cluster was shown by cluster I (6.315), cluster VII (6.553). The intra-cluster distance varied from 6.315 to 8.317, the maximum being for cluster XI (GMU-3636, GMU-3676, GMU-3718, GMU-3721, GMU-3750), which comprised of 5 genotypes. The highest inter-cluster D^2 values was observed between cluster I and cluster VI (30.980) followed by cluster I and cluster XVI (28.206), cluster VI and cluster XI (27.541), cluster VI and cluster XII (26.512), cluster I and cluster XIV (24.700). The lowest inter cluster was found between cluster III and cluster IX (6.620).

followed by cluster V and cluster VII (6.630), cluster IX and cluster X (6.653). The genotypes from above different clusters may be utilized as parents in crossing programme to isolate desirable segregants for seed yield and other important traits.

4.6.2 Cluster means

The intra-cluster group means for 13 characters presented in Table 4.9 revealed marked difference between the 13 clusters in respect of cluster means for different characters.

The cluster mean for days to 50 per cent flowering was highest for cluster XIV (103.42 days) followed by cluster VIII (102.72 days), cluster XVI (102.66 days), cluster IV (102.56 days). The lowest cluster mean showed by cluster III (99.90 days). In figure 4.10 the graph of cluster mean for days to 50 per cent flowering.

In case of character, plant height, the highest cluster mean was obtained for cluster VIII (94.45) followed by cluster IV (91.31), cluster VII (89.05), cluster XIV (88.92) and cluster XI (79.90) showed lowest cluster mean value. In figure 4.11 the graph of cluster mean for plant height.

The highest cluster mean for number of primary branches per plant was observed for cluster XV (18.55) followed by cluster XIII (17.85), cluster XVI (17.41) and cluster VI (16.60). The lowest cluster mean was observed for cluster IV (10.06). In figure 4.12 the graph of cluster mean for number of primary branches per plant.

Cluster XV (10.00) showed the highest cluster mean for length of leaf blade followed by cluster XII (9.21), cluster XIII (8.92) and cluster IX (8.67). The lowest cluster mean was observed for cluster IV (7.00). In figure 4.13 the graph of cluster mean for length of leaf blade.

Table 4.9: Cluster mean for 13 quantitative characters in Safflower

Cluster No.	DF	PH	PB	LLB	WLB	PP	CP	DMC	NSP	HSW	HC (%)	OC (%)	SY
I	100.12	82.87	10.25	7.75	4.33	14.50	19.37	2.12	19.50	4.52	20.75	27.70	435.63
II	102.07	83.50	13.78	7.60	3.83	13.85	26.32	2.10	20.71	4.77	20.75	31.83	619.83
III	99.90	83.80	12.65	7.80	3.48	15.00	24.70	1.86	19.30	4.76	19.75	31.30	698.51
IV	102.56	91.31	10.06	7.00	3.28	12.87	22.06	1.70	19.62	4.10	20.25	31.94	485.13
V	101.40	83.43	15.93	7.12	3.52	12.03	18.71	1.94	19.31	4.97	20.03	31.12	768.28
VI	101.40	80.60	16.60	8.00	4.67	14.60	29.30	1.63	17.60	5.60	20.00	31.61	932.21
VII	100.50	89.05	14.44	8.05	3.48	13.27	23.66	1.98	19.00	4.59	17.50	31.64	959.46
VIII	102.72	94.45	13.40	7.50	3.80	14.27	23.31	1.98	19.72	4.74	20.22	31.03	673.91
IX	101.29	83.32	10.38	8.67	4.12	13.23	24.82	1.85	20.00	5.01	19.41	30.65	737.04
X	100.80	86.20	11.83	8.50	4.09	14.06	18.36	1.64	19.53	4.61	20.73	31.96	831.23
XI	100.40	79.90	14.00	8.20	3.95	12.00	23.40	1.69	21.60	4.31	15.50	28.81	470.38
XII	100.78	84.28	12.42	9.21	3.43	12.42	20.57	1.77	20.28	4.21	20.92	31.13	646.55
XIII	102.21	86.28	17.85	8.92	4.10	12.71	25.00	1.81	19.42	5.10	16.50	28.16	688.09
XIV	103.42	88.92	15.00	8.14	4.19	12.85	26.78	1.75	19.71	4.29	20.78	32.39	608.46
XV	100.16	86.05	18.55	10.00	4.00	12.27	22.94	1.96	19.22	4.71	20.61	32.57	687.86
XVI	102.66	86.91	17.41	8.00	3.29	14.41	21.83	1.80	18.50	4.13	20.25	32.18	576.22

The highest cluster mean for width of leaf blade was obtained for cluster VI (4.67) followed by cluster I (4.33), cluster XIV (4.19) and cluster IX (4.12). The lowest cluster mean was observed for cluster IV (3.28). In figure 4.14 the graph of cluster mean for width of leaf blade.

Cluster III (15.00) showed the highest mean for plant population followed by cluster VI (14.60), cluster I (14.50), cluster XVI (14.41). The lowest cluster mean value was obtained for cluster XI (12.00). In figure 4.15 the graph of cluster mean for plant population.

The highest cluster mean for number of capitula per plant was obtained for cluster VI (29.30) followed by cluster XIV (26.78), cluster II (26.32) and cluster XIII (25.00). The lowest cluster mean was obtained for cluster X (18.36). In figure 4.16 the graph of cluster mean for number of capitulum per plant.

The highest cluster mean for diameter of main capitulum was recorded for cluster I (2.12) followed by cluster II (2.10), cluster VII (1.98) and cluster VIII (1.98). Cluster VI recorded lowest cluster mean (1.63) for diameter of main capitulum. In figure 4.17 the graph of cluster mean for diameter of main capitulum.

Cluster XI (21.60) showed the highest mean for number of seeds per capitulum followed by cluster II (20.71), cluster XII (20.28) and cluster IX (20.00). The lowest cluster mean was obtained for cluster VI (17.60). In figure 4.18 the graph of cluster mean for number of seeds per capitulum.

The highest cluster mean for character 100-seed weight was observed by cluster VI (5.60) followed by cluster XIII (5.10) and cluster IX (5.01). The lowest cluster mean value was obtained for cluster IV (4.10). In figure 4.19 the graph of cluster mean for 100-seed weight.

The highest cluster mean for hull content was recorded by cluster XII (20.92) followed by cluster XIV (20.78), cluster II (20.75) and cluster I (20.75). The lowest cluster mean value recorded for cluster XI (15.50). In figure 4.20 the graph of cluster mean for hull content.

Cluster XV (32.57) showed the highest mean for oil content followed by cluster XIV (32.39), cluster XVI (32.18) and cluster X (31.96). The lowest cluster mean value obtained for cluster I (27.70). In figure 4.21 the graph of cluster mean for oil content.

The highest cluster mean for seed yield was observed by cluster VII (959.46) followed by cluster VI (932.21), cluster X (831.23) and cluster V (768.28). The lowest cluster mean value obtained for cluster I (435.63). In figure 4.22 the graph of cluster mean for seed yield.

Cluster mean for various trait showed that genotypes in cluster XV and cluster VI have highest mean performance for number of primary branches per plant, length of leaf blade, oil content and width of leaf blade, number of capitulum per plant, 100-seed weight, respectively. Genotypes of cluster XIV, VIII, III, I, XI, XII and VII showed highest mean value for days to 50% flowering, plant height, plant population, diameter of main capitulum, number of seeds per capitulum, hull content and seed yield, respectively. GMU- 3713, GMU- 3637, GMU- 3778, GMU-3777 and GMU- 3700 are the highest yielder in cluster VII. Similar findings were reported by Tirkey *et al.*, (2012) for high seed yield in GMU 3494, GMU 3482, GMU 3514 and GMU 3443.

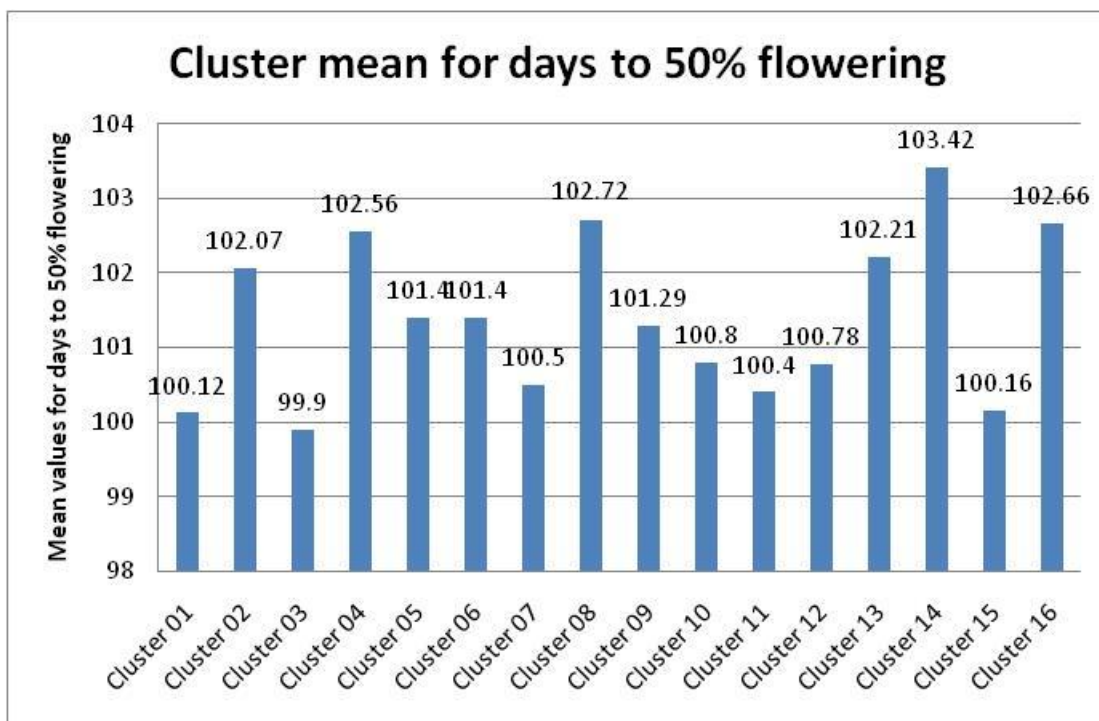


Fig.- 4.10 Cluster mean for days to 50% flowering.

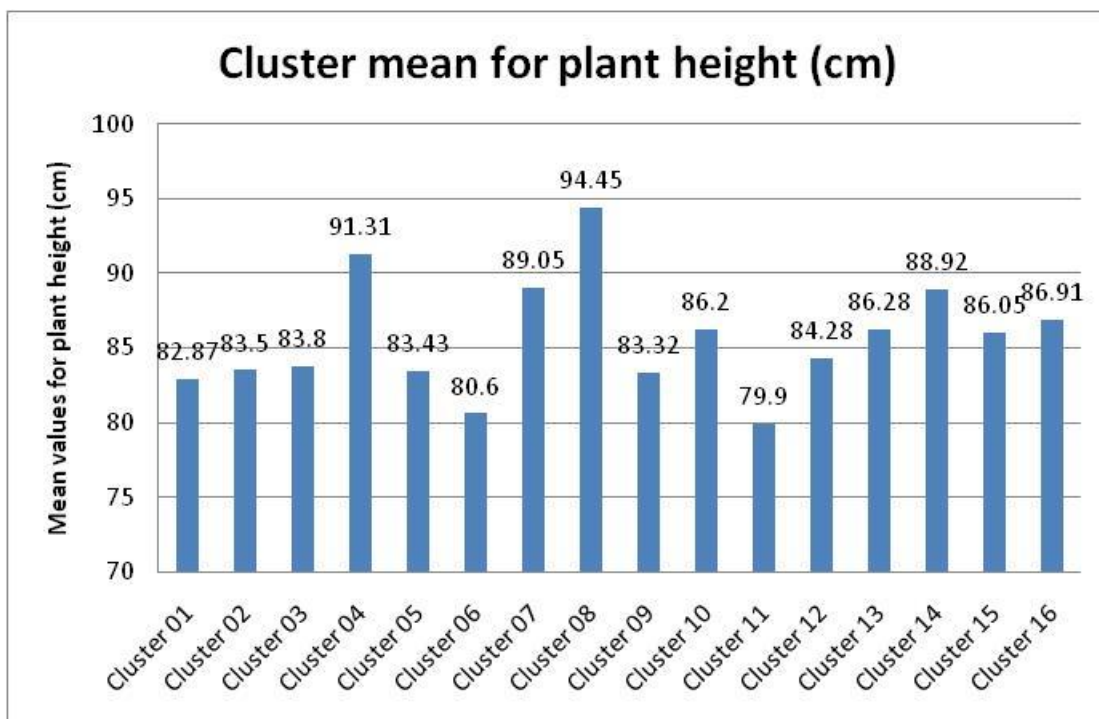


Fig.- 4.11 Cluster mean for plant height (cm).

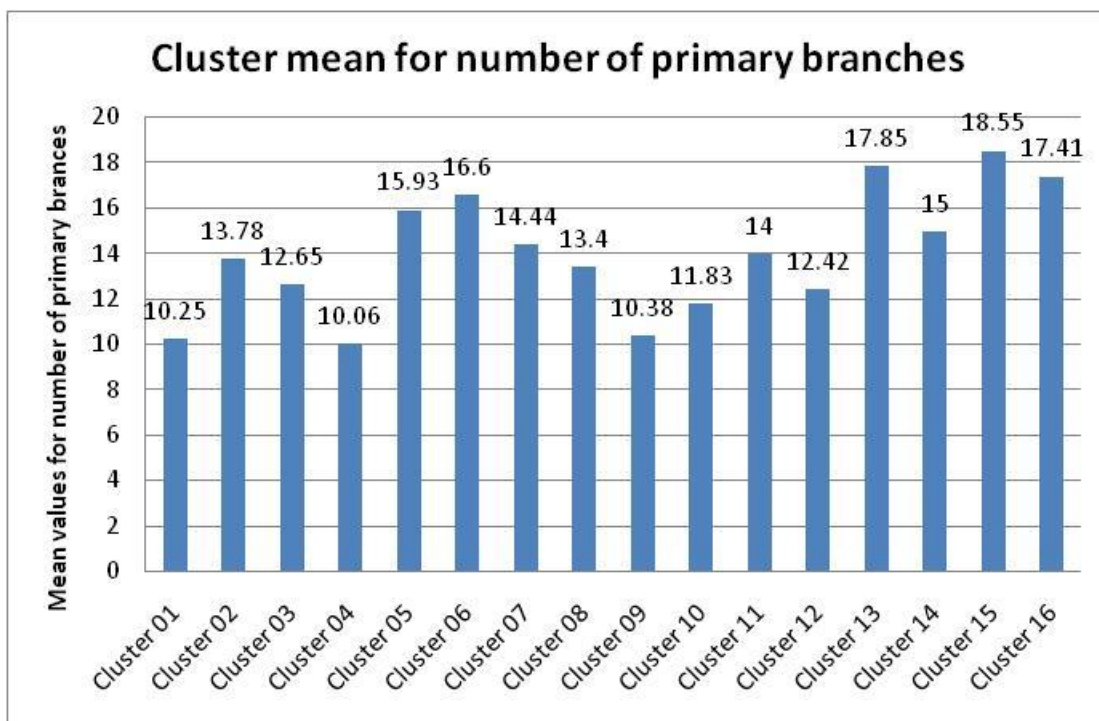


Fig.- 4.12 Cluster mean for number of primary branches

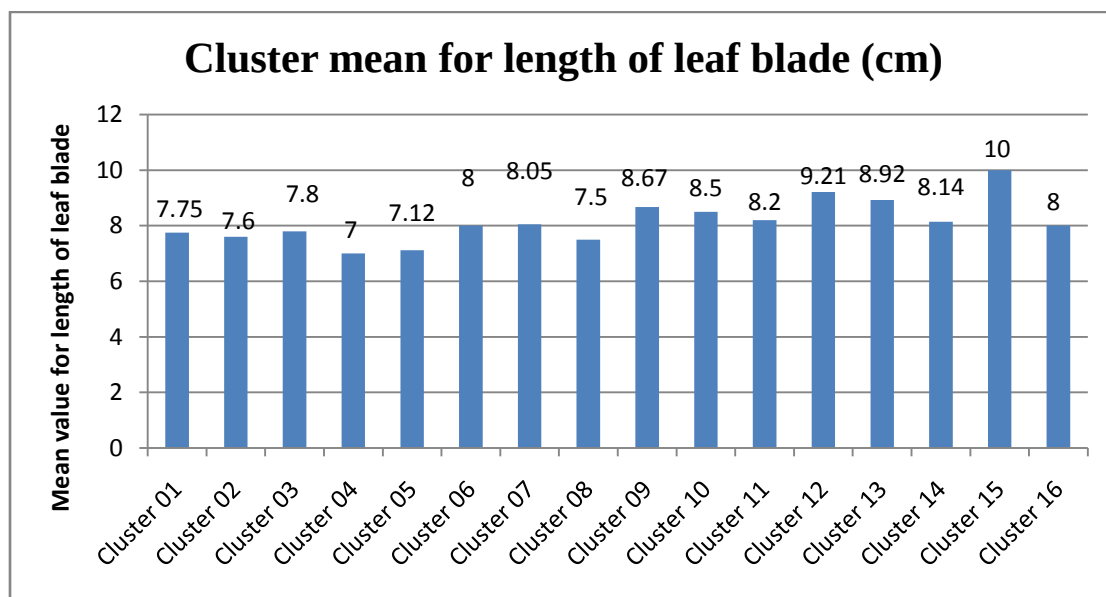


Fig.- 4.13 Cluster mean for length of leaf blade (cm)

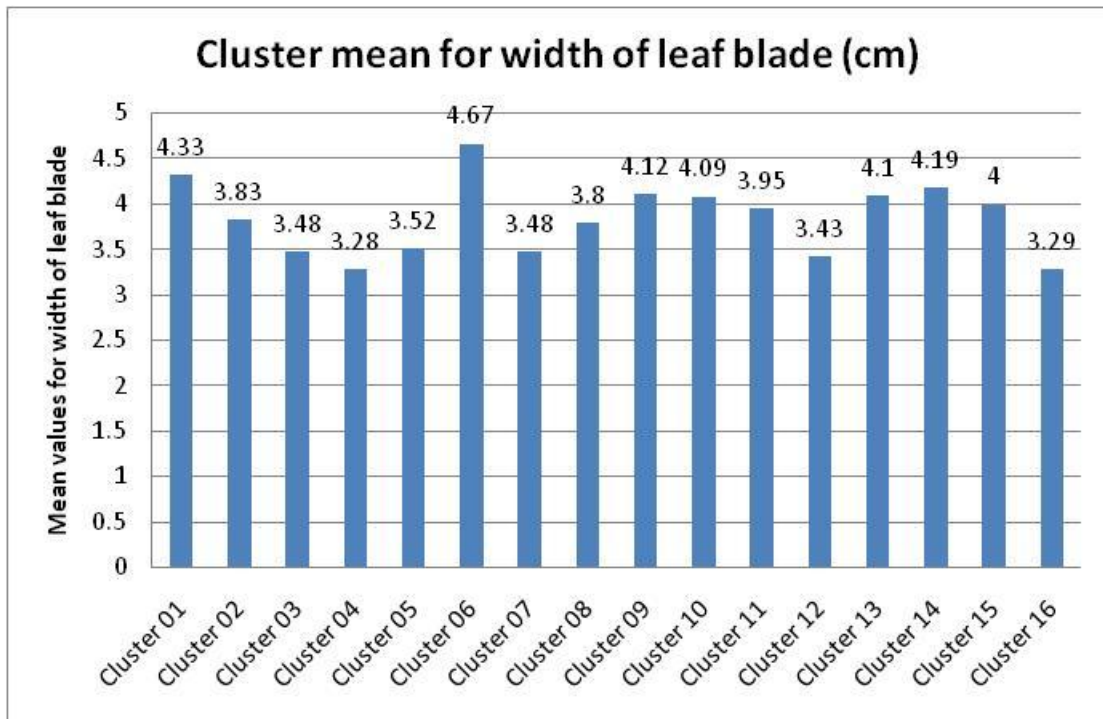


Fig.- 4.14 Cluster mean for width of leaf blade (cm).

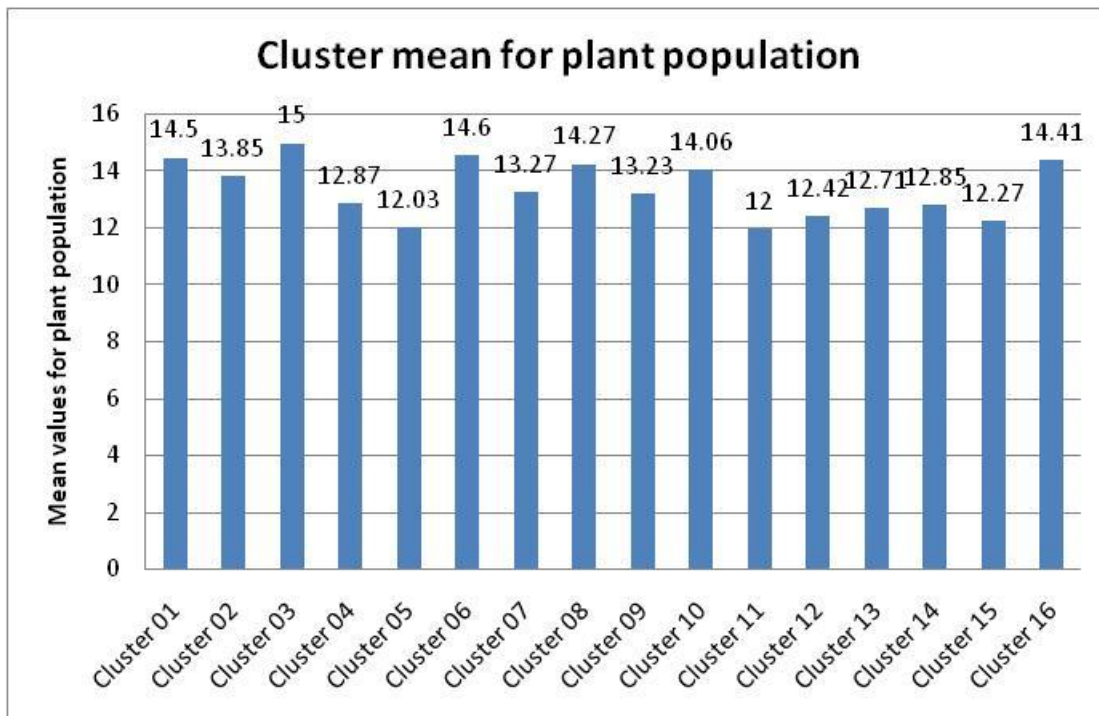


Fig.- 4.15 Cluster mean for plant population

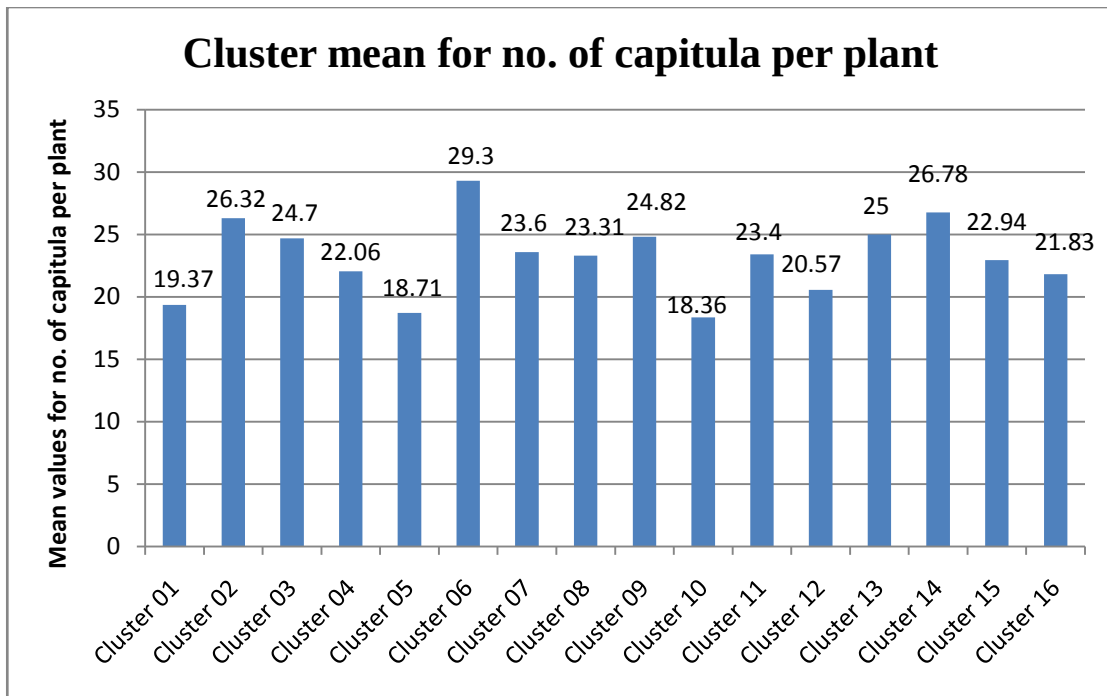


Fig.- 4.16 Cluster mean for no. of capitula per plant.

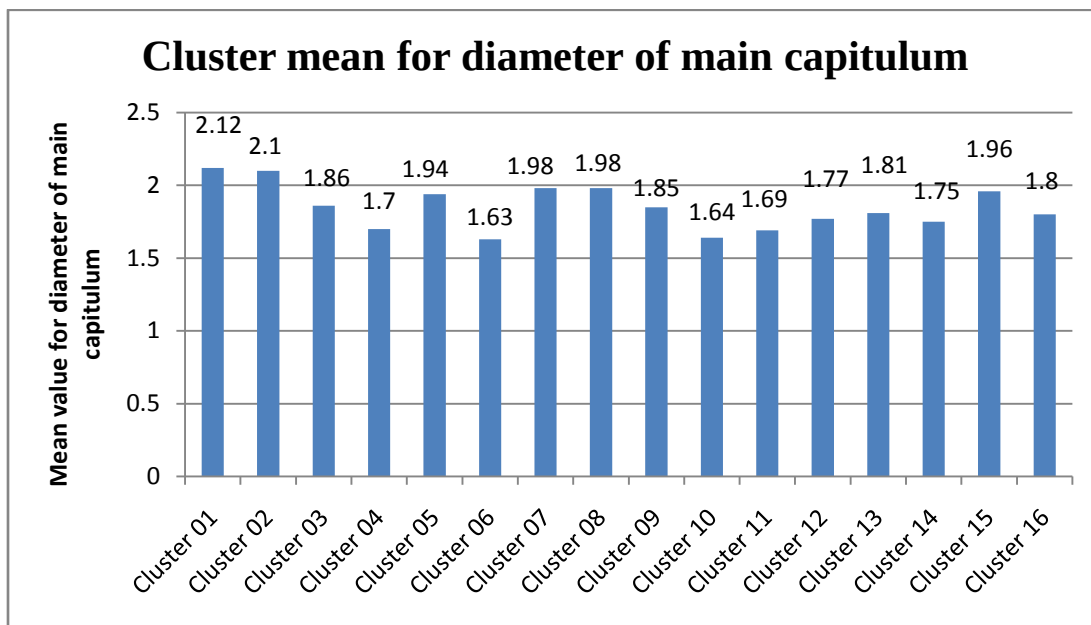


Fig.- 4.17 Cluster mean for diameter of main capitulum

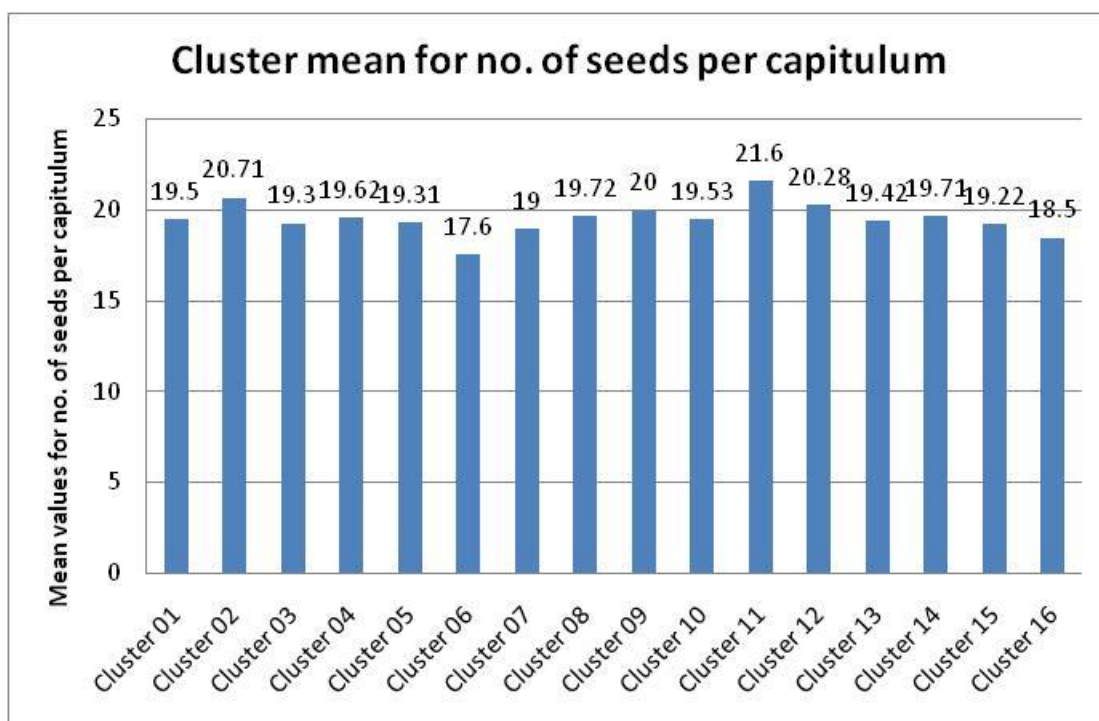


Fig.- 4.18 Cluster mean for no. of seeds per capitulum

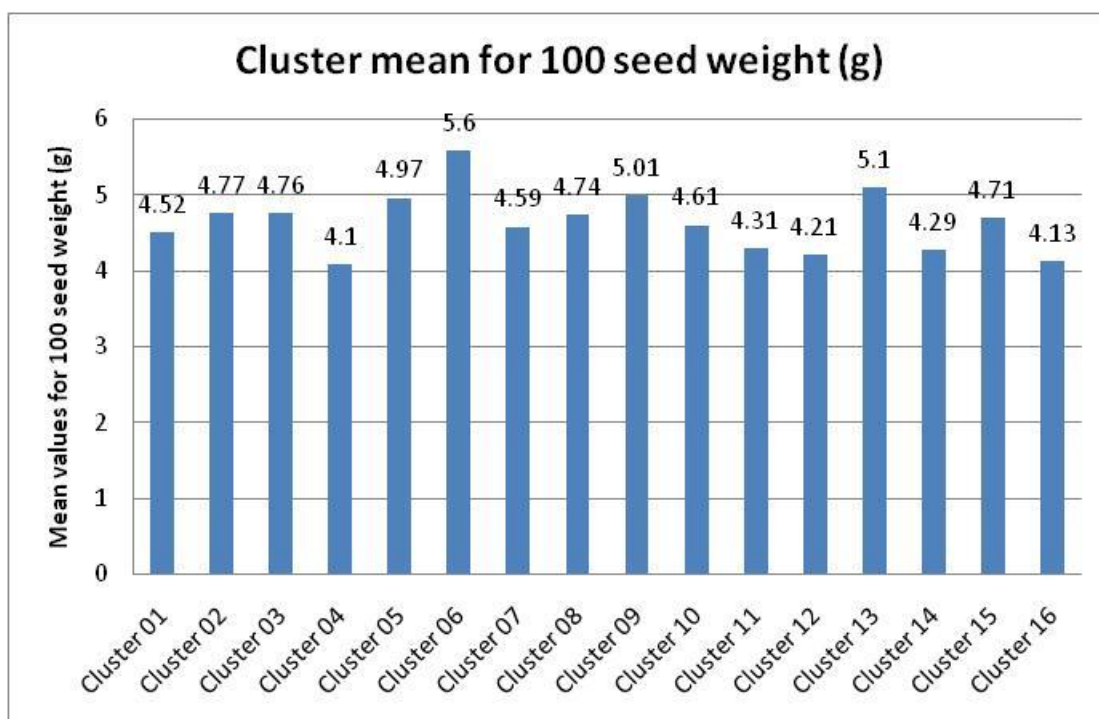


Fig.- 4.19 Cluster mean for 100 seed weight (g)

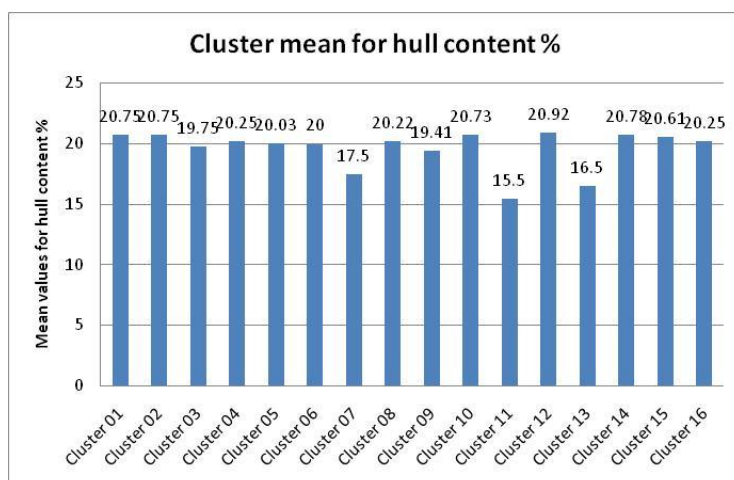


Fig.- 4.20 Cluster mean for hull content %.

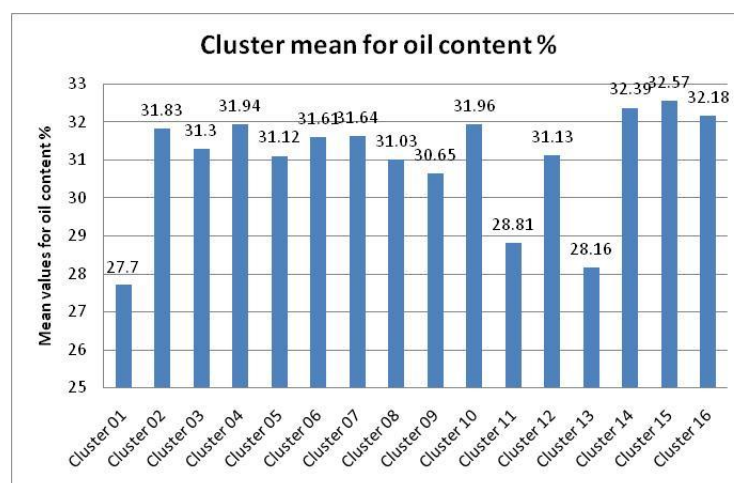


Fig.- 4.21 Cluster mean for oil content %.

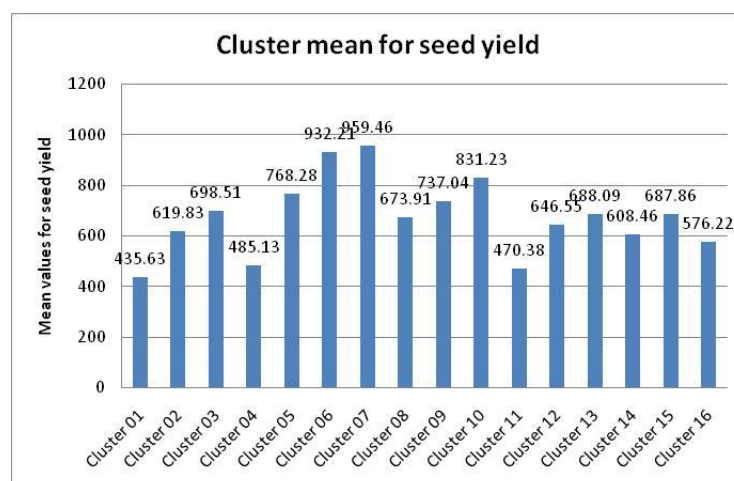


Fig.- 4.22 Cluster mean for seed yield.

***Summary, Conclusions and
Suggestions for Future Work***

CHAPTER-V

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FUTURE WORK

Summary and conclusion

The present investigation “Genetic analysis in safflower (*Carthamus tinctorius* L.)” was carried out during *Rabi* season of 2011-12 at the Research and Instructional Farm of Department of Genetics and Plant breeding, College of Agriculture, IGKV, Raipur (C.G.).

The experimental material comprised of 150 genotypes of safflower including five check varieties viz., A-1, Manjira, PBNS-12, PBNS-20 and JSF-1. The material was grown in Randomized Complete Block Design (RCBD) with two replications.

Analysis of variance revealed that mean sum of squares due to genotypes was significant for all traits except for plant height, number of primary branches, length of leaf blade, plant population and number of seeds per capitulum. Relative high magnitude of phenotypic and genotypic coefficient of variation was maximum for seed yield and number of primary branches per plant. The high magnitude of presence of genotypic coefficient of variation revealed the presence of high genetic variability for the character in the population studied.

High heritability coupled with high genetic advance was observed for number of primary branches indicating that heritability is due to additive gene action and selection based on these characters may be effective. High heritability coupled with moderate genetic advance was observed for plant height, diameter of main capitulum, number of seeds per capitulum and 100-seed weight. It indicates that these characters seems to be more heritable and can be improved by selection. High heritability coupled with low

genetic advance was observed for days to 50% flowering. Moderate heritability coupled with low genetic advance was observed for number of capitulum per plant and Oil content, indicating that this character is influenced by environmental effect and selection would be ineffective.

150 germplasm of safflower were characterized for petal colour, leaf shape, dentation of leaf, spines on leaf and seed colour. All morphological characters showed marked differences in their distribution and amount of variations within them.

Seed yield (kg/ha) had significant positive correlation with 100-seed weight and oil content. The positive correlation suggested that improvement in one will automatically improve the other.

Oil content showed the positive direct effect on seed yield followed by width of leaf blade (0.298) and 100-seed weight (0.201). The study of path analysis revealed that there is no common causal factor that directly influenced seed yield. But up to some extent 100-seed weight and oil content could be used as selection criterion for improvement.

From the results of correlation and path analysis, it was clear that the yield components which were showing significant correlation with the seed yield was mainly due to its direct effects and partially due to indirect effect *via* other characters.

One fifty germplasm of safflower were grouped into sixteen clusters based on D^2 . The cluster XV and cluster VI have highest mean performance for number of primary branches per plant, length of leaf blade, oil content and width of leaf blade, number of capitulum per plant, 100-seed weight, respectively. Inter-cluster distance was recorded highest between cluster I and cluster VI. The least distance was recorded between cluster III and cluster IX. The conclusion drawn by the cluster analysis is that the genotypes from different clusters having maximum inter-cluster distance may be

utilized as parents in crossing programme to isolate desirable segregants. Germplasm/genotypes for seed yield and other important traits were identified most promising for this study based on mean seed yield per se performance and other characters. The progeny should be tested on large scale to develop or evolve a good safflower variety for the state. The promising lines should also be used for hybridization programme.

SUGGESTION FOR FUTURE RESEARCH WORK-

The following suggestions have been made to highlight the future scope of the study.

1. The available genetic variability present in the material may be exploited for the improvement of existing genotypes.
2. On the basis of high heritability and high genetic advance as percentage of mean, it may be suggested that the simple phenotypic selection procedure can be adopted to improve the character viz., number of primary branches per plant.
3. On the basis of correlation and path analysis, 100-seed weight and oil content could be used as a selection criterion for further improvement in seed yield.
4. Morphological characters like petal colour, leaf shape, dentation of leaf, spines of leaf and seed colour may be used as a criterion for identification of genotypes/varieties.
5. For the hybridization programme, the most divergent germplasm should be taken from different clusters on the basis of yield and yield attributing characters.
6. Promising lines identified on the basis of mean per se performance and other character viz., good oil percentage value should be further tested on large scale to develop superior genotypes. The genotypes will be also included in hybridization programme.

Abstract

GENETIC ANALYSIS IN SAFFLOWER (*Carthamus tinctorius* L.)

by

Sourabh Paikara

ABSTRACT

The present investigation was carried out at Research and Instructional Farm Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Viswavidyalaya, Raipur (C.G.) during *rabi* 2011-12. The experiment was conducted in Randomized Complete Block Design with 150 genotypes and two replications for estimation of genetic variability, heritability, genetic advance, correlation, path analysis, genetic divergence and morphological characterization of safflower germplasm.

Analysis of variance revealed significant differences among the genotypes for all the characters except for plant height, number of primary branches, length of leaf blade, plant population and number of seeds per capitulum. The highest magnitude of genotypic variation was observed for number of primary branches per plant and seed yield. High heritability coupled with high genetic advance was observed for number of primary branches indicating that heritability is due to additive gene action and selection based on these characters may be effective.

Correlation coefficient analysis revealed that 100-seed weight and oil content had significant positive association with seed yield. Hence, improvement of seed yield can be achieved by improving these characters.

Path coefficient analysis revealed that plant height, number of primary branches, number of capitula per plant, number of seeds per capitulum showed high to moderate positive direct effects on seed yield, and selection for this character would lead to increase in yield.

Divergence analysis were studied based on Mahalanobi's D^2 statistic, genotypes were grouped into sixteen non-overlapping clusters. Inter-crossing of genotypes from different clusters showing superior mean performance may help in obtaining higher yields.

Morphological characterizations of all 150 genotypes were studied and classified into the different classes *viz.* petal colour, leaf shapes, dentations of leaf, numbers of spines in a leaf and seed colour.

The present investigation revealed that selection for the characters such as seed yield, number of seeds per capitulum, plant height, 100-seed weight, oil content and number of primary branches per plant are important traits to evolve high yielding genotypes of safflower.

Germplasm GMU-3713, GMU-3651, GMU-3637, GMU-3621, GMU- 3726 identified as most promising on the basis of mean seed yield per se performance and other attributing characters.

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Appendix

Appendix : Weekly meteorological data of standard weeks from October to June 2011-12

Week No.	Date	Temperature (°C)		Rainfall (mm)	Relative humidity (%)		Wind velocity (kmph)	Evaporation (mm)	Sun shine (hrs)
		Maximum	Minimum		I	II			
1	Oct 15-21	32.6	20.8	0	90	37	1.7	4.3	9.1
2	22-28	31.8	17.7	0	92	35	1.3	4	8.7
3	29-04	30.8	15.2	0	91	27	1.4	4.2	9
4	Nov 05-11	32.2	15.8	0	90	28	0.8	4	8.1
5	12-18	31.2	15.7	0	88	30	0.9	3.9	8
6	19-25	30.2	15.2	0	87	33	1	3.7	8.9
7	26-02	29.9	14.7	0	88	35	0.6	3.5	7.8
8	Dec 03-09	29.8	13.4	0	89	33	0.6	3.1	6.8
9	10-16	29.3	11.9	0	86	29	0.7	3.1	7.7
10	17-23	28	9.1	0	87	25	0.3	3.3	8.2
11	24-31	27.5	11.5	0	85	36	1.4	3.4	8
12	Jan 01-07	26.3	18.7	34.1	96	72	0.7	12.6	0.9
13	08-14	24.2	11	20.6	94	39	0.6	19.8	6.7
14	15-21	26.9	10.5	0	86	31	1.5	24.4	9
15	22-28	25.7	12.5	0	86	42	0.6	19.9	5.2
16	29-04	25.4	13.1	5.4	87	47	1	18.3	4.5
17	Feb 05-11	29.7	12.4	0	78	27	0.7	26	9.1
18	12-18	30.1	16.2	0	85	44	2.4	26.4	7.9
19	19-25	33.2	14.9	0	78	25	2.2	31.8	9.3
20	26-04	33.5	15.2	0	77	23	2.6	41.3	8.4
21	Mar 05-11	33.6	15.9	0	71	19	3.6	46	8.8
22	12-18	34.6	17.5	0	70	21	3.8	45.8	8
23	19-25	37.9	17.4	0	68	19	2.5	52.2	8.4
24	26-01	38.5	20.1	0	57	16	2.7	51.9	8.1
25	Apr 02-08	39.2	23.5	0	57	21	5.6	65.0	8.3
26	09-15	39.6	23.9	9.2	57	20	6.3	69.8	8.5
27	16-22	40.2	24.8	0	48	16	3.6	66.3	9.4
28	23-29	39.1	25.2	6.6	68	25	5.6	70	8.5
29	30-06	40.9	25.5	0	59	14	5.9	77.5	10.4
30	Mar 07-13	41.1	27.4	0	43	19	4.6	75.3	8.1
31	14-20	43.3	27.6	0	43	13	4.5	85.8	9.4
32	21-27	44.6	28.5	0	34	11	3.7	85.5	8
33	28-03	45.8	28.4	2.2	29	13	5.2	93.6	7.8
34	Jun 04-10	43.4	30.8	0	43	22	8.7	107.9	9
35	11-17	38.3	26.6	103.6	74	48	9.5	68.9	3.9
36	18-24	31	24.2	124.2	89	69	9.1	20.2	1.5