“GENETIC VARIABILITY, PATH COEFFICIENT ANALYSIS AND DIVERSITY IN SUNFLOWER (*Helianthus annuus* L.)”

by

Mr. Lingayat Akshay Sambhaji
(Reg. No. 018/046)

DIVISION OF AGRICULTURAL BOTANY
COLLEGE OF AGRICULTURE, PUNE-411 005

MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI - 413 722, DIST-AHMEDNAGAR
MAHARASHTRA STATE (INDIA)

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A Thesis submitted to the
MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI-413 722, DIST- AHMEDNAGAR,
MAHARASHTRA, INDIA

In partial fulfillment of the requirements for the degree
of

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COLLEGE OF AGRICULTURE, PUNE-411 005

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2020

CANDIDATE’S DECLARATION

I hereby declare that this thesis or part
there of has not been submitted by
me or other person to any
other University or Institute
for a Degree or
Diploma

Place : Pune

Date : / /2020

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Assistant Professor of Plant Physiology,
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CERTIFICATE

This is to certify that the thesis entitled, **“GENETIC VARIABILITY, PATH COEFFICIENT ANALYSIS AND DIVERSITY IN SUNFLOWER [(*HELIANTHUS ANNUUS* L.)]”,** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra) in partial fulfillment of the requirement for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **Mr. LINGAYAT AKSHAY SAMBHAJI** under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been duly acknowledged.

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Place : Pune
Date : / /2020

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Place : Pune
Date : / /2020

(**S. D. Masalkar**)

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Place : **Pune**

Date : **/ /2020**

(Lingayat A. S.)

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LIST OF ABBREVIATIONS

@	:	At the rate
C.D.	:	Critical difference
C.V.	:	Coefficient of variance
cm	:	Centimeters
D	:	Divergence distance
DC	:	Divergence classes
DC_1	:	Divergence class 1
DC_2	:	Divergence class 2
DC_3	:	Divergence class 3
DC_4	:	Divergence class 4
d. f.	:	Degrees of freedom
et al.	:	et all (and others)
etc.	:	Ecetra
F1	:	First filial generation
F2	:	Second filial generation
F3	:	Third filial generation
F4	:	Fourth filial generation
F5	:	Fifth filial generation
Ft.	:	Feet/Foot
g	:	Gram
GA	:	Genetic advance
GCV	:	Genotypic coefficient of variation
h^2 (b.s.)	:	Heritability in broad sense
ha.	:	Hectare
i.e.	:	That is
K	:	Differential constant
Kg	:	Kilo gram
mm	:	Millimeter
No.	:	Number
ha.	:	Hectar
PCA	:	Path coefficient analysis
PCV	:	Phenotypic coefficient of variation
per se	:	Actual
R	:	Residual effect
S.E.	:	Standard error
via	:	Through
viz.,	:	Videlicent (namely)
X	:	General mean
Y	:	Yield

ABSTRACT

"GENETIC VARIABILITY, PATH COEFFICIENT ANALYSIS AND DIVERSITY IN SUNFLOWER (*Helianthus annuus* L.)"

By

MR. AKSHAY SAMBHAJI LINGAYAT

A candidate for the degree
of

MASTER OF SCIENCE (AGRICULTURE)

In

GENETICS AND PLANT BREEDING
2020

Research Guide: Dr. A. B. Rajguru

Department: Agricultural Botany

An experiment entitled, "Genetic Variability, Path Coefficient Analysis and Diversity in Sunflower (*Helianthus annuus* L.)" was carried out at Agricultural Botany Research Farm, College of Agriculture, Pune during *Kharif* season, 2019. The present investigation was undertaken to evaluate thirty two diverse sunflower genotypes to estimate genetic variability, heritability and genetic advance, correlation coefficient, path analysis and genetic diversity.

The study involving thirty two genotypes of sunflower was sown in a randomized block design with three replications. Observations were recorded for ten characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, head diameter, volume weight g/100ml, 100 seed weight, seed filling percentage, hull content, oil content and seed yield per plant.

Greater amount of variability was observed among the genotypes for all characters studied. The magnitude of genotypic coefficient of variation was lower than phenotypic coefficient of variation. The GCV and PCV both were observed high for seed yield per plant followed by plant height, head diameter, 100 seed weight, hull content, oil content, volume weight g/100 ml, days to 50 per cent flowering, seed filling percentage and days to maturity. The estimates of heritability (b.s.) ranged from 81.80% to 96.80%. The highest heritability was observed for plant height (96.80%) followed by seed yield per plant (95.90%), days to 50% flowering (94.00%), days to maturity (93.20%), head diameter (92%). The highest value for genetic advance was observed for plant height (44.31), seed yield per plant (18.74), seed filling percentage (8.50), days to maturity (8.32) and days to 50% flowering (8.26). High heritability with high genetic advance was reported for plant height, seed yield per plant, days to maturity and days to 50 % flowering.

Seed yield per plant was significantly and positively correlated with seed filling percentage (0.9635), head diameter (0.9033), 100 seed weight (0.6357) and positively but non significantly correlated with volume weight g/100 ml (0.1449), days to maturity (0.1447), days to 50 % flowering (0.1198) and oil content (0.1123). However, it showed significant negative correlation with hull content (-0.7823) and non-significant, negative correlation with plant height (-0.0398). Plant height, days to 50% flowering, days to maturity, volume weight g per 100 ml and 100 seed showed positive association with each other.

In path analysis, the positive direct effect on seed yield per plant was through seed filling percentage, head diameter, days to maturity, hull content and volume weight g/100 ml. Thus, direct selection for these traits will be beneficial in yield improvement programme.

The 32 genotypes were grouped into eleven clusters. Cluster I with 9 genotypes followed by clusters III with 8 genotypes, cluster II with 7 genotypes while, remaining all other clusters *viz.*, cluster IV, V, VI, VII, VIII, IX, X and cluster XI were solitary. The calculated D^2 values varied from 35.47 to 347.86. The lowest D^2 value was between the cluster X and cluster XI while, the highest D^2 value was between cluster IV and cluster IX. Cluster II showed high mean for characters *viz.*, 100 seed weight, seed filling percentage and seed yield per plant. Cluster IX showed high mean for oil content, volume weight g/100 ml and head diameter.

Out of 10 characters studied, the seed yield per plant and plant height showed maximum contribution to divergence followed by days to 50 % flowering, hull content, oil content, head diameter, 100 seed weight, seed filling percentage, volume weight g/100 ml and days to maturity.

Potential parents were identified by using the procedure given by Arunachalam and Bandopadhyay (1984). According to this method the potential parents that can be used for future breeding programme are GMU-317, GMU-468, GMU-481, GMU 806, GMU 1034, GP-449, GP-1246, GP-2071-1, MTS-35-22, MTS-35-25 and GP-1350.

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1. INTRODUCTION

Sunflower (*Helianthus annuus* L.) a member of family compositae is an important oilseed crop with chromosome number 2n =34. In India, it is popularly known as ‘Surajmukhi’. It is annual, erect herbaceous plants growing to the height of 1.5 to 6 m. Leaves are simple, alternate somewhat lanceolate in shape and about 5 to 25 cm long. Leaves are rough on both the surfaces, irregularly toothed on margins and hairs on both the sides having acute tip. Typical compositae family type inflorescence is observed in sunflower with branches terminating in capitulum. Protoandry condition is observed and both male and female parts mature at different time. It is an essentially cross pollinated crop. Flower shows yellow colour with brown or black discs. Head diameter ranges from 10-50 cm in diameter with 40-80 number of ray florets. A single sunflower head produces 350 to 2000 seeds which are pointed at base and rounded at the end. Seeds may be white black or black with white strips.

It is believed to be originated from South West United States, Mexico (Heiser, 1976). This crop was introduced in India in 1969 from USSR. Sunflower is well adopted in India due to its wider adaptability, good agronomic traits, high seed and oil yield. Sunflower contains 38 to 42 % oil which can directly be used for cooking purpose. Sunflower oil is considered as premium oil as compared to most other vegetable oils because of its light yellow colour, bland flavour, high smoke point, high level of linoleic acid (55-60 %), low oleic acid (25- 30 %), fairly high content of Poly Unsaturated Fatty Acids (PUFA). Sunflower oil is considered to be of high quality edible oil because of its noncholesterol and anticholesterol properties (Campbell, 1983).

The unhusked seeds contain about 45 to 50 per cent oil which is good for heart patients which helps in washing out cholesterol deposition in coronary arteries of heart. The oil cake contains high quality proteins (17-20%). It is an ideal feed for livestock and poultry. Sunflower hulls are also used in animal feed as a source of roughages as a fuel to generate steam or electricity and in production of furfural and ethyl alcohol. Sunflower kernels can be eaten raw or roasted. The oil is also used for manufacturing hydrogenated oil. In India, it is an important source of edible and nutritious oil. It is a rich source of edible oil (40-52%) and considered as good quality oil from health point of view due to presence of polyunsaturated fatty acids with 55-60 per cent of linoleic acid and 25-30 per cent of oleic acid which are known to reduce the risk of cardiac related problems (Akkaya, 2018).

Sunflower as an oilseed crop occupies an important place in Indian economy and its value is increasing day by day due to constant widening of gap between demand and supply of edible oils. This shortage is reduced by importing edible oils like Soybean, Sunflower and Rapeseed. Due to limitations in increasing productivity of traditional Indian oilseed crops like

Groundnut, Rapeseed, Mustard and Sesamum an urgent need was fulfilled for quite some time by introduction of Sunflower oil.

In the world sunflower is grown as an oilseed crop over the area of 27.84 million hectares with the production of 46.75 million metric tons and productivity of 1.68 MT ha^{-1} during year 2018-19. During the same year sunflower is grown as a major oilseed crop in India over the area of 0.28 million hectares and production of 0.17 million hectares with productivity of 0.61 MT ha^{1} (USDA, 2020). In general, Karnataka, Andhra Pradesh, Maharashtra and Tamil Nadu are considered as traditional sunflower growing states whereas Punjab, Haryana, West Bengal and Uttar Pradesh are promising spring sunflower growing states. In some agro climatic regions of India, sunflower is grown twice a year as spring and autumn crop, both under irrigated and rainfed conditions

During last few years intensive research work has been initiated in India to improve yield as well as quality of oil seed. As yield is very complex character and it is the result of interaction of number of factors inherent to plants and environment in which it is grown it becomes difficult for plant breeders to evaluate and select for this complex polygenic trait. Various components of yield are more or less simply inherited and therefore, more amenable to improve through selection.

Sunflower has great potential in bridging gap between demand and supply of edible oil to a significant extent. Selection of suitable parents with high genetic diversity is a basic requirement in any successful hybridization to produce desirable character combination for selection of high yielding genotypes. Mahalanobis's 'D^2' technique is one of the efficient tools for estimating genetic divergence and for identifying the desirable parents for any crossing programme.Therefore, there is a need to study the genetic divergence among various genotypes in order to evaluate their usefulness as progenitors in hybridization programme. Genetic diversity is of major interest to plant breeders, more diverse the parents, greater are the chances of obtaining heterotic expression in F_1 with possibility of broad spectrum of variability in segregating generations. The D^2 statistics has been found to be a powerful tool to estimate genetic divergence among population. It is a powerful tool in quantifying the degree of genetic divergence among parents (Muppidathi *et al.*, 1995).

Variability means differences among the individuals of a single species or different species. The variability may be due to environment or genotype or interaction of both. Assessment of genetic variability in the base population is the first step in any breeding programme. The improvement in yield and its components depends on the nature and magnitude of genetic variability present in the population. The information about available variability alone is not sufficient to help breeders in deciding breeding programme for improving any trait. Thus, knowledge of genetic parameters is highly desirable for understanding and their manipulation in crop improvement because, the expected genetic gain, a prime goal in any breeding programme from a selection can be obtained by the estimate of the coefficient of variability along with heritability (Chander *et al*., 2008). Both seed and oil yield are quantitative characters with highly variable expression which depends on numerous independent characters. Correlation analysis helps in describing mutual relationship between variables. The estimation of association between the variables at both genotypic and phenotypic level not only describes the inheritance but also indicates level of environmental influence. It also helps in simultaneous improvement of different traits. For planning a successful breeding programme, the knowledge of association of different agronomical and quality traits with yield and among themselves is very essential.

Although, correlations are helpful in determining the components of a complex trait like yield, they do not provide an exact influence of the component characters towards the trait. The path coefficient analysis being a more precise method partitions the direct and indirect effects of independent variables on the dependent variable. Therefore, the path analysis explains the clear impact of independent variables on the dependent one. This method has been extensively used by the sunflower researchers (Mogali and Virupakshappa, 1994; Teklewold *et al*. 2000; Sujatha *et al*. 2002; Tahir *et al*. 2002; Arshad *et al*., 2007; Habib *et al*., 2007; Yasin and Singh, 2010; Darvishzadeh *et al*., 2011; Kholghi *et al*., 2011).

The present investigation entitled **"Genetic Variability, Path Coefficient Analysis and Diversity in Sunflower (*Helianthus annuus* L.)** is therefore undertaken with following objectives:

1) To study the genetic variability for seed yield and seed oil quality characters.

2) To study the correlation and path coefficient analysis in sunflower.

3) To estimate genetic diversity among different genotypes of sunflower.

2. REVIEW OF LITERATURE

Success of any breeding programme depends on the availability of variation and selection practiced. The selection of elite genotypes requires the knowledge of quantitative traits. The present investigation is aimed to find out statistical parameters *viz*., genetic variability (Genotypic coefficient of variance, phenotypic coefficient of variance, heritability and genetic advance), correlation, path analysis, heritability, genetic advance and genetic diversity. Regarding sunflower, optimum literature is available, however, in present chapter attempt has been made to review the results obtained by earlier authors in sunflower. Literature collected has been reviewed under following sub-heads.

1. Genetic variability.
2. Correlation coefficient analysis.
3. Path coefficient analysis.
4. Genetic divergence.

2.1. Genetic variability

The development of an effective plant breeding programme is dependent upon the existence of genetic variability. Hence, an insight into the magnitude of variability present in a gene pool of a crop species is of utmost importance to plant breeder for starting a judicious plant breeding programme. Scientists globally collect the germplasm from various agro-climatic regions and evaluate and characterize them for genetic variability. Both genetic and environmental factors contribute towards variation among individuals. The heritability estimates aid in determining the relative amount of heritable portion in variation and thus help plant breeder in selecting the elite inbreds from a diverse population. Phenotypic and genotypic variance, heritability along with genetic advance has frequently been used to assess the magnitude of variance in sunflower breeding material.

Shinde *et al*. (1983) studied 123 varieties of sunflower and reported high GCV for yield per plant, percentage of filled grains, head diameter and 100 seed weight. The GCV ranged from 5.85 for stem girth to 30.84 for yield per plant. Higher heritability estimates were obtained for plant height, total leaves, head diameter and yield per plant. They also indicated that yield per plant and percentage of filled seed showed higher estimates of genetic advance.

Sheriff *et al*. (1986) in their studies on determining genetic parameters for nine quantitative characters using 23 genotypes, observed a higher phenotypic variance than genotypic variance. Moderate GCV coupled with medium heritability estimates for seed yield, plant height, number of leaves, seeds per capitulum and dry matter have been recorded. But the expected genetic gain from these characters was low, indicating that high GCV or heritability need not necessarily be reflected as high genetic gain.

Singh and Yadava (1986) studied 36 genotypes collected from different climatic regions and reported significant varietal differences for all the ten agronomic characters. A high heritability estimate and high coefficient of variation were recorded for yield of filled achenes per plant, 100 achene weight and head diameter.

Alam *et al*. (1987) reported significant variation for seed yield, number of achenes and head diameter. A genotypic coefficient of variation was low for these characters and highest genetic advance was reported for seed yield per plant.

Patil *et al*. (1996) studied 125 sunflower genotypes of different geographic origin for genetic variability among them. Analysis of variance reported highly significant differences for seed yield per plant, seeds per head, oil content and weight of head. The range of variation was maximum for seeds per head (141 to 1632) followed by total weight of head (7.0 to 494 g) and seed yield per plant (3.0 to 75 g). Mean value for seed yield and oil content found to be 28.59 g and 29.40 per cent, respectively. Higher mean values found to be associated with greater range.

Sujatha *et al*. (2002) studied genetic variability for 51 inbreds and 3 checks, and revealed significant differences for plant height, no.of leaves per plant, seed test weight, seed density, hull percentage, husk percentage, head diameter, stem girth, days to 50 % flowering, 100 seed weight, yield per plant, oil content, oil yield.. The range of variation was maximum for per cent autogamy followed by plant height and oil yield, while it was minimum in the case of 50 per cent flowering and stem girth.

Arshad *et al*. (2007) observed high heritability for days to flower initiation, completion and plant height, while head diameter and seed yield had low heritability.

Khan *et al.* (2007) conducted a study using 8 diverse genotypes of sunflower and observed that the phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits. High heritability estimates were observed for oil content, 1000-seed weight, days to maturity and plant height, while seed yield, number of seeds per head and days to flowering depicted low heritability estimates. High genetic advance as per cent of mean was demonstrated by plant height, number of seeds per head, seed yield and oil yield per hectare.

Muhammad *et al*. (2007) noticed high genotypic and phenotypic variances for plant height, oil content and achene yield with high heritability and expected genetic advance for the latter two traits indicating an additive effect. The dominant and epistatic nature of inheritance was reflected by high heritability and low genetic advance estimates for plant height and capitulum diameter.

Arshad *et al*. (2010) studied the partitioning of variance and revealed high heritability associated with high genetic advance for days to flower initiation, days to maturity, plant height and seed yield while the characters having low heritability were head diameter and hull content.

Camarano *et al*. (2010) investigated genotypic divergence among 10 sunflower populations using Mahalanobis D^2 statistics and canonic variables to identify more similar and more divergent groups. The results of the individual variance analysis pointed out significant differences for the initial flowering, final flowering, plant height, oil content, moisture content and yield in all the experiments. Very high genetic variability was noted among the populations for these traits. The traits, stem diameter, head diameter, 1000-seed weight and number of seeds per head presented differences, which were sometimes significant and sometimes not, indicating that these traits show genotype-environment interaction.

Kalukhe *et al.* (2010) studied genetic variability in 27 sunflower genotypes comprising 26 germplasm lines and one check, i.e., TAS-82. High heritability with high genetic advance was recorded for number of unfilled seeds per head, seed yield per plant, plant height and 100-seed weight, while high heritability along with low genetic advance was observed for oil content, days to 50 per cent flowering, hull content and days to maturity. High values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for number of unfilled seeds per head, seed yield per plant, plant height, 100-seed weight and number of filled seeds per head.

Tan (2010) studied hybrids and open-pollinated confectionary sunflower and the lowest seed yield (343 kg ha^{-1}) were obtained from the varieties ETAE-Y-TM-2007-5 and Armada, respectively. In the confectionary variety experiments, the highest seed yield (563 kg ha^{-1}) and the lowest seed yield (202 kg ha^{-1}) was produced in 2009 by the varieties ETAE-D1-2-B2 and ETAE-Ç-P-1-2, respectively. The results indicated that statistically significant differences were found among the sunflower varieties for the characters in question.

Makane *et al.* (2011) evaluated the newly developed 79 recombinant versions of Morden and EC-68415 varieties of sunflower for nine characters. A high range of variability was noticed for days to maturity, plant height, test weight and seed yield per plant. High GCV was observed for hull content, seed yield per plant, plant height, test weight and oil content. The genetic advance expressed as per cent of mean was high for hull content, seed yield per plant and plant height, whereas it was moderate for test weight, oil content and head diameter and low for days to maturity and days to 50 per cent flowering. High heritability was recorded for plant height and hull content, followed by seed yield per plant, oil content and test weight and moderate for head diameter and days to maturity.

Mahmoud (2012) studied the genetic parameters in sunflower genotypes. The values of PCV and GCV were relatively high for head diameter and seed yield. The results showed little differences in the genotypic and phenotypic coefficients of variability and gave high values of heritability for all studied traits.

Neelima *et al.* (2016) observed that analysis of variance revealed significant differences among the genotypes for all the traits indicating considerable magnitude of genetic variability of the material used for the study. Low heritability coupled with high GAM was observed for seed yield per plant due to high environmental effects and selection is effective.

Mohamed *et al*. (2018) revealed highly significant differences among the undertaken hybrids for plant height, stem diameter, head diameter, empty seed %, 1000-seed weight, seed yield per plant and seed yield.

2.2. Correlation coefficient analysis

Correlation coefficient measures the intensity of association between two characters. This measurement of relationship is vital in planning an efficient breeding programme for the improvement of one of more economic characters which are known to depend on two or more metric traits, it is evident from the most of the reports that a positive and significant correlation exists between yield per plant with yield contributing characters.

Rao (1987) revealed that achene yield was positively correlated with capitulum diameter, achene oil content, 100-achene weight, while negative correlation with days to maturity and husk percentage.

Tariq *et al*. (1992) studied 14 hybrids of *Helianthus annuus* L. and observed that characters plant height, oil content and achene yield reported high genotypic and phenotypic variance with high heritability and genetic advance for the latter 2 traits indicating an additive effect. The dominant and epistatic nature of inheritance was reflected by high heritability and low genetic advance estimates for plant height and capitulum diameter. Most characters, except 100-seed weight and days to maturity were positively correlated with yield.

Gowda (1994) revealed significant association of sunflower seed yield per plant with all the characters except days to 50 per cent flowering both at genotypic and phenotypic level. Oil content recorded significant positive association with oil yield per plant and number of filled seeds per plant.

Mogali and Virupakshappa (1994) estimated genotypic and phenotypic correlations and found that seed yield was positively correlated with number of seeds per plant, plant height, stem diameter, head diameter, test weight and percent seed filling. Plant height was positively correlated with all characters studied except seed filling percentage. Oil content was negatively correlated with seed yield at the genotypic levels.

Doddamani *et al*. (1997) evaluated 47 genotypes of sunflower and revealed that head diameter, 100 seed weight, plant height and stem girth had significant positive correlation with seed yield.

Gill *et al.* (1997) studied 45 sunflower genotypes over four environments and observed high positive association between seed yield per plant and plant height, stem diameter, head diameter, 100-seed weight and number of seeds per head.

Lal *et al.* (1997) reported significant positive association of seed yield with plant height, stem girth and head diameter.

Singh and Kakar (1997) found that number of unfilled seeds recorded negative and non-significant association with seed yield.

Rather *et al*. (1998) observed that days to 50 per cent flowering were positively correlated with oleic acid that showed a strong negative association with linoleic acid.

Dagustu (2002) reported that number of seeds per head, plant height, head diameter, 100 seed weight and number of leaves per plant were significantly and positively correlated with sunflower seed yield per plant. The highest correlation of seed yield was observed with number of filled seeds per plant, followed by percent seed filling and head diameter.

Tahir *et al.* (2002) studied four open pollinated sunflower populations, each having 13 lines for correlation. The highest correlation of seed yield was observed with number of filled seeds per plant, followed by seed filling percentage and head diameter.

Syed *et al*. (2004) studied 66 treatment combinations in sunflower for 12 traits and revealed the positive correlation of number of leaves per plant with days to anthesis and head diameter, plant height with seed yield per plant, days to maturity with head diameter and days to maturity with seed yield per plant in sunflower.

Khan *et al.* (2005) reported significant and positive correlation of oil content with number of days to physiological maturity, but there was significant and negative correlation between oil content and number of filled seeds per head.

Sridhar *et al.* (2005) studied 45 sunflower genotypes during the *rabi* season and revealed that yield per plant was positively and significantly correlated with plant height, head diameter, number of leaves per plant, number of filled seeds per head, seed filling percentage, 100-seed weight, leaf area index, total dry matter per plant and harvest index.

Vidhyavathi *et al.* (2005) observed that seed yield per plant had significant positive correlation with head diameter and plant height whereas, 100-seed weight, seed length, seed breadth, seed oil content and kernel oil content had no significant association with seed yield.

Farhatullah *et al.* (2006) reported highly significant correlation of yield per plant with plant height, head diameter and oil content both at genotypic and phenotypic levels in sunflower.

Arshad *et al.* (2007) evaluated 20 sunflower hybrids to understand the association among characters and reported that days to maturity had positive correlation with head diameter, whereas negative with seed yield. Seed yield had highly positive correlation with oil content, while no association was observed with 100-seed weight. Oil content had negative association with days to flower initiation and plant height but significantly positive correlation with seed yield. 100-seed weight had significant positive genotypic correlation with head diameter.

Binodh *et al.* (2007) studied the performance of 24 genotypes for important characters in sunflower. Seed yield per plant showed highly significant and positive association with oil yield while no association was observed with other characters *viz.,* 100-seed weight, head diameter and oil content. Contrarily, a negative association of seed yield per plant was observed with plant height and days to 50 per cent flowering. Head diameter showed highly significant positive association with volume weight and oil yield. Plant height had significant positive correlation with head diameter and volume weight. Oil yield showed significant positive association with volume weight, whereas days to 50 per cent flowering exhibited significant negative association.

Habib *et al.* (2007) observed significant positive correlation between days to maturity, plant height and oil content on one side and oil yield on the other side, whereas days to flower initiation was negatively correlated with oil yield.

Khan *et al.* (2007) reported highly significant and positive correlation of seed yield with plant height, number of seeds per head, oil content, 1000-seed weight and oil yield.

Amorim *et al.* (2008) studied 14 genotypes and reported that significant positive correlations were observed between seed yield and head diameter and weight of 1000 seeds.

Machikowa *et al.* (2008) studied eight characters in sunflower and the results showed that seed yield was positively correlated with head diameter and plant height. Significant positive correlations were found between per cent seed setting and number of seeds per head, head diameter and 100-seed weight, number of seeds per head and oil content, seed yield and per cent seed setting, and between seed yield and 100-seed weight.

Anandhan *et al.* (2010) observed strong positive association of oil yield per plant with days to maturity, 100-seed weight, volume weight, oil content and seed yield per plant.

Arshad *et al.* (2010) observed that days to flower initiation, days to completion and days to maturity had positive and highly significant correlations with plant height. Head diameter had positive association with 100-seed weight. Similarly, seed yield had negative correlation with oil content. Oil content had positive association with days to flower initiation, days to flower completion, days to maturity and plant height, while negative association with head diameter, seed yield and 100-seed weight.

Tyagi *et al*. (2010) evaluated 22 genotypes of sunflower and observed that seed yield per plant was significantly and positively correlated with number of leaves per plant, plant height, stem diameter at top height, stem diameter at mid height, head diameter, weight of head, number of seeds per head, leaf length, leaf breadth and leaf area.

Yasin and Singh (2010) performed correlation in 24 diverse genotypes of sunflower and found that yield per plant had highly significant and positive correlation with number of seeds per head, head diameter and 1000-seed weight at both genotypic and phenotypic level.

Darvishzadeh *et al.* (2011) observed positive correlation between head diameter and seed yield per plant under well-watered and water-stressed conditions.

Kholghi *et al*. (2011) reported that seed yield per plant was positively and significantly associated with 100-seed weight, head diameter, number of seeds per head, stem diameter and plant height.

Patil (2011) concluded that plant height, head diameter and volume weight had significant association with the seed yield.

Dan *et al.* (2012) conducted character association study on 79 inbred lines of sunflower and revealed positive and significant association of oil yield per plant with seed yield per plant, plant height, head diameter, volume weight, 100-seed weight and oil content.

Kumari *et al.* (2012) evaluated 80 genotypes of sunflower for two years (spring 2008 and 2009) and found that seed yield was positively correlated with plant height, head diameter and 100-seed weight, whereas negatively correlated with oil content.

Neelima *et al.* (2012) studied correlation among seed yield and its component characters in sunflower and revealed that number of seeds per head, 100-seed weight, head diameter and per cent seed filling had highly significant positive interrelation among themselves along with seed yield.

Rao (2013) observed that seed yield had significantly positive association with head diameter, number of filled seeds per head, test weight, plant height, number of leaves per plant oil content and days to maturity, and suggested that these major yield contributing traits might be given selection pressure for improving yield. Plant height had significant positive association with number of leaves per plant, head diameter, oil content, test weight and number of filled seeds per head. Head diameter had significant positive association with test weight, number of filled seeds per head and oil content.

Sujatha *et al.* (2013) studied 146 genotypes including 46 mutants and 100 segregants of sunflower. Character association analysis revealed that the seed yield had significant positive correlation with head diameter and 100-seed weight, while negative with days to flowering and days to maturity. Days to flowering had significant and positive correlation with plant height, while negative and significant correlation with head diameter and test weight. Plant height had positive and significant correlation with days to maturity. Head diameter had positive and significant correlation with seed yield per plant and test weight.

Zia *et al. (*2013) reported positive correlation between harvest index, 100-seed weight and head diameter and seed yield per plant.

Chander and sheoran (2014) reported that days to 50 per cent flowering, days to maturity, plant height, head diameter, 100-seed weight and oil content had significant positive correlations with seed yield.

Biljana *et al*. (2015) observed that 100 seed weight had positive and significant correlation with seed width, seed length and seed yield. On the other hand, negative and significant correlation was obtained between 100 seed weight and oil content.

Singh *et al.* (2018) revealed that seed yield per plant was positively and significantly associated with 100-seed weight, seed volume weight, head diameter, duration of reproductive phase and oil content. Oil content was positively associated with duration of reproductive phase, head diameter and seed volume weight, whereas the association between hull content and oil content was found to be highly significant and negative.

2.3 Path coefficient analysis

In plants, the dynamics of many important physiological and biochemical processes are often influenced by multiple interacting factors. In order to resolve the biological complexity, plant geneticists need to estimate the relative strengths of competing causes of biological phenomena. The advantage of path analysis in plant breeding was demonstrated by Dewey and Lu (1959), which allows partitioning of the correlation coefficient into its components. One component of the path coefficient analysis is the standardized partial regression coefficient that measures the direct influence of an independent variable upon its dependent variable whereas another component is the indirect effect(s) of an independent variable on the dependent variable through the independent variables. If correlation between dependent and independent variable is due to the direct effects of the character, it reflects a true relationship between them and selection can be practiced for such a character in order to improve the dependent variable. But if the association is mainly through indirect effects of the characters via another component characters, the breeder has to select for the later one through which the indirect effect is exerted on the ultimate dependent character such as seed yield.

Murthy and Shambhulingappa (1989) reported that days to 50 per cent flowering and stem girth showed low positive effect on seed yield. Their findings also revealed that days to maturity had negative direct effect on seed yield.

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Khan *et al.* (1992) reported that head diameter had strong effect on seed yield while 50% flowering affected seed yield *via* other characters *viz.*, maturity and 100 achne weight.

Mogali and Virupakshappa (1994) reported that the number of filled seeds per plant had a maximum direct effect on seed yield. All the other character had high, positive indirect effects on seed yield. Seed yield had the highest direct effect on oil yield followed by percent seed filling, oil content and head diameter. Number of filled seeds per plant had the highest indirect effect via seed yield per plant. Plant height, stem diameter and 1000-seed weight had the greater indirect effect via seed yield.

Suma *et al.* (1994) showed that number of filled seeds per plant had maximum direct effect on seed yield. Head diameter also showed considerable effect on seed yield.

Lal *et al.* (1997) studied path analysis in sunflower and revealed that plant height and test weight exerted direct effect in the positive direction on seed yield.

Singh and Kakar (1997) found that number of unfilled seeds recorded large positive direct effect on seed yield.

Venkateshwara Rao (1999) observed highest direct effect of number of filled seeds per head followed by unfilled seeds, plant height and test weight on seed yield.

Satyanarayana (2000) revealed a positive direct association of seed yield with oil content number of filled seed per head, plant height and test weight.

Ayub Khan (2001) revealed that first flower had the highest positive direct effect on seed yield followed by seeds per capitulum 100 achne weight and head diameter, while 50 per cent flowering had the greatest negative direct effect on seed yield.

Chikkadevaiah *et al.* (2002) reported path coefficient analysis for seed yield has maximum direct effect for oil yield followed by 100 seed weight. The maximum indirect effect for seed yield was minimum through oil content, while it was through yield per plant for oil.

Tahir *et al.* (2002) studied four open pollinated sunflower populations, each having 13 lines for path coefficient analysis of morphological traits. Maximum direct effect on seed yield was exerted by number of filled seeds per plant. Head diameter also had a considerable effect on seed yield. It was concluded that number of filled seeds per plant, head diameter and 1000-seed weight were important characters to improve seed yield.

Nehru and Munjanath (2003) recorded the maximum direct effect of number of seeds per head followed by test weight on seed yield per plant, while seed yield had maximum direct effect on oil yield.

Sridhar *et al.* (2005) observed maximum direct effects of plant height followed by head diameter, per cent seed filling and 100-seed weight on seed yield.

Farhatullah *et al*. (2006) reported that days to maturity, plant height, head diameter, number of seeds per head, 1000-seed weight and oil content showed positive direct effect on seed yield, whereas number of leaves per plant and days to flowering had negative direct effects on seed yield.

Arshad *et al.* (2007) reported direct effects of days to flower initiation, plant height and head diameter were positive on seed yield, while remaining characters exhibited negative direct effects. The highest direct effect was exhibited by days to flower initiation and plant height.

Amorim *et al.* (2008) studied 14 genotypes and reported that head diameter and weight of 1000 seeds showed positive direct effects on seed yield.

Kaya *et al*. (2008) concluded that 1000-seed weight had the maximum contribution towards higher yield followed by head diameter and plant height.

Machikowa *et al*. (2008) studied eight characters in sunflower and the results showed that the head diameter showed the highest positive direct effect on seed yield, followed by plant height.

Iqbal *et al.* (2009) reported positive direct effect of stem diameter on oil content under restricted water conditions.

Arshad *et al*. (2010) studied correlation and path coefficient analysis and showed that the direct effects of days to flower initiation, days to maturity, plant height and head diameter were positive, while the remaining characters exerted negative direct effects on seed yield.

Sowmya *et al*. (2010) reported that head diameter exhibited maximum direct effect on seed yield per plant whereas seed filling per cent and plant height recorded maximum indirect effects through head diameter.

Tyagi *et al*. (2010) evaluated 22 genotypes of sunflower for path coefficient analysis and revealed that among all the traits studied, stem diameter at mid height and head weight contributed most directly to seed yield.

Yasin and Singh (2010) performed path coefficient analysis in 24 diverse genotypes of sunflower and revealed that number of seeds per head, 1000-seed weight and head diameter had high positive direct effects on seed yield per plant.

Darvishzadeh *et al.* (2011) studied path coefficient analysis and revealed that besides head diameter, number of seeds per head had also positive direct effects on seed yield per plant in both the conditions.

Kholghi *et al*. (2011) reported that number of seeds per head, 100-seed weight and head diameter had positive direct effects on seed yield. On the basis of path coefficient analysis of two sunflower populations improved through recurrent selection with and without pollen selection

Patil (2011) concluded that plant height, head diameter and volume weight exert positive direct effects on seed yield.

Neelima *et al.* (2012) reported that the number of seeds per head, per cent seed filling, hull content and plant height influenced the seed yield directly whereas 100-seed weight influence was indirect through number of seeds per head and per cent seed filling. Maximum indirect contribution for most of studied traits was through number of seeds per head.

Iqbal *et al*. (2013) noted that number of leaves, stem diameter, head diameter and oil content exerted positive direct effects on seed yield and head diameter.

Rao (2013) revealed a higher magnitude of positive direct effect of number of filled seeds per head, followed by test weight and plant height on seed yield. Interestingly, days to maturity showed direct positive effect on seed yield, but an indirect effect through plant height, number of filled seeds and test weight was also noticed. In contrast, days to 50 per cent flowering and oil content showed negative direct effects on seed yield.

Zia *et al. (*2013) reported highest direct effects for head diameter, 100-seed weight and harvest index, respectively. The highest indirect effects were recorded for per cent filled seeds and 100-seed weight and harvest index.

Chander and sheoran (2014) reported that the maximum positive direct effect on seed yield was exhibited by head diameter, whereas plant height showed maximum indirect effect.on seed yield.

2.4 Genetic divergence

Genetic diversity plays an important role in plant breeding because crosses between diverse parental lines display a greater heterosis than those between closely related parents. Hence, it is important to identify best parents with wide genetic divergence for desired characters to obtain better heterotic hybrids. Mahalanobis (1936) outlined a statistical procedure ‘D^2 statistics’ to measure the genetic divergence in a given population. It is a powerful tool in quantifying the degree of genetic divergence among parents (Muppidathi *et al.,* 1995; Sujatha *et al*., 2002 and Punitha *et al*., 2010).

Muppidathi *et al.* (1995) assessed genetic divergence among 121 sunflower genotypes by using Mahalanobis D^2 statistics. The inbreds were grouped in 9 clusters. Grouping of different clusters was not related to their geographic origin. Maximum number of genotypes were included in cluster IV comprising 52 genotypes followed by cluster VII (28), cluster Ill (16) and cluster V (11). The least number of genotypes were present in the cluster I (1), cluster II (4), cluster VIII (2) and cluster IX (3).

Chungai *et al.* (1996) showed that linear regression model fits the relationship between seed oil content and genetic divergence showing oil content gives more contribution towards divergence.

Path coefficient analysis by Mamata rani *et al.* (2017) revealed that days to maturity, plant height, head diameter, stem girth and seed filling percentage had positive and direct effects on seed yield per plant, while days to flowering showed direct negative effects.

Singh *et al.* (2018) revealed that 100 seed weight expressed the highest positive direct effect

Sankarapandian *et al*. (1996) reported substantial genetic diversity in 54 sunflower genotypes by D^2 analysis. The genotypes were grouped into 7 clusters. The maximum number of genotypes were included in cluster II (18) followed by cluster I and IV (13) and remaining clusters had 1 to 4 genotypes. There was no association between clustering pattern and eco-geographic distribution of genotypes.

Sebil (1999) studied twenty varieties from seven geographic origins of the world to study the genetic diversity of sunflower varieties in Ethiopia. Based on nine traits which were significantly different, the genotypes were grouped into eight clusters. Varieties in clusters II, III and VIII showed better performance for the majority of the traits of interest seed yield per plant, number of seeds per head, 1000 seed weight, harvest index, and oil yield ha^{-1}. The clustering pattern of the materials has indicated no relationships between genetic diversity and geographic origins since genotypes from the same origin were found to be grouped into different clusters or vice versa. The Mahalanobis D^2 square analysis showed that distance between clusters III and V was minimum.

Taklewold *et al.* (2000) studied that most of the genotypes derived from different crosses were grouped in single cluster (cluster I), medicated the similarity for the characters studied in parental on the contrary the genotypes having similar pedigree were grouped into different clusters. It clearly demonstrated the impact of selection pressure in increasing the genetic diversity.

Manjula *et al*. (2001) reported genetic divergence among 46 non-oilseed sunflower genotypes. The genotypes were grouped into 11 clusters. The generalized genetic distance between the genotypes was in the range of 0 to 3792.34.

Ravi (2001) assessed 66 sunflower genotypes for genetic divergence by D^2 analysis and these genotypes were grouped into nine clusters. The characters seed yield per plant, total dry matter per plant, seed set per cent under self pollination contributed maximum towards the genetic divergence.

Vega *et al.* (2001) studied a set of 10 sunflower hybrids (Contiflor 15, Aguara, GV23105, GV25015, GV25086, TC 2001, GV23146, GV22510, Contiflor 9 and Morgan 734) in 21subtropical (northern), temperate (central) and managed environments of Argentina, Cluster analysis revealed three genotypic groups: northern, central and broadly adapted. All central environments discriminated among genotypes in a similar fashion; discrimination in northern environments was more divergent across years and locations.

Sujatha *et al.* (2002) evaluated 51 inbreds and three checks (GAUSUF-15, TNASUF-7 and TNAU-1) of sunflower to study genetic divergence among them using the Mahalanobis D^2 statistics. These 51 inbreds grouped into eight clusters which were not related to their geographic origin. Stem girth and seed yield per plant contributed the most towards the total genetic divergence. Maximum inter-cluster distance was observed between the inbreds grouped in clusters I and V containing five and twelve inbreds, respectively, while the intra-cluster distance ranged from zero to 2306.05. Based on mean performance, genetic divergence and clustering pattern, few inbreds namely CMS-234B, 7-1-B, CMS-597B, CMS-852B, ARM- 250B, ARM-245B, HAM-69, ARM-284B, ARM-247B and HAM-174 were considered as potentially important for further breeding programs.

Ramasubrahmanyam *et al.* (2003) evaluated 85 sunflower inbreds for estimation of genetic diversity among them by using Mahalanobis D^2 statistics. The 85 genotypes were grouped into 15 clusters. The maximum number of genotypes was included in cluster I which had 43 genotypes followed by cluster II with 11 genotypes, cluster IV with 8 genotypes, cluster Ill with 7 genotypes and cluster VI with 6 genotypes. Remaining clusters contained only one genotype each.

Subrahmanyam *et al.* (2003) studied genetic divergence among 85 sunflower genotypes including five checks and grouped them into fifteen clusters. Among the investigated traits,maximum contribution towards genetic divergence was exhibited by number of filled seeds per head followed by test weight, kernel to hull ratio and seed yield per plant.

Komuraiah *et al.* (2004) assessed 101 genotypes consisting of 98 inbred, two hybrids and one open-pollinated variety. All genotypes were grouped into ten clusters. Among the investigated traits, the number of filled seeds, test weight and plant height contributed maximum towards genetic divergence.

Reddy and Devasenamma (2004) in assessment of divergence analysis among 58 newly developed genotypes along with three checks in sunflower reported that inter crossing divergent groups would lead to greater opportunity for crossing over which releases hidden variability by breaking linkage.

Reddy *et al*. (2005) studied 102 genotypes to assess genetic divergence among them. These genotypes were grouped into twelve clusters. Based on the inter cluster distances and *per se* performance, the genotypes namely; GMU-4, GMU-11, GMU-14, GMU-16, GMU-25, GMU-40 and GMU-70 were selected for further intercrossing to obtain high heterosis and also to recoSver desirable transgressive segregants. The analysis suggested the maximum contribution of seed yield per plant (40.2%) followed by number of leaves per plant (25.8%) and 100-seed weight (17.0%) towards divergence.

Mahalakshmi *et al.* (2006) studied 29 genotypes of sunflower for their genetic divergence by D^2 analysis. The genotypes were grouped into seven clusters. The character, days to first flowering contributed more towards genetic divergence.

Binodh *et al.* (2007) assessed 24 breeding lines for eight traits in sunflower to study the genetic divergence. The genotypes were grouped into ten clusters. Cluster I was the largest containing 13 genotypes, followed by cluster IV with 3 genotypes. The inter-cluster distance was the maximum between clusters VI and VIII, followed by clusters IV and VI, and clusters VI and IX. The study revealed that maximum genetic divergence was contributed by character plant height (45.29%), followed by seed yield per plant (25.72%) and oil content (15.94%). Based on the inter-cluster distance and *per se* performance, the genotypes *viz.*,17A, 47A, CSFI 5325, CSFI 5415, CSFI 5436 and CSFI 5013 were identified as suitable parents which could be intercrossed to obtain high heterosis.

Anandkumar *et* a*l.* (2008) reported genetic divergence in 32 sunflower genotypes. These 32 genotypes were grouped into 11 clusters. Among them cluster VI was largest containing 6 genotypes followed by cluster V with 5 genotypes, cluster Ill with 4 genotypes, cluster I with 4 genotypes, cluster IV with 3 genotypes. Cluster VII, VIII and X had 2 genotype each. Cluster IX and XI had only genotype in each.

Kumar *et al.* (2008) studied 32 parental lines using D^2 analysis, and altogether eleven clusters were formed. Among the studied characters, oil content contributed maximum towards the total divergence followed by days to 50 per cent flowering and days to maturity.

Punitha *et al.* (2010) studied genetic diversity among 17 sunflower genotypes using nine agronomic characters and indicated the presence of substantial genetic diversity. All the genotypes were grouped into four clusters. Among the investigated characters, seed yield, plant height, oil content and oil yield exhibited high contribution towards genetic divergence. It was observed that the inclusion of CSFI 5076, CSFI 5162, CMS 47A, CSFI 5005, CMS 17A, CMS 47A, CSFI 5069, CSFI 5422, CSFI 5109, CSFI 5155, CSFI 5002, COSF 1A , CSFI 5161 and CSFI 5015 in future breeding programmes could result in the development of superior sunflower cultivars.

Mandel *et al.* (2011) carried out population genetic analysis of the primary gene pool sunflower based on a broad sampling of 433 cultivated accessions and 24 wild sunflower populations. Gene diversity across the cultivars was 0.47 as compared with 0.70 in the wilds, indicating that cultivated sunflower harbours roughly two-thirds of the total genetic diversity present in wild sunflower.

Dan *et al*. (2012) conducted study on genetic divergence of 79 inbred lines of sunflower using Mahalanobis D^2 statistics and indicated the presence of substantial genetic diversity. Oil yield per plant (26.74 %) contributed maximum towards genetic divergence, followed by plant height (17.72 %) and 100-seed weight (17.46 %). Head diameter and seed yield per plant contributed the least.

Reddy *et al*. (2012) studied genetic divergence in 64 genotypes of sunflower and grouped them in nine clusters. The random pattern for distribution of genotypes into various clusters was observed and indicated that the geographical and genetic diversity were not related. Plant height contributed maximum towards genetic divergence, followed by stem diameter and head diameter.

Chandirakala and Maniwannan (2014) studied 38 sunflower genotypes and grouped them into thirteen clusters for the quantification of nature and extent of genetic diversity using Mahalanobis D^2 statistics. Cluster IX was the largest with 9 genotypes followed by cluster X with 5 genotypes. The genotypes GMU 322, COSF3B and COSF4B in the cluster II, the genotypes GMU 503, GMU 1074 and GMU 1108 in the cluster XII and the genotypes COSF1B in the cluster XIII were widely divergent. The characters *viz.,* days to 50 per cent flowering and seed yield were found to be important contributors for genetic divergence.

Pandya *et al*. (2014) studied 40 genotypes of sunflower. These genotypes were grouped into five clusters. The cluster III having higher means for days to maturity, head diameter, number of seeds per capitula, number of filled seeds per capitula, seed yield per plant and 100-seed weight was found to be more divergent from cluster IV. Cluster IV reported higher means for number of unfilled seeds per capitula. The clustering pattern of genotypes was independent of their geographical distribution.

Rani Reena *et al*. (2017) studied the genetic divergence for seed yield and its components among ninety sunflower inbred lines from different agro-ecological origins. These 90 inbred lines were grouped into 8 clusters indicating considerable amount of genetic diversity based on D^2 values.

3. MATERIALS AND METHODS

The details of experimental material and methods employed in the present investigation entitled “Genetic Variability, Path coefficient Analysis and Diversity in Sunflower *(Helianthus annuus* L.*)*" were as follows.

3.1. Experimental site

3.2. Experimental material

3.3. Experimental details

3.4. Observations recorded

3.5. Statistical analysis

3.1. Experimental site

The present investigation was carried out at the Research Farm, Division of Botany, College of Agriculture, Pune during *kharif* 2019. All type of inputs and recommended package of practices were followed for satisfactory crop growth and development.

3.2. Experimental Material

The experimental material for the genetic diversity consisted of 32 inbred lines of Sunflower (*Helianthus annuus* L.), collected from Zonal Agricultural Research Station, Solapur. The list of genotypes is given in Table 3.1.

3.3. Experimental details

A uniform piece of land was selected for conducting the trial. It was ploughed, harrowed and the stubbles of the previous crop were collected and finally the land brought to fine tilt. Thirty two genotypes were sown in Randomized Block Design with three replications during *kharif* season of 2019 with spacing of 60 x 30 cm having a single row of 4.5 m length.

Sowing was done by dibbling 2-3 seeds at each hill. Thinning was done 15 days after sowing and only one healthy plant was kept at each hill. After 30 days from sowing the crop was top dressed with urea @ 30 kg N/ha timely and proper cultural practices were carried out to ensure satisfactory crop growth.

3.4. Observations Recorded

Following observations were recorded on five randomly selected plants, from each treatment in each replication and averages were worked out.

3.4.1 Days to 50 per cent flowering (No.)

This was recorded in terms of number of days taken from the day of sowing to the date of opening of ray florets in 50 per cent of the plants in each plot.

Table 3.1 List of sunflower genotypes

Sr. No.	Genotype	Sr. No.	Genotype
1	AKSFI-42-5	17	GMU-1034
2	GMU-308	18	GP-449
3	GMU-317	19	GP-450
4	GMU-379-1	20	GP-530-1
5	GMU-442	21	GP-804
6	GMU-452	22	GP-1011
7	GMU-459	23	GP-1124
8	GMU-468	24	GP-1217-1
9	GMU-477	25	GP-1246
10	GMU-481	26	GP-1350
11	GMU-571-1	27	GP-2071-1
12	GMU-595	28	GP-6-198
13	GMU-635	29	MTB-20-3
14	GMU-806	30	MTB-20-9
15	GMU-889	31	MTS-35-22
16	GMU-928	32	MTS-35-25

3.4.2 Days to maturity (No.)

The number of days taken by majority of the plants head in each plot to become lemon yellow in colour from date of sowing.

3.4.3 Plant height at harvest (cm)

Plant height was measured in centimeters using a meter scale, when the crop attained physiological maturity from the ground level to the base of the capitulum.

3.4.4 Head diameter (cm)

Head diameter of five selected plants from each treatment was measured in centimeter by using centimeter scale at the time of harvest of the crop.

3.4.5 Volume weight (g/100 ml)

The measuring cylinder was filled to 100 ml volume with seeds of each entry and was weighed in g as volume weight /100 ml.

3.4.6 100 seed weight (g)

This was determined by recording the weight of 100 seeds of each genotype in gram from selected plant in each replication and expressed as average. The seeds obtained from each treatment were measured in measuring cylinder.

3.4.7 Seed filling percentage

Seed filling percentage was calculated by dividing the number of filled seeds per head by the total number of seeds per head and multiplied by 100 to express in per cent.

$$\% \text{ filled seeds} = \frac{\text{Number of filled seeds per head}}{\text{Total number of seeds per head}} \times 100$$

3.4.8 Hull content (%)

10 g of seed was weighed and soaked overnight. The hull was removed, thereafter; hull and dehulled seeds were dried in oven and weighed separately to compute the hull percentage.

3.4.9 Oil content (%)

A random bulk well dried and filled seeds sample were drawn from selected plant produce weighing 15 grams. The oil content percentage was measured using NMR facilities available at AICRP on Sunflower, Main Agricultural Research Station, UAS Campus, Raichur, Karnataka.

3.4.10 Seed yield per plant (g)

Weight of seeds of each of the five plants selected for observations was recorded and average worked out as seed yield per plant in gram.

3.5 Statistical analysis

The mean values of five randomly selected observational plants for ten different characters were used for statistical analysis. The following statistical parameters were calculated for presentation of data on different quantitative attributes.

3.6.1 Assessment of variability

a. Estimation of mean and range

The mean value of each character was calculated by dividing the total by corresponding number of observations.

$$\overline{\mathrm{X}} = \frac{1}{N}\left[\sum_{i=n}^{n} \mathrm{Xi}\right]$$

Where,

$\overline{\mathrm{X}}$ = mean of character

$\sum \mathrm{Xi}$ = Total of all the observations for the character

N = number of observations

b. Analysis of variance

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the randomized block design (Panse and Sukhatme, 1985) as given in table 3.2.

Table 3.2 Analysis of variance (ANOVA)

Source of variation	**Degrees of freedom**	**Sum of square**	**Mean sum of square**	**Calculated F Value**
Replications(r)	r-1	RSS	$\frac{\mathrm{RSS}}{\mathrm{r}-1} = \mathrm{Mr}$	Mr/Me
Treatments(t)	t-1	TrSS	$\frac{\mathrm{TrSS}}{\mathrm{t}-1} = \mathrm{Mt}$	Mt/Me
Error	(r-1)(t-1)	ESS	$\frac{\mathrm{ESS}}{(\mathrm{r}-1)(\mathrm{t}-1)} = \mathrm{Me}$	–
Total	rt-1	TSS	--	--

where,

r = Number of replications

t = Number of treatments

RSS = Replication sum of square

TrSS = Treatment sum of square

ESS = Error sum of square

Me = Error mean sum of square

c. Estimation of standard error of means (SEm), standard error of difference (SEd) and critical difference (CD)

i. The standard error of mean was calculated as,

S.E. of mean (SEm) = $\sqrt{\sigma^2 e/r}$

ii. The standard error of difference between two means was calculated as,

S.E. of difference (SEd) = SEm x $\sqrt{2}$

iii. The critical difference between two means was calculated as,

C.D. = SEd x ‘t’ at error d.f.

where,

σ^2e = Error mean square

t = Table ‘t’ value of error degrees of freedom at 5 and 1 per cent level of significance.

d. Estimation of components of variation

The phenotypic and genotypic variances were calculated by using respective mean sum squares from variances table (Johnson *et al.* 1955) as below.

i. Genotypic variance = $\sigma^2 g = MSg - MSe/r$

ii. Phenotypic variance = $\sigma^2 p = \sigma^2 g + \sigma^2 e$

iii. Environmental variance = $\sigma^2 e$ = MSe where,

MSg = Genotypic mean sum of square

MSe = Error mean sum of square

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 e$ = Environmental variance

r= Number of replication

e. Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated by using following formulae given by Burton (1952).

E.1 Genotypic coefficient of variation

$$GCV(\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} * 100$$

Where,

$\sigma^2 g$ = Genotypic variance

X = Mean of the character

E.2 Phenotypic coefficient of variation

$$PCV(\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} * 10$$

Where,

$\sigma^2 p$ = Phenotypic variance

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

E.1 Environmental variation

$$ECV = \frac{\sqrt{\sigma^2 e}}{X} \times 100$$

Where,

$\sigma^2 e$ = Environmental variance and

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

The PCV and GCV are classified as follows as suggested by Sivasubramanian and Madhavmenon (1973).

Low : Less than 10%
Moderate : 10-20%
High : More than 20%

f. Estimation of heritability (Broad sense)

Heritability percentage in broad sense was calculated as per the formula given by Burton and Devane (1953).

$$h^2(b.s.) = V_g/V_p \text{ X } 100$$

Where,

$h^2(b.s.) =$

h^2 (b.s.) = Heritability in broad sense
Vg = Genotypic variance
Vp = Phenotypic variance

The range of heritability is classified as suggested by Johnson *et al.* (1955)

Low : Below 30%
Medium : 30-60%
High : Above 60%

g. Genetic advance

Genetic advance (at 5% selection intensity) was calculated by the formula given by Allard (1960).

$$GA = \sigma^2 g / \sigma^2 p \times \sqrt{\sigma^2 p} \times K$$

OR

$$GA = K \text{ x } h^2 (b.s.) \text{ x } p$$

Where,

$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance
K = Selection differential (at 5% selection intensity K = 2.06)
h^2 (b.s.) = Heritability in broad sense

$$\text{GA as percentage of mean} = \frac{GA}{X} \times 100$$

Where,

GA = Genetic advance
X = Mean of the character

The range of genetic advance percent of mean is classified as suggested by Johnson *et al.* (1955).

Low : Less than 10%
Medium : 10-20%
High : More than 20%

Accordingly by utilizing the prediction procedure of prediction procedure of selection Johnson *et al.* (1955a) following criteria are used.

i. High heritability accompanied with high genetic advance indicate that most likely the heritability is due to additive genetic effect and selection may be effective.

ii. High heritability accompanied with low genetic advance indicates non-additive gene action and selection for such traits may not be rewarding.

iii. Low heritability accompanied with high genetic advance reveals that the character is governed by additive gene effects. The low heritability is being exhibited due to high environmental effects. Selection may be effective in such cases.

iv. Low heritability accompanied with low genetic advance indicate that the characters is highly influence by environmental effects and selection would be ineffective.

3.5.7 Correlation

To understand the association among the characters, genotypic and phenotypic correlation coefficients were worked out by adopting the method described by Singh and Chaudhary (1977).

3.5.7.1 Phenotypic correlation coefficient

$$rp = \text{covariance } (X, Y)_p / \sqrt{\text{Variance } X\ (_p)\ \text{Variance } Y\ (_p)}$$

Where,

rp = Phenotypic correlation coefficient between character X and Y

Genotypic correlation coefficient

$$rg = \text{covariance } (X, Y)_g / \sqrt{\text{Variance } X\ (_g)\ \text{Variance } Y\ (_g)}$$

Where,

rg = Genotypic correlation coefficient between character X and Y.

Significant of correlation coefficients were tested by using ‘t’ test (Panse and Sukhatme, 1985).

3.5.7 Path Coefficient Analysis

Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959).

In the present study, Seed yield per plant is dependent character (Y) while days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), volume weight g/100 ml, 100 seed weight (g), seed filling percentage, hull content (%) and oil content (%) are independent characters.

If, Y is the effect and X_1 is the cause, the path coefficient for the path from cause X_1 to the effect Y is $\sigma X_1/\sigma Y$.

Direct and indirect effects were worked out by using genotypic correlations as below:

Where,

Direct effect of X_1 on y = PX_1 Y

PX_1 = Path coefficient of X_1on Y.

Similarly, direct effects of other attributes on yield were worked out.

Indirect effect of X_1 *viz.,* X_2 or Y = PX_2 Y r X_1 X_2

Where,

Path coefficient of the component character X_2 on Y.

r X_1 X_2= Genotypic correlation between X_1 and X_2.

Similarly, indirect effects in all possible combinations were calculated for all component characters.

The residual effect (R) was calculated as below;

$$R = [1-(PX_1 . rX_1Y) - (PX_2 . rX_2Y) - \ldots\ldots(PXn. rXnY)]^{½}$$

Where,

PX_1. PX_2, ...PXn= Direct effects of respective characters on yield.

rX_1, rX_2, rXn= Correlation coefficient between respective characters and yield

3.5.8. Genetic Distance (D^2)

The generalized distance between two populations was defined by Mahalanobis (1936) as:

$$D^2 = \Sigma \lambda \text{ i.j.di. dj.}$$

Where,

λ i. j. = Reciprocal matrix to the common dispersion matrix.

di= Difference between the mean values of two populations for i^{th} character

dj= difference between the mean values of two populations for j^{th} character.

Estimation of D^2 values from the above formula is very complicated in the present study

Since, it requires the inversion of a thirteenth order determinant and then the evaluation of B (BH) / 2 terms whose sum is D^2. It was found convenient to work with a set of uncorrelated characters construed form the original measurements. D^2 with such transformed variables reduces to the evaluation of a simple sum of squares. Transformation was done by Singh and Chaudhary using pivotal condensation method (1977).

The coefficients for the transformation were obtained by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

3.5.8 Determination of Gene Constellations

Tocher"s method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for finding the clusters because a cluster is not a well-defined term. The only criterion appears to be that any two groups belonging to the same cluster should be at least on an average shows a smaller D^2 than those belonging to two different clusters. A simple device suggested by K. D. Tocher is to start with two closely associated groups and find a third group which has the smallest average D^2 from the first two. Similarly, the fourth is chosen to have the smallest D^2 from the first three and so on. If at any stage the average D^2 value of a group from those already listed appears to be high, then this group does not fit in with the former groups and is therefore taken outside the former cluster. The groups of the first cluster are then omitted and the rest are treated similarly. It is also useful to calculate the change in average D^2 within a cluster due to the inclusion of an additional group. If the changes are appreciable then the newly added group has to be considered as outside the cluster.

3.5.9. Average Intra and Inter Cluster D^2 and D Values

3.5.9.1 Average intra cluster D^2

$$D^2 = \Sigma D^2 i / n$$

Where,

Di is the sum of distance between all possible combinations (n) of the population included in a cluster.

3.5.9.2 Average inter cluster D^2

$$D^2 = \Sigma \text{ distance between the population of cluster i and j.} / ni.nj$$

Where,

ni= number of genotypes in the cluster i.

nj = number of genotypes in the cluster j.

3.5.9.3. Average intra and inter cluster distance

$$\overline{D} = \sqrt{D^2}$$

3.5.10 Cluster Means

Cluster means were calculated for individual character on the basis of mean performance of the genotype included in the clusters.

3.5.11 Cluster Diagram

With the help of D^2 values between the clusters, a diagram showing the relationships between different populations was drawn.

3.5.12. Per cent Contribution of the Characters

In all the combination, each character was ranked on the basis of $\Sigma i= y_{ij}-y_{ik}$ values. Rank 1 was given to the highest mean difference and last rank to the lowest mean difference. The percentage contribution was calculated on the basis of number of times a character appeared first rank in all the combinations (Singh and Chaudhary, 1977).

3.6 Genetic Divergence and Selection of Potent Parents

Diversity among genotypes was studied to obtain best and potent parents. The possible limits of parental divergence within which, high chances of the occurrence of heterosis were calculated by following procedure given by Arunachalam and Bandopadhyay (1984). According to them, divergence among parents was classified into four divergence classes. To study the magnitude of variation in parental divergence, the mean (m) and standard deviation (s) of the values of divergence were calculated from the table of D^2 analysis. The divergence classes were defined as follows:

DC_1 = D > or = m+s

DC_2 = D < (m+s) and > or =m

DC_3 = D > or (m-s) and < m

DC_4 = D < (m-s)

They proposed that two parents whose genetic divergence falls between (m-s) and (m+s) *viz.*, in the classes DC_2 and DC_3 when crossed with each other have higher chances of producing high heterosis when compared to a across whose parental divergence falls outside the limits [(m s), (m+s)]. The cluster combinations were classified into four divergence classes, following the method suggested by Arunachalam and Bandopadhyay (1984).

4. RESULT AND DISCUSSION

The present investigation entitled "Genetic variability, path coefficient analysis and diversity in sunflower (*Helianthus annuus* L.)' was undertaken with the view to know the variability, correlation, path analysis and genetic diversity of thirty two different genotypes of sunflower. The experiment was conducted at Agricultural Botany Research Farm, College of Agriculture, Pune during *kharif* season 2019. The results obtained in the present investigation have been presented in brief under the different headings.

4.1 Analysis of Variance

The analysis of variance was carried out to know whether the treatment (genotypes) differences after partition source of variation were significant or otherwise. The analysis of variance (Table 4.1) revealed that the mean sum of squares for all the characters studied were significant. This indicates the presence of wide variability in the genotypes studied in present table 4.1.

Table 4.1. Analysis of variance for 10 Characters.

Sr. No.	**Characters**	**Mean sum of squares**		
		Replication (d.f. 2)	**Treatment (d.f. 31)**	**Error (d.f. 62)**
1	Days to 50 per cent Flowering	2.54	54.64**	3.29
2	Days to Maturity	2.57	56.40**	3.84
3	Plant Height (cm)	40.54	1481.16**	47.34
4	Head Diameter (cm)	0.23	13.95**	1.12
5	Volume weight g/100 ml (g)	0.18	41.25**	7.49
6	100 seed weight (g)	0.08	1.45**	0.18
7	Seed filling Percentage	17.34	72.86**	11.83
8	Hull content (%)	2.27	20.25**	2.89
9	Oil Content (%)	0.88	28.76**	2.96
10	Seed yield per plant (g)	23.95	269.59**	10.93

4.2 Mean performance of the genotypes

The mean performance of 32 genotypes of Sunflower for 10 characters is given in Table No. 4.2.

4.2.1. Days to 50 per cent flowering

The variation in days to 50 per cent flowering ranged from 48.33 to 66.67. The general mean for days to 50 per cent flowering was observed to be 58.80. Fifteen genotypes were early and seventeen genotypes were late as compared to general mean. Among all thirty two genotypes, GP-1350 (48.33) was early in flowering, followed by GMU-635 (50.33), GMU-308 (53.00) which were on par with GP-1350. While, genotypes GMU-452 (66.67) followed by GP- 1217-1 (64.00) were late in flowering.

4.2.2. Days to maturity

The variation in days to maturity ranged from 80.33 to 98.67. The general mean for days to maturity was observed to be 90.55. Fifteen genotypes were early in maturity and remaining genotypes seventeen were late in maturity. The genotype GP-1350 (80.33) reported early in maturity followed by genotypes GMU-635 (80.67) which were at par with each other. While genotype GMU-452 (98.67), followed by GMU-317(96.00) were late in maturity among all the genotypes.

4.2.3. Plant Height (cm)

Plant height was recorded in the range of 89.53 cm to 188.40 cm with mean of 144.99cm. Out of thirty two genotypes, sixteen genotypes were dwarf and sixteen were taller as compared to general mean. The genotype GP-1011 was the tallest (188.40 cm) followed by MTS-35-25 (173.3cm). The genotype GMU-477 (89.53 cm) was dwarf followed by GP-1350 (107.8cm) and GMU-635 (113.4 cm).

4.2.4. Head Diameter (cm)

The general mean for head diameter was 15.83 cm. The variation in head diameter ranged from 10.40 cm to 20.63 cm. Eighteen genotypes recorded head diameter smaller than mean and fourteen reported larger head diameter than general mean. The genotype GMU-317 recorded largest head diameter (20.63 cm), followed by MTS-35-25 (20.00 cm), GP-1246 (19.03 cm) and GMU-806 (18.8 cm), which were at par with GMU-317. The smallest head diameter was reported by genotype GMU-889 (10.40 cm), followed by GMU-452(12.40).

4.2.5. Volume weight g/100 ml (g)

The variation in volume weight ranged from 39.64 g to 51.96 g. The general mean was45.22 g. Seventeen genotypes recorded lesser volume weight as compared to mean and fifteen genotypes recorded more volume weight than mean. The genotype GMU-468 (51.96 g) recorded highest volume weight followed by MTS-35-25 (51.11g) GP-1217-1 (50.42g), GP-449 (50.07g), MTB-20-3 (49.81g) and GMU-806 (49.25g) which were at par with GMU-468. While, genotype GMU-459 (39.64g) recorded lowest value for volume weight, followed by GP-1350 (39.80 g).

4.2.6. 100 seed weight (g)

The variation in 100 seed weight ranged from 4.00 to 6.79 g. The general mean was recorded as 5.11 g. Twenty genotypes recorded lower value than mean and twelve genotypes recorded higher value than mean. The genotype GMU-481 (6.79 g) recorded highest value for 100 seed weight, followed by GMU-1034(6.45 g), GMU-317 (6.41g), GMU-806 (6.11g) which were at par for the trait. The lowest value was recorded by genotype GMU-928 (4.00 g), followed by GP-1011 (4.42 g).

4.2.7. Seed filling Percentage

The general mean for seed filling percentage was 78.28 %. The variation in seed filling percentage ranged between 68.65 to 85.91%. Sixteen genotypes recorded lower and remaining sixteen genotypes recorded higher seed filling percentage than mean. The genotype GMU- 1034(85.91%) recorded highest value for seed filling percentage followed by genotype GP-2071- 1 (85.28%), GMU-806 (84.57%), GMU-481 (84.33%) and was at par with GMU-1034. Lowest seed filling percentage was recorded for GMU-452 (68.65%), followed by GMU-379-1 (69.29%).

4.2.8. Hull content (%)

The general mean for hull content (%) was observed to be 25.24 %. The variation in hull content was recorded from 20.97% to 30.28%. Twenty genotypes recorded hull content lower than mean and twelve genotypes recorded hull content higher than mean. The lowest % of hull content was observed in genotype GP-2071-1 (20.97%), followed by MTS-35-25 (21.40 %), GMU-806 (21.99%), GMU-317 (22.03%). While, the genotype GMU-452 (30.28 %) recorded highest % of hull content, followed by genotype GMU-571-1(29.43%).

4.2.9. Oil Content (%)

The variation in oil content (%) ranged from 28.56 % to 39.87 %. The general mean was34.17 %. Eighteen genotypes recorded lower and fourteen genotypes recorded higher oil content than mean. The genotype MTS-35-25 (39.86%) recorded highest oil content, followed by MTS- 35-22 (39.07 %), GMU-481 (38.47%) which were at par for the trait. While, genotype AKSFI- 42-5(28.56%) recorded lowest percentage of oil content followed by GMU-308 (28.87 %).

4.2.10. Seed yield per plant (g)

The general mean for seed yield per plant was 28.03 g. The variation in seed yield per plant was observed from 14.82 g to 46.32 g. Eighteen genotypes recorded lower seed yield per plant than mean while fourteen genotypes recorded higher seed yield per plant than mean. Highest seed yield per plant was recorded for genotype GMU-481(46.32 g), followed by GP-449 (43.10 g) and GP-2071-1 (42.96 g) which were at par with each other. Lowest seed yield per plant was recorded for genotype GP-1011 (14.82 g), followed by GMU-928(15.58 g).

The genotype GMU-477 recorded desirable performance for plant height, while genotype GMU-317 recorded highest *per se* performance for head diameter. The genotype GMU-468 exhibited highest *per se* performance for volume weight g/100 ml. The highest *per se* performance for 100 seed weight and seed yield per plant was reported by genotype GMU-481, while genotype GMU-1034 recorded highest *per se* performance for seed filling percentage. The highest *per se* performance for oil content was reported by genotype MTS-35-25. The genotype GP-1350 exhibited desirable performance for 50 per cent flowering and was earliest to mature. The desirable performance for hull content was exhibited by genotypes *viz.,* GP-2071-1 and MTS-35-25.

Therefore it can be concluded that genotypes GMU-481, GMU-1034, MTS-35-25, GMU- 317, GMU-806, MTS-35-22 and GP-2071-1 were found to be superior on the basis of their mean performance.

4.3 Parameters of Genetic Variability

Genetic variability is one of the important aspects in any crop improvement project which need to be studied in detail. Variability is measured by estimation of genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation (GCV and PCV), heritability, genetic advance and genetic advance as per cent of mean. These parameters help in selection for yield improvement through selection of desired traits.

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Environment plays an important role in expression of phenotypic characters. The phenotypic variability which is observable includes both genotypic (heritable) and environmental (non-heritable) variation. Hence, variability can be observed through biometric parameters like GCV, heritability (broad sense) and genetic advance.

Range of variability, estimates of genotypic and phenotypic coefficient of variation, heritability percentage in broad sense, genetic advance and genetic advance expressed as percentage of mean were presented in Table 4.3.

4.5.1 Genetic variability

In present investigation wide range of variability was observed for all characters under study. Highly significant differences were recorded for plant height (89.5- 188.4), seed yield (14.82- 46.32), days to maturity (80.33-98.67),days to 50 per cent flowering (48.33-66.67) and seed filling percentage (68.65-85.91), while rest of characters recorded narrow range of variability

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Table 4.2. Mean performance of 32 genotypes for 10 quantitative characters.

Sr. No.	Genotype	Days to 50 per cent Flowering (No.)	Days to Maturity (No.)	Plant Height (cm)	Head Diameter (cm)	Volume weight g/100 ml (g)	100 seed weight (g)	Seed filling Percentage	Hull content (%)	Oil Content (%)	Seed yield per plant (g)
1	AKSFI-42-5	60.33	92.33	149.93	16.30	43.13	4.61	76.73	23.53	28.57	31.48
2	GMU-308	53.00	85.33	115.87	16.57	39.03	4.64	83.39	24.71	28.87	34.67
3	GMU-317	63.33	96.00	144.00	20.63	46.21	6.41	81.29	22.03	31.50	39.24
4	GMU-379-1	55.33	87.33	128.73	14.30	42.89	4.52	69.29	26.84	33.27	18.77
5	GMU-442	62.33	94.67	168.03	15.40	48.70	4.88	77.58	27.13	30.63	25.06
6	GMU-452	66.67	98.67	158.20	12.40	45.15	4.70	68.65	30.28	32.67	16.51
7	GMU-459	61.67	92.67	163.73	14.97	39.64	4.89	80.60	28.02	37.87	25.34
8	GMU-468	55.33	86.00	123.20	15.20	51.96	4.93	81.58	24.96	32.67	26.30
9	GMU-477	57.33	89.33	89.53	16.03	47.59	4.46	75.77	26.44	37.57	26.53
10	GMU-481	56.67	88.67	164.93	18.30	44.04	6.79	84.33	22.47	38.47	46.32
11	GMU-571-1	62.67	94.33	139.67	15.63	48.90	5.17	75.71	29.43	34.13	27.67
12	GMU-595	59.33	91.00	159.73	15.27	44.43	4.88	76.69	24.27	31.27	23.17
13	GMU-635	50.33	80.67	113.40	15.30	41.45	4.68	73.42	25.09	32.03	22.51
14	GMU-806	58.33	90.00	130.87	18.80	49.25	6.11	84.97	21.99	30.63	39.54
15	GMU-889	53.67	86.33	168.67	10.40	46.52	5.40	74.28	28.60	32.97	16.17
16	GMU-928	61.33	91.67	121.33	12.90	43.50	4.00	73.17	29.40	32.50	15.58
17	GMU-1034	62.33	94.0000	141.47	17.17	48.04	6.45	85.91	22.92	35.23	39.76

Sr. No.	Genotype	Days to 50 per cent Flowering (No.)	Days to Maturity (No.)	Plant Height (cm)	Head Diameter (cm)	Volume weight g/100 ml (g)	100 seed weight (g)	Seed filling Percentage	Hull content (%)	Oil Content (%)	Seed yield per plant (g)
18	GP-449	57.67	89.33	160.87	17.77	50.07	5.89	82.04	24.31	33.40	43.10
19	GP-450	58.00	89.33	155.00	14.47	42.67	5.55	74.60	28.77	30.67	18.59
20	GP-530-1	56.33	87.67	129.87	16.67	40.01	4.77	82.56	23.64	36.90	34.83
21	GP-804	59.33	91.67	150.60	15.77	40.72	5.05	81.01	23.75	33.67	32.34
22	GP-1011	56.33	88.33	188.40	13.60	41.60	4.42	70.69	28.45	30.90	14.82
23	GP-1124	61.33	92.33	169.20	14.90	46.09	5.40	79.00	25.95	38.00	18.49
24	GP-1217-1	64.00	94.67	138.33	15.40	50.42	5.38	71.55	22.54	35.30	22.81
25	GP-1246	62.33	94.33	162.53	19.03	41.32	4.79	82.74	23.73	33.23	35.10
26	GP-1350	48.33	80.33	107.80	14.63	39.80	4.47	74.61	22.85	35.17	19.22
27	GP-2071-1	56.00	87.67	130.53	17.20	44.99	4.49	85.28	20.97	34.33	42.96
28	GP-6-198	63.00	94.67	130.00	16.03	47.53	4.61	79.79	24.95	37.07	33.08
29	MTB-20-3	53.00	85.33	163.27	14.76	49.81	4.77	73.88	25.23	38.27	17.30
30	MTB-20-9	62.67	95.33	140.53	13.83	45.14	4.50	78.53	27.88	36.90	17.49
31	MTS-35-22	60.67	92.67	158.47	16.83	45.25	6.04	84.16	25.05	39.07	35.38
32	MTS-35-25	62.67	95.00	173.27	20.00	51.11	5.88	81.28	21.40	39.87	36.94
	Mean	**58.80**	**90.55**	**144.99**	**15.83**	**45.22**	**5.11**	**78.28**	**25.24**	**34.17**	**28.03**
	S. E.	**1.05**	**1.13**	**3.97**	**0.61**	**1.57**	**0.24**	**0.98**	**0.98**	**0.99**	**1.91**
	C. D. 5%	**2.96**	**3.19**	**11.23**	**1.72**	**4.46**	**0.69**	**2.77**	**2.77**	**2.81**	**5.40**
	C. V. %	**3.08**	**2.16**	**4.74**	**6.68**	**6.05**	**8.29**	**6.74**	**6.73**	**5.04**	**11.79**

4.5.3 Coefficient of Variation

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).

Perusal of table revealed that the estimate for genetic coefficient of variation (GCV) were lower than phenotypic coefficient of variation (PCV) for all the characters studied. Seed yield per plant recorded highest values of GCV (33.12) and PCV (33.82). It was followed by plant height (15.08 and 15.32), head diameter (13.07 and 13.63), 100 seed weight (12.76 and 13.63), hull content (9.53 and 10.29), oil content (8.58 and 9.06), volume weight g/100 ml (7.42 and 8.20), days to 50 per cent flowering (7.04 and 7.26), seed filling percentage (5.76 and 6.29). While, the lowest values for GCV (4.62) and PCV (4.79) were recorded for the trait, days to maturity.

The highest difference between GCV and PCV values was recorded for oil content (1.02%), followed by 100 seed weight (0.87%), volume weight g/100 ml (0.78 %), hull content (0.76%), seed yield per plant (0.70%), head diameter (0.56%), seed filling percentage (0.53%), plant height (0.24%), days to 50% flowering (0.22%). Character, days to maturity (0.17%) recorded lowest difference between GCV and PCV.

Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits indicating that environmental factors were influencing their expression. Wide difference between phenotypic and genotypic coefficient of variations indicated their sensitiveness to environmental fluctuations whereas narrow difference showed less environmental interference on the expression of these traits. The traits which showed high phenotypic and genotypic coefficient of variations are of economic importance and there is scope for improvement of these traits through selection.

Similarly higher values of PCV than GCV was reported by Khan *et al.* (2007).The characters seed yield per plant, plant height, head diameter and 100 seed weight showed higher estimates of GCV and PCV. These results were in agreement with reports of Muhammad *et al.* (2007) for plant height; Kalukhe *et al.* (2010) for seed yield per plant; 100 seed weight and plant height; Makane *et al.* (2011) for plant height , seed yield per plant and days to maturity.

4.5.4 Heritability (b.s.)

The heritability in broad sense was worked out for all the characters, have been presented in the Table 4.3 and the performance adjudged on the basis of criteria given by Robinson *et al*. (1949) for heritability.

The estimates of heritability ranged from 81.80 % to 96.80 %. The highest heritability was recorded for plant height (96.80%), followed by seed yield per plant (95.90%), days to 50 per cent flowering (94.00%), days to maturity (93.20%), head diameter (92%), oil content % (89.70%), 100 seed weight (87.60%), hull content% (85.70%), seed filling percentage (83.80%).The lowest value for heritability was recorded for volume weight g/100 ml (81.80%).

Heritability estimates give a measure of transmission of characters from one generation to the other, as consistency in the performance of the selection depends on the heritable portion of the variability. Thus, enabling the plant breeder for isolating elite selections in the crop. Hence, the magnitude of the variation and the estimates of the heritability and genetic advance are the important parameters on which the success of selection lies.

The heritability express the proportion of the total variance that is attributed to the average effect of genes and that is what determines the degree of resemblance between parents and offspring (Falconer, 1960).

In present study, high heritability was observed for all the characters which indicates least influence of environment on these characters.

Heritability estimate provide the information regarding the amount of transmissible genetic variation to total variation and determine genetic improvement and response to selection. High heritability for traits for oil content, 1000-seed weight, days to maturity and plant height were reported by Khan *et al.* (2007).

4.5.5 Genetic Advance

The perusal of genetic advance revealed that it ranged from 1.26 g (100 seed weight) - 44.31 cm (plant height). The result showed that highest value for genetic advance was observed for plant height (44.31) cm, seed yield per plant (18.74) g, seed filling percentage (8.50), days to maturity (8.32), days to 50 per cent flowering (8.26), volume weight g/100 ml (6.25) g, oil content% (5.72), hull content % (4.59), head diameter (4.09) cm, while least genetic advance was recorded for 100 seed weight (1.26) g.

Heritability estimates alone do not provide reliable information about the gene action governing the expression of a particular character and also it does not provide the information of the amount of genetic progress that would result from the selection of best individuals. High heritability coupled with high genetic gain suggests that the gene action is mostly of additive type and therefore, direct selection of such trait will be rewarding. While, high heritability and low genetic advance indicate contribution of non -additive gene effect on the expression.

High heritability with high genetic advance was reported for plant height, seed yield per plant, days to maturity and days to 50 per cent flowering. Similar results were reported by Arshad *et al*. (2010) for days to flower initiation, days to maturity, plant height and seed yield. Kalukhe *et al.* (2010) also reported similar results for seed yield per plant and plant height.

4.5.6 Genetic advance as per cent of mean

The perusal of genetic advance as per cent of mean revealed that it ranged from 9.19% (days to maturity) -66.83% (seed yield per plant). The result showed that four attributes namely seed yield per plant (66.83)%, plant height (30.56)%, head diameter (25.85)% and 100 seed weight (24.61)% exhibited high genetic advance as per cent of mean (> 20%). Although, the traits, hull content (18.18)%, oil content (16.74)%, days to 50 per cent flowering (14.05)%, volume weight g/100 ml (13.83)% and seed filling percentage (10.86)% showed moderate genetic advance as per cent of mean (10%-20%). However, the trait, days to maturity (9.19)% exhibited low genetic advance as per cent of mean (< 10%).

4.6 Correlation

In order to find out the degree and direction of relationship of the yield contributing characters with yield and interrelationship among themselves, correlation coefficient analysis (phenotypic and genotypic) was carried out for all traits under investigation. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield.

Correlation analysis showed phenotypic and genotypic correlation for most of the characters pairs were in same direction and genotypic estimates were higher than the phenotypic one, indicating inherent association between the characters. The correlation coefficient analysis of different traits were presented in Table 4.4

Table No. 4.3 Parameters of genetic variability in 32genotypes of sunflower

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	h^2 % (b.s.)	Genetic advance	Gen. adv. as % of mean
1	Days to 50 per cent flowering	58.80	48.33-66.67	7.04	7.26	94.00	8.26	14.05
2	Days to maturity	90.55	80.33-98.67	4.62	4.79	93.20	8.32	9.19
3	Plant height (cm)	144.99	89.5-188.4	15.08	15.32	96.80	44.31	30.56
4	Head diameter (cm)	15.83	10.4-20.63	13.07	13.63	92.00	4.09	25.85
5	Volume weight g/100 ml	45.22	39.03-51.96	7.42	8.20	81.80	6.25	13.83
6	100 seed weight	5.11	4.00-6.79	12.76	13.63	87.60	1.26	24.61
7	Seed filling percentage	78.28	68.65-85.91	5.76	6.29	83.80	8.50	10.86
8	Hull content %	25.24	20.97-30.28	9.53	10.30	85.70	4.59	18.18
9	Oil content %	34.17	28.56-39.87	8.58	9.06	89.70	5.72	16.74
10	Seed yield per plant	28.03	14.82-46.32	33.12	33.81	95.90	18.74	66.83

4.4.2 Genotypic correlation

The significant and positive genotypic correlation of seed yield per plant was exhibited by the trait seed filling percentage (0.9635) followed by head diameter(0.9033) and 100 seed weight (0.6357) while it showed significant negative correlation with hull content (-0.7823). Seed yield per plant recorded non-significant positive genotypic correlation with volume weight g/100 ml (0.1449), days to maturity (0.1447), days to 50 per cent flowering (0.1198) and oil content (0.1123). These results were in agreement with reports of Rao *et al.* (1987) for 100 seed weight; Tahir *et al*. (2002) for seed filling percentage and head diameter; Sujatha *et al.* (2013) for 100 seed weight and head diameter; Singh *et al.* (2018) for hull content.

Days to 50 per cent flowering exhibited highly significant and positive correlation with days to maturity (0.9935), plant height (0.3792), volume weight g/100 ml (0.3562), 100 seed weight (0.2321) and head diameter (0.2013). While it showed non- significant positive correlation with hull content (0.1487), oil content (0.1353) and seed filling percentage (0.0754).

Days to maturity showed significant and positive association with plant height (0.4213), volume weight g/100 ml (0.3542), 100 seed weight (0.2584) and head diameter (0.2196). It showed non-significant and positive correlation with oil content (0.1392), hull content (0.1289) and seed filling percentage (0.0980).

Plant height was highly significant and positively correlated with 100 seed weight (0.3744). It showed non-significant positive association with hull content (0.1602), volume weight g/100 ml (0.1148) and oil content (0.0806) while, non-significant negative association was observed with head diameter (-0.0152) and seed filling percentage (-0.0044).

Head diameter showed highly significant and positive association with seed filling percentage (0.8170), 100 seed weight (0.6089), and volume weight g/100 ml (0.2114). It showed positive, non-significant correlation with oil content (0.1508). However, it was negatively and significantly correlated with hull content (-0.8916).

Volume weight g/100 ml exhibited highly significant and positive association with 100 seed weight (0.4419) and oil content (0.2227). Its association was non-significant positive correlation with seed filling percentage (0.0989) and non- significant and negative with hull content (-0.1491).

100 seed weight was positively and significantly associated with seed filling percentage (0.6142) and oil content (0.2283) while negative and significant association with hull content (-0.4059).

Seed filling percentage exhibited positive and significant correlation with oil content (0.2368). It showed negative and significant correlation with hull content (-0.7362)

Hull content showed non-significant and negative correlation with oil content (-0.1648).

Arshad *et al*. (2010) reported positive significant association between head diameter and 100 seed weight; Sujatha *et al.* (2013) reported positive and significant correlation of plant height with days to maturity; Binodh *et al*. (2008) reported highly positive association of head diameter to volume weight.

4.7 Path coefficient analysis

The path analysis reveals whether the association of these characters with yield is due to their direct effect on yield or is a consequence of their indirect effects via other component characters. In other words, it measures the cause of association between two variables (or traits). The correlation values denote only the nature and extent of associations exists between pair of characters. A dependent character like seed yield is influenced by several component characters which are mutually associated. Each component has two action paths *viz*., direct effect by itself and indirect effect through other components by virtue of the association it has with them. In this study, the genotypic correlation coefficients, which were higher in magnitude than the phenotypic correlation coefficients of selected component characters with seed yield were partitioned into direct and indirect effect through path coefficient analysis

In this analysis seed yield per plant was considered as effect dependent on nine independent variables which were considered as causes. The independent characters are days to 50 per cent flowering, plant height, head diameter, per cent seed filling, 100 seed weight, hull content and oil content. The direct and indirect phenotypic path effects of each of the eight component traits on seed yield are presented at phenotypic level are presented in Table 4.5.

Genotypic Path Coefficient Analysis

Five out of nine characters had positive direct effect on seed yield per plant. The characters which had positive and high direct effects are seed filling percentage (0.7139), head diameter.

Table 4.4.Genotypic correlation of 10 characters in 32 genotypes of sunflower

Observations	Days to Maturity (No.)	Plant Height (cm)	Head Diameter (cm)	Volume weight g/100 ml (g)	100 seed weight (g)	Seed filling Percentage	Hull content (%)	Oil Content (%)	Seed yield per plant (g)
Days to 50 per cent Flowering (No.)	0.9935**	0.3792**	0.2013*	0.3562**	0.2321*	0.0754	0.1487	0.1353	0.1198
Days to Maturity (No.)		0.4213**	0.2196*	0.3542**	0.2584*	0.0980	0.1289	0.1392	0.1447
Plant Height (cm)			-0.0152	0.1148	0.3744**	-0.0044	0.1602	0.0806	-0.0398
Head Diameter(cm)				0.2114*	0.6089**	0.8170**	-0.8916**	0.1508	0.9033**
Volume weight g/100 ml (g)					0.4419**	0.0989	-0.1491	0.2227*	0.1449
100 seed weight (g)						0.6142**	-0.4059**	0.2283*	0.6357**
Seed filling Percentage							-0.7362**	0.2368*	0.9635**
Hull content (%)								-0.1642	-0.7823**
Oil Content (%)									0.1123

*, ** significant at 5% and 1% level respectively

(0.6921), days to maturity (0.5086) and hull content (0.3659). While, the characters *viz.,* days to 50 per cent flowering (-0.6165*)*, oil content (-0.0872), 100 seed weight (-0.0597) and plant height (-0.0442) had negative direct effect on seed yield per plant. Seed filling percentage (0.7139) had the highest positive direct effect whereas, days to 50 per cent flowering (-0.6165) had the highest negative effect.

Seed yield per plant was the result mainly of seed filling percentage, head diameter and 100 seed weight as they were significantly correlated with it. These characters affected the seed yield directly and indirectly through other characters.

4.5.1. Days to 50 per cent Flowering

The genotypic correlation between days to 50 per cent flowering and seed yield per plant was positive and non-significant (0.1198). Its direct effect on seed yield per plant was negative and high (-0.6165). The indirect effect of this trait *via* days to maturity (0.5053) was positive and high on seed yield per plant, while *via* head diameter (0.1393), hull content (0.0544) and seed filling percentage (0.0538) and volume weight g/100 ml (0.0260) was positive and low. The indirect effect *via* plant height (-0.0168), 100 seed weight (-0.0138) and oil content (-0.0118) was negative and low.

4.5.2. Days to Maturity

The genotypic correlation between days to maturity and seed yield per plant (0.1447) was positive and non-significant. Its direct effect on seed yield per plant was positive and highly significant (0.5086). The indirect effect of this trait *via* head diameter (0.1520) was positive and moderate, while *via* seed filling percentage (0.0699), hull content (0.0472) and volume weight g/100 ml (0.0258) was positive and low on seed yield per plant. The indirect effect of this trait *via* days to 50 per cent flowering (-0.6126) was significantly high and negative, while *via* plant height (-0.0186), 100 seed weight (-0.0154) and oil content (-0.0121) was negative and low.

4.5.3. Plant Height (cm)

The genotypic correlation between plant height and seed yield per plant was negative and non-significant (-0.0398). Its direct effect on seed yield per plant was negative and low (-0.0442). The traits days to maturity (0.2143) showed positive and high indirect effect on seed yield per plant. The indirect effect *via* hull content (0.0586) and volume weight g/100 ml

(0.0084) was positive and low, while *via* days to 50 per cent flowering (-0.2338) was negative and high on seed yield per plant. The indirect effect of this trait *via* 100 seed weight (-0.0223) and head diameter (-0.0105) was negative and low, while *via* oil content (-0.0070) and seed filling percentage (-0.0031) was negative and negligible on seed yield per plant.

4.5.4. Head Diameter (cm)

The genotypic correlation between head diameter and seed yield per plant was positive and highly significant (0.9033).Its direct effect on seed yield per plant was positive and high (0.6921).The trait seed filling percentage (0.5833) *via* head diameter showed indirect significant effect on seed yield per plant. Days to maturity (0.1117) showed indirect positive and moderate effect while volume weight g/100 ml (0.0154) and plant height (0.0007) showed positive and negligible indirect effect on seed yield per plant. The indirect effect *via* hull content (-0.3263) was high and negative, while *via* days to 50 per cent flowering (-0.1241) showed negative and moderate effect on seed yield per plant. The traits, 100 seed weight (- 0.0363) and oil content (-0.0131) showed negative and low indirect effect on seed yield per plant.

4.5.5 Volume weight g/100 ml (g)

The genotypic correlation between volume weight and seed yield per plant was positive and non-significant (0.1449). The direct effect of this trait on seed yield per plant was positive and low (0.0729). The indirect effect of this trait through days to maturity (0.1801) and head diameter (0.1463) was positive and moderate, while through seed filling percentage (0.0706) was positive and low on seed yield per plant. The trait days to 50 per cent flowering (- 0.2196) showed negative and high indirect effect, while hull content (-0.0546), 100 seed weight (-0.0264) and oil content (-0.0194) showed negative and low indirect effect on seed yield per plant. Plant height (-0.0051) showed negative and negligible indirect effect on seed yield per plant.

4.5.6. 100 seeds weight (g)

The genotypic correlation between 100 seed weight and seed yield per plant was positive and highly significant (0.6357). The direct effect of this trait on seed yield per plant was negative

Table: 4.5 Direct (diagonal) and Indirect (above and below diagonal) path effects of different characters towards seed yield at genotypic level in sunflower

Characters	Days to 50 per cent Flowering (No.)	Days to Maturity (No.)	Plant Height (cm)	Head Diameter (cm)	Volume weight g/100 ml (g)	100 seed weight (g)	Seed filling Percentage	Hull content (%)	Oil Content (%)	Seed yield per plant (g)
Days to 50 per cent Flowering (No.)	**-0.6165**	0.5053	-0.0168	0.1393	0.0260	-0.0138	0.0538	0.0544	-0.0118	0.1198
Days to Maturity (No.)	-0.6126	**0.5086**	-0.0186	0.1520	0.0258	-0.0154	0.0699	0.0472	-0.0121	0.1447
Plant Height (cm)	-0.2338	0.2143	**-0.0442**	-0.0105	0.0084	-0.0223	-0.0031	0.0586	-0.0070	-0.0398
Head Diameter(cm)	-0.1241	0.1117	0.0007	**0.6921**	0.0154	-0.0363	0.5833	-0.3263	-0.0131	0.9033**
Volume weight g/100 ml (g)	-0.2196	0.1801	-0.0051	0.1463	**0.0729**	-0.0264	0.0706	-0.0546	-0.0194	0.1449
100 seed weight (g)	-0.1431	0.1314	-0.0165	0.4214	0.0322	**-0.0597**	0.4385	-0.1485	-0.0199	0.6357**
Seed filling Percentage	-0.0465	0.0498	0.0002	0.5655	0.0072	-0.0366	**0.7139**	-0.2694	-0.0206	0.9635**
Hull content (%)	-0.0917	0.0656	-0.0071	-0.6171	-0.0109	0.0240	-0.5256	**0.3659**	-0.0144	-0.7823
Oil Content (%)	-0.0834	0.0708	-0.0036	0.1044	0.0162	-0.0136	0.1690	-0.0603	**-0.0872**	0.1123

(R=0.094) ** indicates significance at 1 % level

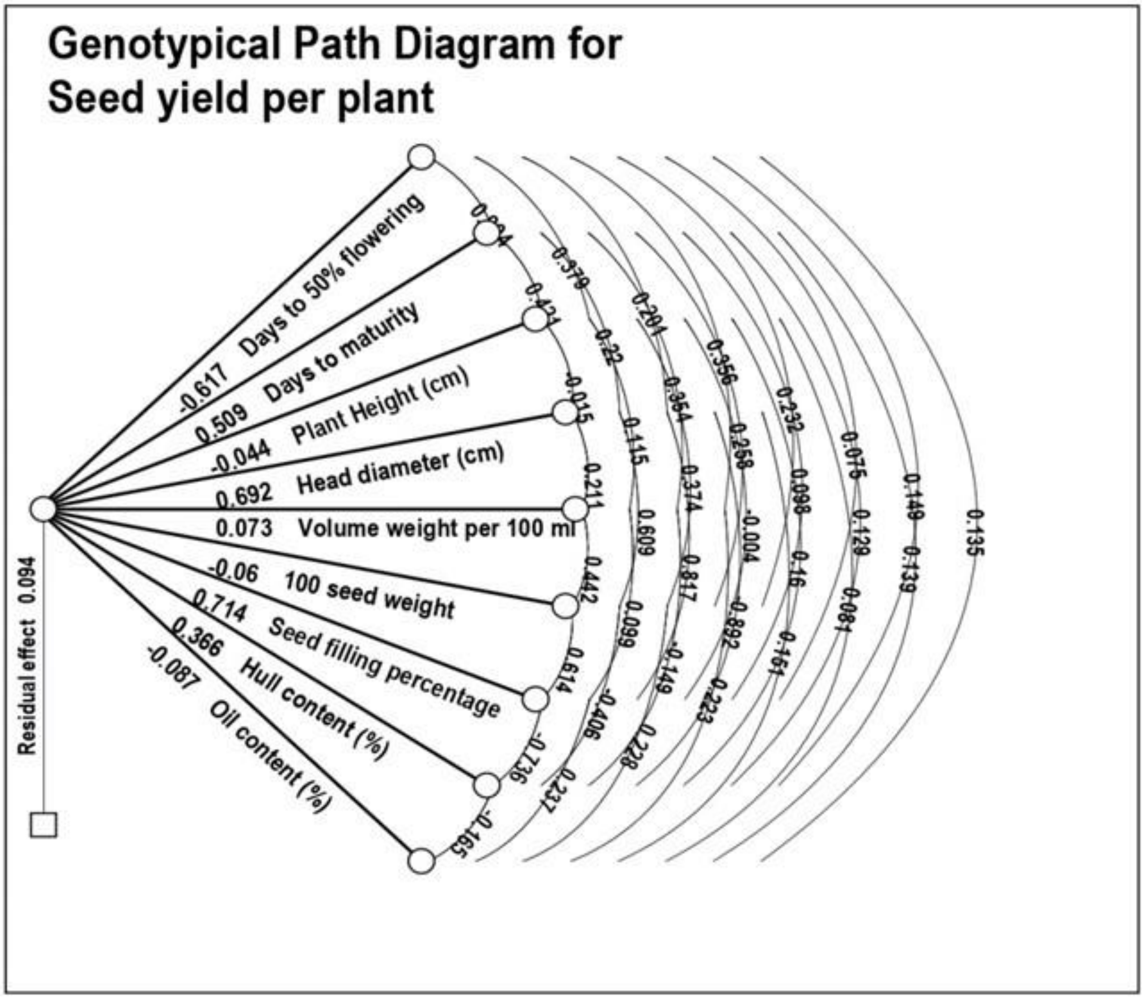


Fig. 1. Genotypic path diagram for seed yield per plant in sunflower

and low (-0.0597). The indirect effect of this trait through seed filling percentage (0.4385) and head diameter (0.4214) was positive and high on seed yield per plant. The trait days to maturity (0.1314) showed positive and moderate indirect effect on seed yield per plant, while volume weight g/100 ml (0.0322) showed positive and low indirect effect on seed yield per plant. The indirect effect of this trait *via* hull content (-0.1485) and days to 50 per cent flowering (-0.1431) as negative and moderate on seed yield per plant. The indirect effect of this trait *via* oil content (- 0.0199) and plant height (-0.0165) was negative and low on seed yield per plant.

4.5.7 Seed filling percentage

The genotypic correlation between seed filling percentage and seed yield per plant was positive and highly significant (0.9635). The direct effect of this trait on seed yield per plant was positive and high (0.7139). The indirect effect of this trait *via* head diameter (0.5655) was positive and significantly high on seed yield per plant. The trait via days to maturity (0.0498) and volume weight g/100 ml (0.0072) was positive and low, while plant height (0.0002) showed positive and negligible indirect effect on seed yield per plant. The trait hull content (-0.2694) showed negative and high indirect effect on seed yield per plant, while days to 50 per cent flowering (-0.0465), 100 seed weight (-0.0366) and oil content (-0.0206) showed negative and low indirect effect on seed yield per plant.

4.5.8 Hull content (%)

The genotypic correlation between hull content and seed yield per plant was negative and highly significant (-0.7823). The direct effect of this trait on seed yield per plant was positive and high (0.3659). The indirect effect of this trait through days to maturity (0.0656), 100 seed weight (0.0242) and oil content (-0.0144) was positive and low, while through head diameter (-0.6171) and seed filling percentage (-0.5256) was negative and high on seed yield per plant. The trait days to 50 per cent flowering (-0.0917) and volume weight g/100 ml (-0.0109) showed negative and moderate indirect effect on seed yield per plant, while through plant height (-0.0071) showed negative and low indirect effect on seed yield per plant.

4.5.9 Oil content

The genotypic correlation between oil content and seed yield per plant was positive and non-significant (0.1123). The direct effect of this trait on seed yield per plant was negative and low (-0.0872). Its indirect effect *via* seed filling percentage (0.1690) and head diameter (0.1044) was positive and moderate on seed yield per plant. The traits days to maturity (0.0708) and volume weight g/100 ml (0.0162) showed positive and low indirect effect on seed yield per plant. The indirect effect through days to 50 per cent flowering (-0.0834), hull content (-0.0603), 100 seed weight (-0.0136) and plant height (-0.0036) was negative and low on seed yield per plant.

Similar results were reported by Khan *et al.* (1992) and Farhatullah *et al.* (2006) for head diameter which exhibited positive direct effect on seed yield per plant. Sridhar *et al.* (2005) reported similar results for head diameter and per cent seed filling on seed yield. Patil (2011) reported similar results for volume weight and head diameter. The results were in conformity with reports of Neelima *et al.* (2012) for seed filling percentage and plant height; Mamata rani *et al.* (2017) for days to flowering.

The characters seed filling per cent, head diameter, days to maturity, hull content and volume weight g/100 ml had high positive direct effect on seed yield per plant. Thus, direct selection for these traits will be beneficial in yield improvement programme.

4.6 Genetic Divergence

The significant values of mean sum of squares due to genotypes from the analysis of variance (Table 4.1) revealed the presence of significant variation among the genotypes for all the characters investigated.

Thirty two genotypes were grouped into eleven clusters based on D^2 values such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of different clusters is shown in Table 4.6. Out of eleven clusters formed, cluster I and III were the largest groups comprising of 9 and 8 genotypes, respectively, followed by cluster II with 7 genotypes, cluster IV , V, VI, VII, VIII, IX, X and cluster XI with 1 genotype each.(Table No. 4.6). The 8 monogenic clusters *i.e.* IV, V, VI, VII,VIII, IX, X and XI showed zero intra-cluster distance, confirming to the result of Mohmad Shamshad *et al.* (2014) and Pandya *et al.* (2014). These results are in conformity with the observations made by Anandkumar *et a*l. (2008); Kumar *et al.* (2008) and Sujatha *et al.* (2002).

Table 4.6 Distribution of 32 genotypes of sunflower into different clusters

Clusters	No. of Genotypes included	Genotypes
I	9	AKSFI-42-5,GMU-442,GMU-459,GMU-571-1,GMU-595 GP-450,GP-804,GP-1124,MTB-20-9
II	**7**	GMU-317, GMU-481, GMU806, GMU-1034, GP-449,GP-1246, MTS-35-22
III	8	GMU-308, GMU-379-1, GMU-468, GMU-477, GMU-635, GP-530-1, GP-2071-1, GP-6-198
IV	1	GP-1350
V	1	GMU-928
VI	1	GP-1217-1
VII	1	GMU-889
VIII	1	MTB-20-3
IX	1	MTS-35-25
X	1	GP-1011
XI	1	GMU-452

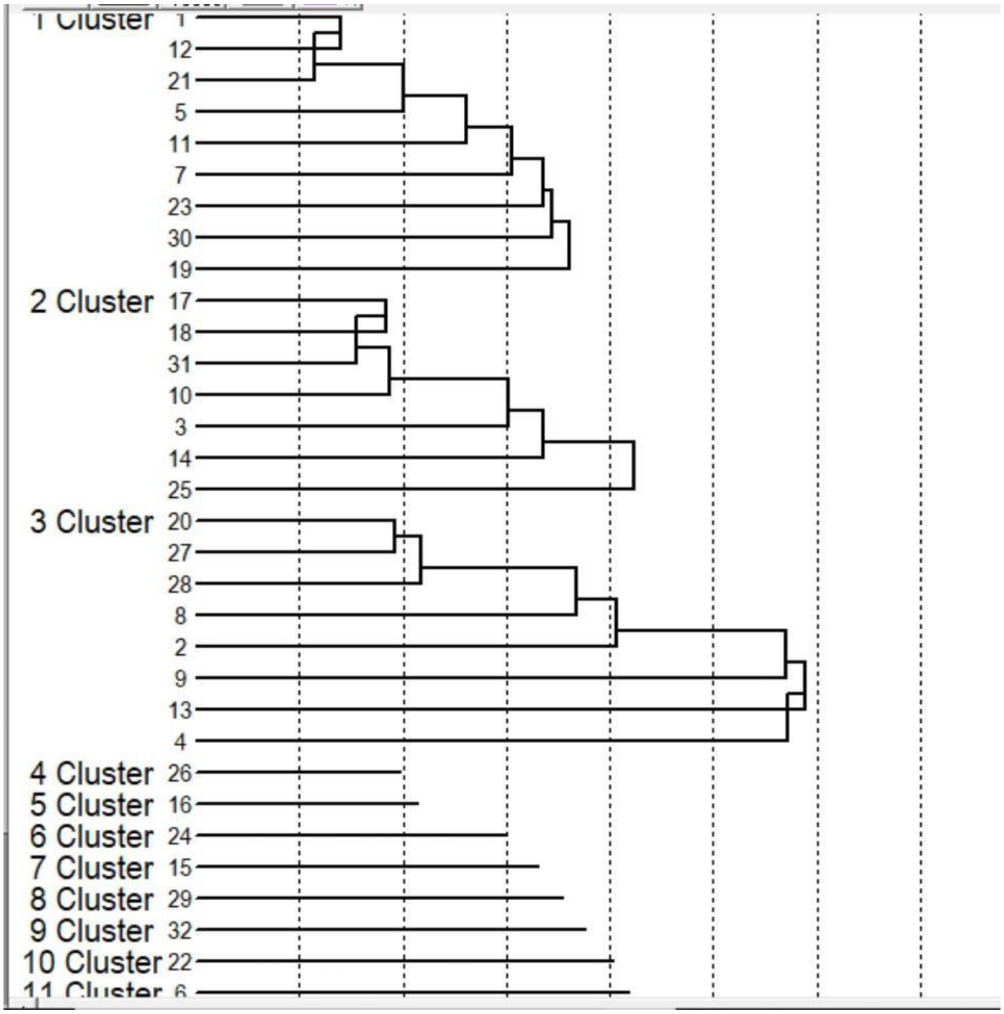


Fig 2. Distribution of 32 genotypes of sunflower into different clusters.

4.6.1 Average Inter and Intra Cluster Distances

Average intra and inter cluster D^2 values among 32 genotypes (Table 4.7) revealed that cluster I had the minimum intra cluster value (35.47) indicating that genotypes within this cluster were genetically less variable while cluster III showed the maximum intra cluster D^2 value (58.83) followed by cluster II (37.59) revealing there by the existence of diverse genotypes that fall in these clusters.

The inter cluster D^2 value ranged from 44.38 to 347.86. Minimum inter cluster D^2 values were observed between cluster X and XI indicating close relationship among the genotypes included in these clusters. Maximum inter cluster value was observed between IV and IX (347.86) clusters followed by cluster IV and XI (262.96), cluster V and IX (261.57), cluster VII and IX (248.88), cluster II and IV (245.71) and clusters IV and X (244.27), which indicates that genotypes included in these clusters are genetically diverse and may give rise to high heterotic response.Similar studies based on D^2 statistics were also reported by Sujatha *et al.* (2002) and Anandkumar *et.al.* (2008).

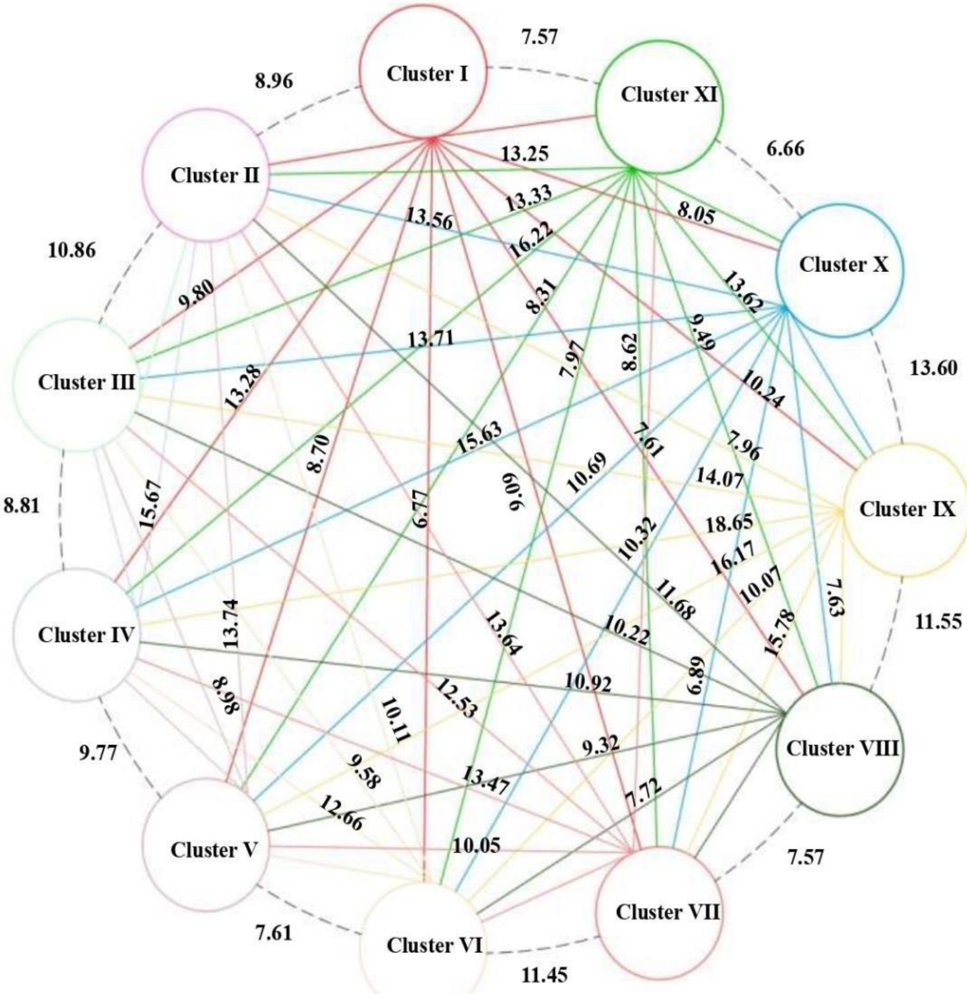


Fig.3. A cluster diagram showing inter relationship between eleven clusters in sunflower

Table No. 4.7 Average Intra and Inter Cluster D^2 and D (in parenthesis) values in Sunflower.

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**
I	**35.47** **(5.96)**	80.25 (8.96)	96.02 (9.80)	176.36 (13.28)	75.62 (8.70)	45.90 (6.77)	82.66 (9.09)	57.96 (7.61)	104.86 (10.24)	64.83 (8.05)	57.33 (7.57)
II		**37.59** **(6.13)**	117.85 (10.86)	245.71 (15.67)	188.79 (13.74)	102.23 (10.11)	186.05 (13.64)	136.33 (11.68)	63.44 (7.96)	178.41 (13.38)	175.51 (13.25)
III			**58.83** **(7.67)**	77.55 (8.81)	180.64 (8.98)	91.76 (9.58)	157.05 (12.53)	104.53 (10.22)	197.96 (14.07)	188.10 (13.71)	177.58 (13.33)
IV				**0.00** **(0.00)**	95.53 (9.77)	160.40 (12.66)	181.52 (13.47)	119.27 (10.92)	347.86 (18.65)	244.27 (15.63)	262.96 (16.22)
V					**0.00** **(0.00)**	57.90 (7.61)	101.04 (10.05)	86.94 (9.32)	261.57 (16.17)	114.23 (10.69)	70.24 (8.38)
VI						**0.00** **(0.00)**	131.22 (11.45)	59.68 (7.72)	101.36 (10.07)	106.54 (10.32)	63.52 (7.97)
VII							**0.00** **(0.00)**	57.27 (7.57)	248.88 (15.78)	47.16 (6.87)	74.34 (8.62)
VIII								**0.00** **(0.00)**	133.47 (11.55)	58.29 (7.63)	90.12 (9.49)
IX									**0.00** **(0.00)**	185.10 (13.60)	185.59 (13.62)
X										**0.00** **(0.00)**	44.38 (6.66)
XI											**0.00** **(0.00)**

4.6.2 Mean values of different clusters

The mean performances of cluster values of ten characters are presented in Table No. 4.8. A considerable inter cluster variation in respect of cluster was observed among the various clusters for ten characters studied.

Cluster II recorded highest seed yield per plant (39.779) cm, seed filling percentage (83.632), 100 seed weight (6.068) g and second highest head diameter (18.362) cm.

Cluster III has second lowest plant height (120.142) cm. Cluster IV recorded lowest plant height (107.800) cm, volume weight g/100 ml (39.803) g. It also recorded early maturity (80.333) and early in 50% flowering (48.333).

Cluster V has second highest value for hull content (29.403)% with second lowest value for oil content (32.500)% and seed yield per plant (15.580) g. It also reported lowest 100 seed weight (4.00) g.

Cluster VI reported second maximum volume weight g/100 ml (50.420) g with second late 50 per cent flowering (64.000) and with second minimum hull content (22.543)%. Cluster VII has minimum head diameter (10.400) cm.

Cluster VIII reported second highest value for oil content (38.267)% with second early in 50 per cent flowering (53.000) and maturity (85.333). Cluster IX has second highest seed yield per plant (36.943) g, seed filling percentage (81.283) and plant height (173.267) cm with maximum oil content (39.867)%, head diameter (20.00) cm and volume weight g/100 ml (51.13) g, with second late in maturity (95.000) and second highest in 100 seed weight (5.877) g with lowest hull content percentage (21.397)%.

Cluster X reported highest value for plant height (188.400) cm with second lowest value for volume weight g/100 ml (41.603) g and seed filling percentage (70.693) and 100 seed weight (4.420) g with lowest seed yield per plant (14.820) g, oil content (30.900)%.

Cluster XI is late in maturity (98.667) and 50 per cent flowering (66.667) with highest hull content (30.280)%. It also reported lowest value for seed filling percentage (68.653) and second lowest head diameter (12.400) cm.

Table 4.8 Cluster mean performance of 11 clusters for 10 characters in sunflower

Cluster No.	Days to 50 per cent Flowering (No.)	Days to Maturity (No.)	Plant Height (cm)	Head Diameter (cm)	Volume weight g/100 ml (g)	100 seed weight (g)	Seed filling Percentage	Hull content (%)	Oil Content (%)	Seed yield per plant (g)
I	60.852	92.630	155.159	15.170	44.381	4.992	77.828	26.526	33.522	24.403
II	60.190	92.143	151.876	18.362	46.311	6.068	83.632	23.215	34.505	39.779
III	55.833	87.333	120.142	15.912	44.431	4.638	78.884	24.698	34.088	29.957
IV	48.333	80.333	107.800	14.633	39.803	4.467	74.607	22.853	35.167	19.220
V	61.333	91.667	121.333	12.900	43.503	4.000	73.173	29.403	32.500	15.580
VI	64.000	94.667	138.333	15.400	50.420	5.380	71.553	22.543	35.300	22.807
VII	53.667	86.333	168.667	10.400	46.517	5.400	74.280	28.603	32.967	16.170
VIII	53.000	85.333	163.267	14.760	49.810	4.767	73.880	25.227	38.267	17.300
IX	62.667	95.000	173.267	20.00	51.113	5.877	81.283	21.397	39.867	36.943
X	56.333	88.333	188.400	13.60	41.603	4.420	70.693	28.453	30.900	14.820
XI	66.667	98.667	158.200	12.40	45.153	4.700	68.653	30.280	32.667	16.513
Mean	**58.80**	**90.55**	**144.99**	**15.83**	**45.22**	**5.11**	**78.28**	**25.24**	**34.17**	**28.03**
S.D.	5.93	6.39	22.46	3.45	8.88	1.36	5.54	5.54	5.60	10.80

4.6.3 Per cent Contribution of 10 characters for divergence in sunflower

Study was conducted for 32 genotypes of sunflower for 10 characters and the data collected was used to determine percent contribution of characters as shown in Table No. 4.9. Out of 10 characters studied, the maximum contribution to divergence was reported in characters plant height and seed yield per plant (24.19 %). It was followed by days to 50 per cent flowering (22.38 %), hull content (9.07 %), oil content (8.87 %), head diameter (5.25 %). 100 seed weight (2.22 %), seed filling percentage (1.82 %), volume weight g per 100 ml (1.81 %) and days to maturity (0.20%) contributed less to the divergence.

Table: 4.9 Per cent contribution of 10 characters for divergence in Sunflower.

Sr. No.	Source	Times ranked first	Contribution %
1	Days to 50 per cent Flowering (No.)	111	22.38
2	Days to Maturity (No.)	1	0.20
3	Plant Height (cm)	120	24.19
4	Head Diameter (cm)	26	5.25
5	Volume weight g/100 ml (g)	9	1.81
6	100 seed weight (g)	11	2.22
7	Seed filling Percentage	9	1.82
8	Hull content (%)	45	9.07
9	Oil Content (%)	44	8.87
10	Seed yield per plant (g)	120	24.19
		Total	100

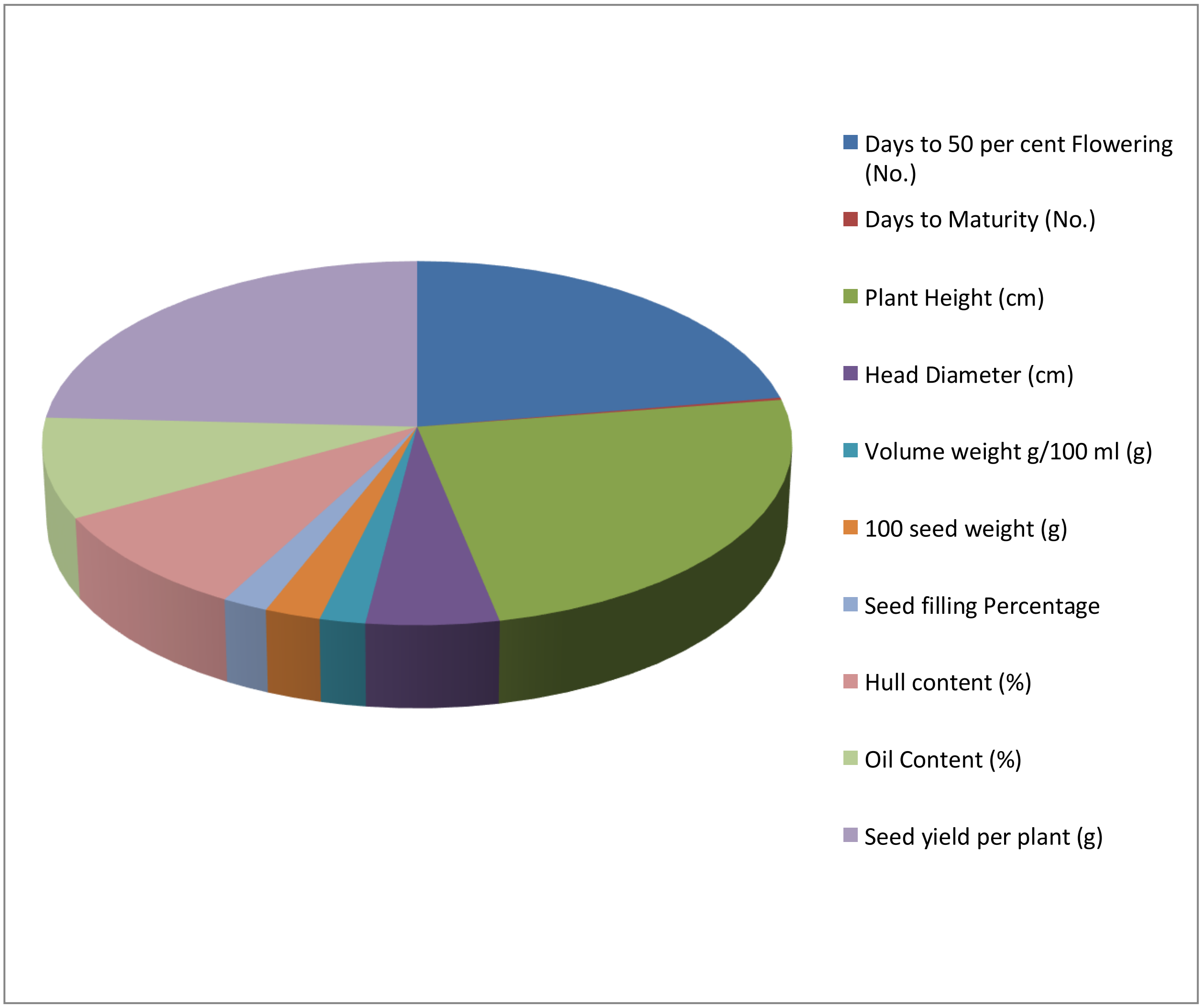


Fig.4. Per cent contribution of 10 characters for divergence in Sunflower.

4.6.4 Genetic divergence as a measure of choosing potent parent for crossing

The success of any crossing programme depends on selection of parents having high expression for the economically important characters. Therefore, diversity is the basic need of crop improvement programme. Among the different approaches of selecting parents, selection based on diversity has its own merit. Therefore, in the present study diversity among different genotypes was studied, which yielded valuable information that could be useful in suggesting potent parents for crossing. Hays and Johnson (1939) and East and Hays (1942) obtained greater heterosis from crosses between diverse parents than those between close related ones. Timothy (1963) found that genetic divergence is one of the criteria for selecting the parents for hybridization, which may produce transgressive seggregants in the later generations.

Arunachalam and Bandopadhay (1984) suggested a method, which assert parent divergence into four divergence classes (DC) *viz.*, DC_1, DC_2, DC_3 and DC_4, to take into account the magnitude of variation in parental divergence, the mean (M) and standard deviation (S) of the intra and inter cluster divergence (D) were calculated. They conducted two experiments in groundnut and rape seed and concluded that the chance for the occurrence of a high frequency of heterotic crosses with high heterotic value were more when the parent were chosen, whose divergence lies between interval M-S and M+S (DC_2 and DC_3) as compared to crosses between parents whose divergence fall outside of this interval.

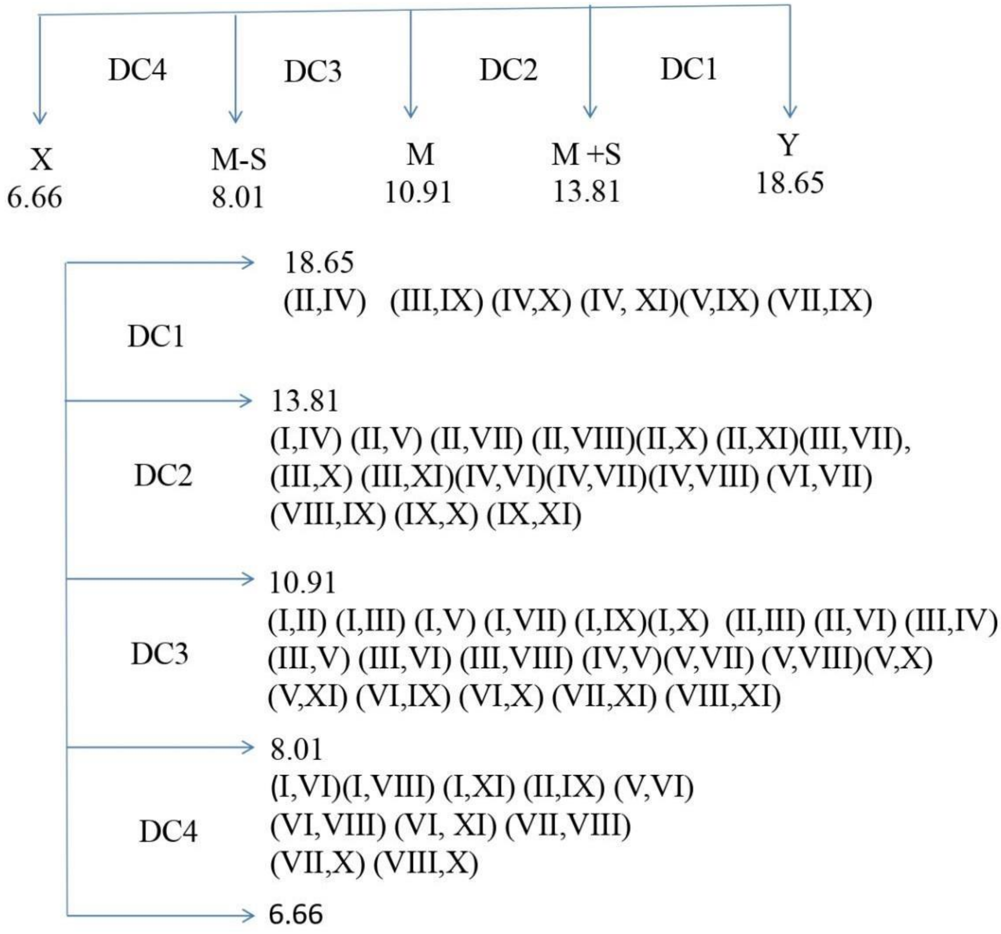
In the present investigation mean (M) calculated for inter and intra cluster distance was 10.91 with the standard deviation of 2.90 .The maximum (Y) and the minimum (X) divergence classes values among these distance were 18.65 and 6.66, respectively. The results of present investigation support the above findings.

The divergence classes were defined as follows: DC1 = D > or = m+s

DC2 = D < (m+s) and > or =m DC3 = D > or (m-s) and < m DC4 = D < (m-s)

On the basis of the results from the Table 4.1, selection of parents should be done from the cluster combinations in the divergence classes DC_1, DC_2 and DC_3 whereas, selection among the genotypes of a cluster, the *per se* performance of genotypes for different characters such as days to 50 per cent flowering, volume weight, oil content, seed yield per plant, *etc*. should be considered to obtain desirable segregates after hybridization.

Table 4.10: Distribution of different cluster combinations into four divergence classes based on D values between them



On the basis of divergence classes studied the genotypes *viz.*, GMU-317, GMU-468, GMU-481,GMU 806, GMU 1034,GP-449, GP-1246, GP-2071-1, MTS-35-22,MTS-35-25 and GP-1350 can be used for further breeding programme.

5. SUMMARY AND CONCLUSION

The present investigation entitled, "Genetic Variability, Path Coefficient Analysis and Diversity in Sunflower [*Helianthus annuus* L.]" was conducted at Botany Farm, College of Agriculture, Pune during *kharif,* 2019 with the following objectives:-

1) To study the genetic variability for seed yield and seed oil quality characters.
2) To study the correlation and path coefficient analysis in sunflower.
3) To estimate genetic diversity among different genotype of sunflower.

Thirty two genotypes of sunflower were collected from Zonal Agricultural Research Station, Solapur. The experiment was laid out in randomized block design with three replications. The observations were recorded on randomly selected five plants for ten yield and its components *viz.*, plant height, head diameter, days to 50 per cent flowering, days to maturity, volume weight gram per 100 ml, 100 seed weight, hull content, seed filling percentage, oil content and seed yield per plant.

Wide range of variation was observed for all characters under study. Analysis of variance exhibited significant treatment mean square for all the characters studied. It revealed the presence of considerable amount of variability evaluated.

5.1 Mean Performance

Highly significant differences among 32 genotypes were recorded. The genotype GMU-477 recorded desirable performance for plant height, while genotype GMU-317 recorded highest *per se* performance for head diameter. The genotype GMU-468 exhibited highest *per se* performance for volume weight g/100 ml. The highest *per se* performance for 100 seed weight and seed yield per plant was reported by genotype GMU-481, while genotype GMU-1034 recorded highest *per se* performance for seed filling percentage. The highest *per se* performance for oil content was reported by genotype MTS-35-25. The genotype GP-1350 exhibited desirable performance for 50% flowering and was earliest to mature. The desirable performance for hull content was exhibited by genotypes *viz.*, GP-2071-1 and MTS-35-25

5.2 Genetic Variability

The magnitudes of GCV and PCV were high for seed yield per plant followed by plant height, head diameter, 100 seed weight, hull content, oil content and volume weight g/100 ml. Thus, these characters provide good source of variation and hence they are useful in crop improvement programme in sunflower. The characters days to 50 per cent flowering, seed filling percentage and days to maturity registered low estimates of GCV and PCV indicating the low range of variation found in these characters, thus offers little scope for further improvement of these characters.

In the present study, high heritability values were recorded for all characters studied. Highest heritability recorded for plant height, followed by seed yield per plant, days to 50% flowering, days to maturity, head diameter, oil content, 100 seed weight, hull content, seed filling percentage and volume weight g/100 ml. Therefore, it can be concluded that environmental effects are least on the characters studied.

The highest value for genetic advance was observed for plant height followed by seed yield per plant, seed filling percentage, days to maturity and days to 50 per cent flowering. This suggests that the characters are governed by additive gene action and selection will effective. Characters volume weight g/100 ml, oil content, hull content, head diameter, 100 seed weight reported lower value for genetic advance that asserts the presence of non-additive gene action and therefore, heterosis breeding will be effective for improving these characters.

High heritability with high genetic advance was reported for plant height, seed yield per plant, days to maturity and days to 50 per cent flowering indicating that most likely the heritability is due to additive gene effects and selection may be effective for these characters.

High heritability coupled with high genetic advance as per cent of mean was recorded for seed yield, plant height, head diameter, 100 seed weight indicating that most likely the heritability is due to additive gene effects and selection may be effective for these characters.

5.3 Correlation

The genotypic correlation among various yield and yield contributing traits revealed that seed yield per plant was significantly and positively correlated with seed filling percentage, head diameter, 100 seed weight and positively but non significantly correlated with volume weight g/100 ml, days to maturity, days to 50 per cent flowering and oil content. However, it showed significant negative correlation with hull content and non-significant, negative correlation with plant height.

Days to 50 per cent flowering exhibited significant positive correlation with days to maturity, plant height, volume weight g/100 ml, 100 seed weight and head diameter. Similarly the character days to maturity shows significant positive correlation with plant height volume weight g/100 ml, 100 seed weight and head diameter. Plant height showed positive and significant correlation with 100 seed weight. The character head diameter had significant positive correlation with seed filling percentage, 100 seed weight, and volume weight g/100ml. The character volume weight g/100 ml exhibited highly significant and positive association with 100 seed weight and oil content. 100 seed weight showed positive and high significant association with seed filling percentage and oil content. Seed filling percentage had positive and significant correlation with oil content.

5.4 Path Analysis

In present study, the character seed filling percentage showed highest direct positive effect on seed yield per plant followed by head diameter, days to maturity, hull content and volume weight g/100 ml. Thus, direct selection for these traits will be beneficial in yield improvement programme. Days to 50% flowering, oil content, 100 seed weight and plant height had negative direct effects on seed yield per plant.

The character plant height showed positive indirect effect through days to maturity, hull content and volume weight g/100 ml. The character head diameter showed positive indirect effect through seed filling percentage, days to maturity, volume weight g/100 ml and plant height. Days to 50 per cent flowering exhibited indirect positive effect *via* days to maturity, head diameter, hull content, seed filling percentage, and volume weight g/100 ml. Days to maturity showed positive indirect effect through head diameter, seed filling percentage, hull content and volume weight g/100 ml. Volume weight g per 100 ml exhibited positive indirect effect *via* days to maturity, head diameter, seed filling percentage. 100 seed weight exhibited positive indirect effect through seed filling percentage, head diameter, days to maturity and volume weight g/100 ml. Hull content showed positive indirect effect *via* days to maturity, 100 seed weight and oil content. The character seed filling percentage had indirect positive effect through head diameter, days to maturity and volume weight g/100 ml. Oil content exhibited positive direct effect through seed filling percentage and head diameter.

5.5 Genetic Diversity

Genetic divergences in 32 genotypes of sunflower were measured by following Mahalanobis's D^2 statistic. Total 11 clusters were formed using Tocher's method as described by Rao (1952). Clusters I contained 9 genotypes and clusters III contained 8 genotypes, followed by cluster II with 7 genotypes while cluster IV, V, VI, VII, VIII, IX, X and cluster XI were monogenotypic.

The minimum intra-cluster distance was found in cluster I (35.47) followed by cluster II (37.59), cluster III (58.83). Cluster IV, cluster V, cluster VI, cluster VII, cluster VIII, cluster IX, cluster X and cluster XI showed no intra cluster distance due their monogenotypic nature. The maximum inter-cluster distance was observed between cluster IV and IX (347.86), followed by cluster IV and XI, cluster V and IX, cluster VII and IX cluster II and IV, cluster IV and X. This suggested that genotypes present in one cluster differ entirely from those present in another cluster.

The variance of cluster mean provided information that plant height and seed yield per plant, followed by days to 50 per cent flowering, hull content, oil content, head diameter, 100 seed weight were the main characters contributing to the genetic divergence in the present study. In the present investigation seed filling percentage, volume weight per 100 ml and days to maturity had relatively much low contribution towards divergence.

Conclusion

In the present investigation was made to evaluate sunflower germplasm obtained from Indian Institute of Oilseeds Research, Hyderabad. The experimental material consisted of 32 genotypes of sunflower. The significant treatment differences of 32 genotypes indicated good amount of variability for all the characters studied. In the present investigation seed yield per plant, plant height, head diameter, 100 seed weight, hull content, oil content and volume weight g/100 ml recorded high magnitude of GCV and PCV. Thus, these characters provide good source of variation and hence they are useful in crop improvement through selection in sunflower.

High heritability (b. s.) with high genetic advance was recorded for plant height and seed yield per plant indicate that these traits were predominantly governed by additive gene action and selection of these traits would be more effective for desired genetic improvement. High heritability (b. s.) with low genetic advance was recorded for head diameter, 100 seed weight and oil content indicate that these traits were predominantly governed by non additive gene action and therefore, heterosis breeding will be effective for improving these characters.

Seed yield per plant was significantly and positively correlated with seed filling percentage, head diameter, 100 seed weight. Plant height, days to 50% flowering, days to maturity, volume weight g per 100 ml, and 100 seed weight showed positive correlation with each other. In path analysis, the positive direct effect on seed yield per plant was through seed filling percentage, head diameter, days to maturity, hull content and volume weight g/100 ml. Thus, direct selection for these traits will be beneficial in yield improvement programme. While characters days to maturity, head diameter, volume weight g/100 ml and seed filling percentage contributed indirectly towards seed yield per plant.

All 32 genotypes under study were grouped into 11 clusters. The minimum intra cluster distance was observed for cluster I and inter cluster distance was maximum between cluster X and XI.

On the basis of divergence classes studied and per se performance of the genotypes *viz.*,GMU-317, GMU- 468,GMU-481, GMU 806, GMU 1034,GP-449, GP-1246, GP-2071-1, MTS-35-22, MTS-35-25 and GP-1350 can be used for further breeding programme.

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7. VITAE

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IN
GENETICS AND PLANT BREEDING

2020

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