Morphological Characterization and Diversity Studies in Sesame

तिल में लक्षणात्मक निरूपण और विविधता का अध्ययन

MANISHA KUMARI

Thesis

Master of Science in Agriculture

(Genetics and Plant Breeding)

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DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, MANDOR-JODHPUR
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Thesis

Submitted to
Agriculture University, Jodhpur

in partial fulfillment of the requirements for the degree of

Master of Science in Agriculture
(Genetics and Plant Breeding)

BY

MANISHA KUMARI

2019

Agriculture University, Jodhpur

College of Agriculture, Mandor- Jodhpur

CERTIFICATE-I

Dated: / /2019

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This is to certify that the thesis entitled **"Morphological Characterization and Diversity Studies in Sesame"** submitted for the degree of **Master of Science in Agriculture** in the subject of **Genetics and Plant Breeding**, embodies bonafide research work carried out by **Ms. Manisha Kumari** under my guidance and supervision and that no part of this thesis has been submitted for any other degree. The assistance and help received during the course of investigation have been fully acknowledged. The draft of this thesis was also approved by the advisory committee on / 06 / 2019.

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ABBREVIATIONS

Abbreviation		Stand for
*	:	5% probability level
**	:	1% probability level
%	:	Per cent
/	:	Per
@	:	At the rate of
i.e.	:	That is
0˚C	:	Degree Celsius/Centigrade
^{o}N	:	Degree North
^{o}E	:	Degree East
σ^2_e	:	Genotypic variance
σ^2_g	:	Environmental variance
σ^2_p	:	Phenotypic variance
$\overline{X}$	:	General mean
ANOVA	:	Analysis of variance
C.D.	:	Critical difference
Cm	:	Centimetre
CV	:	Coefficient of variation
d.f.	:	Degree of freedom
DF	:	Degree of freedom
et al.	:	(et-alai) and other
etc.	:	Etcetera
FAO	:	Food and Agriculture Organization
Fig.	:	Figure
G	:	Gram
GA	:	Genetic advance
GAM	:	Genetic advance as per cent of mean
GCV	:	Genotypic coefficient of variation
H.I.	:	Harvest index
h^2	:	Heritability
Ha	:	Hectare

EC	:	Exotic collection
Kg	:	Kilogram
M	:	Meter
Max.	:	Maximum
Min.	:	Minimum
MSe	:	Error mean sum of squares
MSg	:	Genotype mean sum of squares
MSr	:	Replication mean sum of squares
PCV	:	Phenotypic coefficient of variation
Q	:	Quintal
RBD	:	Randomized block design
Rg	:	Genotypic correlation coefficient
Rp	:	Phenotypic correlation coefficient
SE (d)	:	Standard error of difference
SEm	:	Standard error mean
SSe	:	Error sum of squares
SSg	:	Genotype sum of squares
SSr	:	Replication sum of square
TSS	:	Total sum of squares
UN	:	United Nations
&	:	And
MT	:	Metric Ton
viz.,	:	Videlicet (namely)

1. INTRODUCTION

Sesame (*Sesamum indicum* L.), belonging to the family Pedaliaceae, is one of the most ancient and important oil seed crop (Mabberley, 1997). It is also known as *til, gingelly, benniseed* and *sinsim*. *Sesamum indicum*, the cultivated type, is originated in India (Ogasawara *et al*. 1988). The genus *Sesamum* contains more than 30 species of which *Sesamum indicum* is the commonly cultivated (Nayar and Mehra, 1970). Sesame is a drought tolerant crop particularly at vegetative stage because of its extensive root system. The diploid chromosome number of sesame is 2n=26 and it is usually self- pollinated although cross- pollination reported ranging from 5 to over 50% (Pathirana, 1994).

India, China, Burma and Sudan are the major sesame producing countries that contribute to about 60% of the total world production. Sesame is one of the nine major oilseed crops of India. It is an important *kharif* crop mainly cultivated in states of Gujarat, Rajasthan, Andhra Pradesh, Tamil Nadu, Madhya Pradesh, Maharashtra, Karnataka, Uttar Pradesh, West Bengal, Orissa and Assam. In India, sesame is grown in an area of 13.98 lakh hectare with production of 4.18 lakh tonne with an average productivity of 291 kg/ha, while in Rajasthan it is grown over an area of 2.72 lakh ha with an annual production of 73.55 thousand tonne and productivity of 270 kg/ha (Anno. 2017).

Sesame is grown for its seeds and oil. It had earned a poetic label “Queen of Oilseeds” as its oil and protein are of very high in quality. Sesame is highly nutritive and also possesses high oil (38-54%) and protein content (18-25%). The seed is also used on burger, breads and cakes. Sesame seeds are digestive, rejuvenative, anti aging and rich in vitamins E, minerals like calcium, phosphorus, iron, copper, magnesium, zinc and potassium with this unique composition coupled with high-unsaturated fatty acid (linolinic and tocopherol) make the sesame nearly perfect food (Lokesha and Theertha Prasad, 2006). Sesame oil has long shelf-life due to presence of lignans (which have remarkable antioxidant function), sesamol, tocopherols, sesamolin and their derivatives prevent oxidation of the oil and give it long shelf life and stability (Brar and Ahuja, 1979). All these characters make it holds tremendous potential for export.

India produces large varieties of sesame seed varying in colour from white to red, brown and black. The brown seeds are used mainly for crushing, white due to desirable taste, is used for making sweets and confectionary products while black seeds are used in Japan for seasoning. Hulled white sesame is used in Europe and other Western countries in making bakery products.

In spite of its good quality oil and health benefits, cultivation of sesame is not wide in India due to low yield potential to other crops. The low yield of sesame can be attributed to various factors such as its cultivation in un-irrigated areas, lack of improved varieties tolerant to abiotic and biotic stresses, low harvest index values, significant yield loss during threshing and uneven ripening of capsules. Furthermore, properties such as undefined growth habit, asynchronous capsule ripening and seed shattering are also some important factors which are limiting the production of sesame (Ashri, 1998).

The knowledge of genetic variability in germplasm will help in the selection and breeding of high yielding, good quality cultivars that will increase production. India is wealthy of sesame germplasm and some local cultivars provide raw material for improved varieties (Ali *et al*., 2009). Amelioration of productivity necessitates us to detection or cataloguing of sesame genotypes along with the assessment of genetic variability and diversity in sesame germplasm. In India, the availability of plant genetic resources and genetic diversity allows us to develop improved genotypes to adapt under changing environments such as new pests, diseases and climatic conditions.

Yield is the end product of multiplicative interaction among various yield components and this involves a thorough perception of character association and direct and indirect effects contributed by each character on seed yield before initiating any breeding programme. Correlation is the measure of the mutual relationship between two variables and may help the plant breeder to know how the improvement of one character will bring simultaneous improvement in other characters. Correlation alone does not provide the true contribution of the characters towards yield, the genotypic and phenotypic correlation coefficients should be divided into direct and indirect effects through path coefficient analysis. Path coefficient analysis is a standardized regression coefficient and measures the direct influence of one variable.

Genetic diversity of crops plays an important role in sustainable development and food security (Esquinas-Alcazar, 2005), as it allows the cultivation of crops in the presence of various biotic and abiotic stresses. Genetic diversity is an inherited variation among and between populations, created, activated and maintained by evolution. Genetic divergence is a pervasive feature of all species in nature and plays an important role in the selection of parents among the genotypes having wider variability for different characters and ultimately for rational use of genetic resources for use in hybridization to create new variability. Mahalanobis D^2 statistic has been proven to be a substantial tool for measuring genetic divergence in a stated population.

Keeping in view the aforesaid aspects, the present investigation was undertaken with the following objectives:

1. To assess genotypic and phenotypic variance, heritability and genetic advance in sesame genotypes for seed yield & it's component traits
2. To estimate genotypic and phenotypic correlation and direct & indirect effects of yield components on seed yield through path coefficient
3. To estimate genetic divergence through D^2 statistics

2. REVIEW OF LITERATURE

A brief review of available literature, in consonance with the objectives of the present investigation in respect of sesame crop, is being presented under the following subheads:-

2.1 Genetic variability, heritability and genetic advance
2.2 Association analysis
    2.2.1 Correlation coefficient analysis
    2.2.2 Path coefficient analysis
2.3 Genetic divergence using Mahalanobis's D^2

2.1 Genetic variability, heritability and genetic advance

Fisher (1918) studied genetic variability for the first time which is prerequisite for selection in any breeding programme. Partitioning of observed variability into heritable and non-heritable components is necessary to get an indication of the genetic coefficient of variability as a useful measure of the magnitude of genetic variance present in the population.

Heritability refers to the proportion of observed variation in a particular trait that can be attributed to inherited genetic factors in contrast to environmental ones. High heritability indicates that it should be easy to conduct effective selection for the trait. Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present in relation to observed variation.

Heritability can be used to calculate genetic advance which indicates the degree of gain in a character obtained under a particular selection pressure. According to Allard (1960), effect of genetic advance under selection depends upon genetic variability, heritability and selection intensity.

Sudhakar *et al.* (2007) observed high heritability and high genetic advance for seed yield per plant, number of capsules per plant, number of primary branches per plant, number of seeds per capsule, plant height and days to 50% flowering but high heritability and low genetic advance was recorded for oil content.

The study carried out by Kumhar *et al.* (2013) using 36 genotypes of sesame, showed high heritability coupled with high genetic advance for the characters like seed yield, free fatty acid, oxalic acid content, number of productive capsules per plant and productive branches per plant revealing that these characters were governed by additive gene action.

Bharathi *et al*. (2014) conducted an experiment with sesame genotypes and recorded moderate to high magnitude of PCV and GCV for seed yield per plant, number of capsules per plant and number of branches per plant. High heritability coupled with high genetic advance was recorded for seed yield per plant, number of capsules per plant and number of branches per plant showing the presence of additive gene action.

Chandra Mohan (2014) studied genetic diversity in 280 genotypes of sesame and observed the high heritability coupled with high genetic advance for capsules per plant indicating the presence of additive gene effect, whereas, lower estimates of both heritability and genetic advance were reported for days to maturity and capsule length showing the presence of non-additive gene action.

The study carried out by Tripathi *et al.* (2014) using 100 sesame genotypes showed high heritability combined with high genetic advance for seed yield/plant and 1000 seed weight indicating that these characters are governed by additive gene effect.

Bindu *et al*. (2014) studied 31 sesame genotypes for variability in seed yield and yield components and reported high heritability and high genetic advance as percent of mean for the characters *viz*., plant height, number of branches, and number of capsules per plant, oil content and yield.

Similarly high heritability coupled with high genetic gain were also reported by Ismaila and Usman (2014) for number of capsules per plant, number of branches per plant and seed yield per hectare which indicated the additive nature of inheritance.

The investigation carried out by Hika *et al.* (2015) also showed high heritability coupled with high genetic advance estimates for seed yield, primary branches per plant, number of branches per plant, biological yield and moderate heritability for test weight and harvest index.

Abate *et al*. (2015) evaluated 49 sesame genotypes for genetic variability. Higher genotypic variance was observed for seed yield and number of capsules per plant while moderate heritability with moderate genetic advance was observed for most of the yield related traits which were showing the presence of both additive as well as non-additive gene action.

Saxena and Bisen (2016) studied variability in 26 sesame genotypes and reported slightly higher amount of PCV than GCV. They observed high GCV and PCV values for number of capsules per plant and seed yield per plant while number of primary branches per plant and number of secondary branches per plant showed high values for PCV only.

Tripathy *et al*. (2016) recorded highest genotypic coefficient of variation for number of primary branches per plant followed by seed yield per plant, number of capsules per plant, number of seeds per capsule. The characters *viz.,* number of primary branches per plant, height to first capsule and seed yield revealed moderate heritability associated with moderately high genetic advance which showed presence of both additive and non-additive gene effects.

The investigation carried out by Prithviraj and Parameshwarappa (2017) using 130 sesame genotypes to evaluate genetic variability and other related parameters showed high genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) for seed yield per plant followed by number of capsules per plant, number of capsules on the main stem and number of seeds per capsule. High heritability and high genetic advance as percent mean were observed for seed yield per plant, number of capsules on the main stem, number of capsules per plant, plant height and number of seeds per capsule.

Aristya *et al*. (2017) studied 18 mutant lines of sesame and recorded highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for number of secondary branches, number of nodes to first flower, number of capsules per plant, stem height from base to first branch, yield of biomass per plant and seed yield per plant.

Teklu *et al.* (2017) evaluated 64 accessions of sesame and reported highest phenotypic and genotypic coefficient of variation for number of capsules per plant and seed yield per ha. They also observed high heritability value for days to 50% flowering, plant height, height to first capsule and number of capsules per plant.

Singh *et al*. (2018) studied 75 sesame genotypes and found high value for PCV and GCV for number of secondary branches per plant, followed by number of primary branches per plant, seed yield per plant, number of seed per capsule and number of capsules per plant. High heritability coupled with moderate genetic advance was recorded for oil content and days to 50% flowering.

The investigation carried out by Haibru *et al*. (2018) in 45 genotypes of sesame showed high magnitude of GCV and PCV for branch number per plant, capsule number per plant, seed weight per capsule, capsule split before and after drying, capsule opening before and after drying as well as seed yield per plant. High estimates of heritability were observed for all the characters. High heritability along with high genetic advance was recorded for all the traits except days to maturity, plant height and capsule length.

2.2 Association analysis

2.2.1 Correlation coefficient analysis

Correlation coefficient analysis is a statistical evaluation which measures the degree and direction of the linear relationship between two or more characters of plant. Correlation analysis includes both genotypic and environmental effects. Most of the characters are complex in nature due to interaction of several components. It is utmost important to understand the association between yield and its component traits to make the best use of these associations in selection procedure.

A brief review of studies on the correlation analysis in sesame is being presented here:-

Goudappagoudra *et al*. (2011) evaluated 120 F_4 families of sesame and recorded positive association of seed yield per plant with number of capsules per plant, number of seeds per capsule, number of branches per plant, plant height and 1000 seed weight. The magnitude of correlation was reported highest in case of number of capsules per plant.

Ibrahim and Khidir (2012) reported that seed yield per plant exhibited positive association with number of capsules per plant, 1000-seed weight and number of seeds per capsule.

Hika *et al*. (2014) recorded positive and significant genotypic as well as phenotypic correlations of seed yield with all twelve characters except for plant height and biomass yield indicating that they are important yield components and can be used for yield improvement in sesame breeding programme.

Fazal *et al*. (2015) studied 13 sesame genotypes and reported highly significant positive correlation of yield per plant to all other traits both at genotypic and phenotypic level.

Sabiel *et al*. (2015) recorded highly significant and positive correlation of seed yield with biomass, 1000-seed weight and plant height in twelve genotypes of sesame but it was highly significant and negatively correlated with days to flowering.

Saxena and Bisen (2016) studied 26 advanced varietal lines of sesame and indicated strong positive association of seed yield per plant with number of secondary branches per plant and number of capsules per plant.

Sopundharrya *et al*. (2017) evaluated 62 genotypes of sesame for ten characters and reported that seed yield per plant was significantly and positively associated with number of seeds per capsule and number of capsules per plant.

Kindeya (2017) reported that seed yield had a significant and positive correlation with number of branches and number of capsules per plant while its association with days to maturity and flowering time was negative significant.

The study conducted by Agrawal *et al*. (2017) with 40 genotypes of sesame showed significant positive association of seed yield per plant with days to maturity, number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000- seed weight and protein content.

Abhijatha *et al*. (2017) evaluated 33 accessions of sesame and reported positive and significant association of yield with yield attributing characters such as plant height, number of primary branches, number of capsules per plant, length of capsule and number of seeds per capsule, signifying that selection based on these characters may improve yield.

The study carried out by Abate (2018) to evaluate 81 mid altitude sesame accessions showed high and significant positive correlation of seed yield with characters *viz.,* number of capsules per plant, biomass yield, harvest index and test weight. Plant height and number of seed per capsule also showed moderately positive significant association with seed yield.

Sasipriya *et al.* (2018) reported positive significant correlation of seed yield with number of branches per plant, number of capsules per plant, capsule length, number of seeds per capsule and 1000 seed weight.

Singh and Bisen (2018) studied 60 genotypes of sesame and reported that seed yield per plant exhibited positive and significant correlation with days to flower initiation, days to 50% flowering, number of primary branches per plant, number of secondary branches per plant and number of capsules per plant both at genotypic and phenotypic levels.

Patil and Lokesha (2018) evaluated 100 sesame advanced mutant breeding lines which exhibited that number of capsules per plant, number of branches per plant, capsule length, number of seeds per capsule, capsule weight and test weight had strong and significant positive correlation with seed yield per plant at both genotypic and phenotypic levels.

Ramprasad *et al.* (2019) conducted an experiment with 41 genotypes of sesame and recorded observations on 10 traits. Character association studies showed significant positive association of seed yield per plant with plant height, number of branches per plant, first capsule height, capsules per plant and 1000-seed weight.

2.2.2 Path coefficient analysis

Path analysis is a straight forward extension of multiple regressions which splits the correlation coefficient into measure of direct and indirect effect. Correlation study becomes more complex due to association of several components so path coefficient analysis helps to overcome this complication by measuring the direct and indirect influence of one variable upon the other by partitioning correlation coefficient into the components of direct and indirect effects. This method was developed by Sewall Wright in 1921 but Dewey and Lu (1959) employed this method for the first time in plants to disentangle the direct and indirect influences of components of seed yield.

Gnanasekaran *et al.* (2008) evaluated 40 sesame genotypes and their study showed that the indirect effects of number of branches per plant through number of capsules per plant and *vice versa* was also positive.

The study carried out by Gangadhara *et al.* (2012) by using 81 local accessions and elite varieties of sesame on eleven characters revealed maximum positive direct effect of capsules per plant on seed yield followed by seed weight per capsule and plant height, while negative direct effect on capsule length, oil content and days to maturity was observed.

Rao *et al.* (2013) reported that number of capsules per plant and test weight exhibited positive direct association with seed yield per plant and were important traits to be considered for realizing the improvement in seed yield.

The investigation carried out by Abate and Mekbib (2015) using 49 sesame genotype revealed that highest positive direct effect on seed yield was exhibited by biomass per plant followed by harvest index and 1000 seed weight, while negative direct effect on seed yield was shown by days to maturity at both phenotypic and genotypic level.

Fifty four diverse genotypes of sesame studied by Bharathi *et al.* (2015) during *Kharif* revealed that number of seeds per capsule, number of capsules per plant, number of branches per plant and capsule length had positive direct effect on seed yield, while negative direct effect was shown by days to 50% flowering.

Fazal *et al.* (2015) studied path analysis in 13 genotypes of sesame which revealed that capsules per plant had highest direct effect on seed yield per plant and seeds per capsule had highest indirect effect *via* number of capsules per plant on seed yield per plant.

Saxena and Bisen (2016) studied 26 advanced varietal lines of sesame and recorded high positive direct effect of number of secondary branches and number of capsules per plant on seed yield per plant. Hence number of secondary branches per plant and number of capsules per plant may be used for selection for improvement of seed yield.

The study carried out by Agrawal *et al.* (2017) to evaluate 40 genotypes of sesame exhibited positive direct effect of characters *viz*., days to maturity, capsule length, number of branches per plant, protein content, number of capsule per plant, number of seeds per capsule, 1000 seed-weight and leaf length with seed yield, while plant height, internodal length and number of leaves per plant and days to 50% flowering were having negative direct effect.

Abhijatha *et al.* (2017) conducted an experiment with 33 accessions of sesame which showed that number of capsules per plant had the highest positive direct effect on seed yield per plant followed by number of seeds per capsule. Number of primary branches per plant and days to maturity had shown the maximum positive indirect effect on seed yield per plant through numbers of capsules per plant.

Sopundharrya *et al*. (2017) studied path analysis for yield and its contributing traits in 62 sesame genotypes and revealed maximum positive direct effect of number of seeds per capsule on seed yield followed by number of capsules per plant. Lalpantluangi *et al*. (2018) studied 21 genotypes of sesame and recorded positive direct effect of strover yield, days to 80% maturity, seeds per capsule and number of secondary branches per plant on seed yield.

Singh *et al.* (2018) reported highest direct effect of days to flower initiation and number of capsules per plant on seed yield per plant in 60 genotypes of sesame.

Study conducted by Sasipriya *et al*. (2018) with 45 genotypes of sesame showed highest positive direct of 1000-seed weight on seed yield followed by number of capsules per plant and number of seeds per capsules both at phenotypic and genotypic level. Number of seeds per capsule, capsule length and plant height also showed positive direct effect on seed yield.

Abate (2018) reported the maximum positive direct effect of number of capsules per plant, biomass yield, days to maturity, harvest index and 1000-seed weight on seed yield showing that these traits can be used for selection to improve the seed yield.

Forty one genotypes of sesame studied for path coefficient analysis by Ramprasad *et al*. (2019) to identify their efficiency with respect to 10 quantitative characters revealed that the number of capsules per plant, diameter of stem, capsule length, number of branches per plant and plant height directly affected the seed yield per plant.

2.3 Genetic divergence

Knowledge on the nature and magnitude of genetic variation present in a crop species play an important role in framing successful crop breeding programs. Mahalanobis's D^2 statistics is the major tool for identification of genetically divergent parents for their exploitation in hybridization programs. It measures the degree of diversity and determines the relative proportion of each component character to the total divergence.

Begum *et al*. (2011) evaluated 50 genotypes of sesame for diversity using Mahalanobis's D^2 analysis and grouped them into five clusters. The highest intra cluster distance was observed in cluster IV while the lowest distance was recorded in cluster V. The results revealed that clusters having highest inter-cluster distance should be given more emphasis during selection of genotypes as parents for crossing, which may produce new recombination.

The experiment conducted by Narayanan and Murugan (2013) to evaluate 16 sesame genotypes using Mahalanobis D^2 statistics revealed that days to 50% flowering, days to maturity, plant height, number of pods per plant, seed yield, and number of primary branches per plant and test weight contributed to considerable variability. Among all the traits observed, seed yield contributed the most (89.49%) towards the divergence of genotypes followed by number of pods per plant, days to 50% flowering and plant height.

The field experiment conducted by Kumhar *et al*. (2013) to study the genetic diversity in 36 genotypes of sesame for ten characters were grouped into seven clusters using Ward's minimum variance method. The inter cluster Euclidean^2 distance was maximum between cluster III and VII (42.71) and followed by cluster VI and VII (41.90) and cluster II and VII (39.03). Among the ten characters, number of primary branches per plant contributed the most towards the divergence of genotypes.

Jadhav and Mohrir (2013) collected 31 accessions of sesame to evaluate for genetic divergence using D^2 statistics. The genotypes were grouped into seven clusters with three solitary clusters. Character oil content contributed maximum (91.83%) towards genetic divergence. Based on the inter cluster distance, cluster I, II, III and VII could be used for intercrossing to obtain heterosis and wider adaptability as they were distant clusters.

Genetic divergence study comprising of 100 sesame genotypes for nine characters carried out by Tripathi *et al*. (2014) using D^2 analysis grouped the genotypes into eleven clusters. Maximum inter cluster distance was observed between cluster VI and cluster XI followed by cluster V and XI, while lowest cluster distance was observed between cluster IV and V. Among all the nine traits studied, days to 50% flowering contributed highest towards genetic divergence.

Chandra Mohan (2014) conducted an experiment with 280 sesame genotypes to study the genetic diversity. Based on diversity, the genotypes were grouped into 12 clusters and highest inter cluster distance was observed between cluster VI and XII followed by cluster VI and IX, cluster II and VI and cluster III and IV. Among all the traits studied capsule per plant and plant height contributed maximum towards genetic divergence while no contribution was noticed from capsule length.

Diversity study conducted by Baraki *et al*. (2015) in 13 sesame genotypes from the western Tigray region of Northern Ethiopia grouped genotypes into four clusters and the maximum genetic distance divergence was observed between cluster II and cluster III.

Bamrotiya *et al*. (2016) assessed the genetic diversity among 40 genotypes of sesame which formed three clusters. The cluster I had 36 while cluster II contained three genotypes whereas cluster III possessed only one genotype. Height to first capsule contributed maximum to the genetic divergence followed by number of capsules per leaf axil, length of capsule, seed yield per plant and number of seeds per capsule.

Tripathy *et al*. (2016) characterized 12 sesame genotypes for genetic diversity and grouped into six clusters based on Euclidian genetic distance following SAS software programme. Cluster IV genotypes showed dwarf plant types along with capsule bearing from lower height while cluster I bore longer and bold capsule resulting in highest number of seeds per capsule coupled with increased 500-seed weight.

Soundharya *et al*. (2017) applied Mahalanobis's D^2 statistics to access the divergence among the 62 genotypes. All the genotypes were grouped into six clusters where, cluster I was largest containing 44 genotypes followed cluster II was twelve genotypes, cluster VI with three genotypes. cluster III, V and IV had only one genotype. The inter cluster distance was maximum between cluster IV and VI, minimum between cluster I and III.

The diversity study carried out by Patil *et al*. (2018) using 100 sesame advanced breeding lines using Mahalanobis's D^2 grouped lines into 12 clusters. The intra cluster distance was maximum in cluster III though it had only 14 entries but it was lowest in cluster I despite having of 76 entries. Inter cluster distance was maximum between cluster III and XII. The maximum divergence was contributed by height from ground to first capsule followed by days to 50% flowering, number of capsules per plant and days to maturity.

The study of 33 indigenous genotypes of sesame carried out by Gogoi *et al.* (2018) to assess the extent of genetic diversity revealed considerable genetic diversity and led to their grouping into eight clusters. The yield per plant contributed most to genetic divergence followed by days to 50% flowering and 1000 grain weight.

Tanwar and Bisen (2018) conducted an experiment with 97 diverse genotypes of sesame which clustered all the genotypes into 15 groups. Cluster I was the largest among all clusters comprising 48 germplasm. The highest intra cluster was recorded in cluster V and the inter cluster distance was highest between the cluster VI and cluster XV followed by cluster VIII and cluster XV.

The field experiment carried out by Singh *et al.* (2018) to evaluate 75 sesame genotypes to assess the genetic divergence present in the sesame germplasm based on the Mahalanobis distance and cluster analysis showed maximum inter cluster between cluster XII and IV followed by clusters VIII and IX. The trait days to flower initiation contributed maximum to genetic divergence followed by oil content and number of capsules per plant.

Swathy *et al.* (2018) evaluated 90 genotypes of sesame using Mahalanobis's D^2 statistics. Among the nine clusters formed cluster IX and V showed highest inter cluster distance indicating that they are the most diverse cluster whereas cluster VIII and II were the least diverse as indicated by the inter cluster distance. Cluster means for number of capsules per plant and seed yield per plant were highest in cluster IX while cluster III had highest for oil content and days to 50% flowering.

3. MATERIALS AND METHODS

The field experiment entitled "**Morphological Characterization and Diversity Studies in Sesame**" was conducted with 28 genotypes during *kharif* season of 2018 at Agricultural Research Station, Mandor (Jodhpur). The details of experimental procedures adopted, materials used, methodology employed and data collected for genotype evaluation during the course of investigation are illustrated in the following subheads.

3.1 Experimental site

The experiment was conducted at Agricultural Research Station, Mandor-Jodhpur. Geographically, Jodhpur is situated between 26^{o} 15' N to $26\ ^{0}$45' North latitude and 73^{o} 00' E to latitude 73^{o} 29' East longitude at an altitude of 231 meter above mean sea level. This region falls under agro-climatic zone Ia, (Arid Western Plains) of Rajasthan.

3.2 Climate and weather conditions

The climate of Jodhpur is typically arid with hot dry and sunny summers. The average annual rainfall is about 367 mm (CV 52%) and major part of it (85 to 90%) is received from June to September (*kharif* season) by the southwest monsoon. The normal time of onset of monsoon is the last week of June to first week of July but weather aberrations are quite common. The other distinct climatic features of this region are low relative humidity (15-30%), high wind velocity (30-40 km $hour^{-1}$), high solar incidence (520 cal cm^{-2}), high potential evapo-transpiration (1843 mm $year^{-1}$) and wide range of maximum ($24.6^{o}C$ in January to $41.6^{o}C$ in May) and minimum ($9.6^{o}C$ in January to $27.7^{o}C$ in June) temperatures.

Weather influences the growth, yield and quality of crop as well as biotic phase of soil during season as an input. Hence, it is important to present climatic variables in this context. The periodical mean of weekly weather parameters for the period of the experimentation recorded from the meteorological observatory of Central Arid Zone Research Institute, Jodhpur, are presented in Appendix I. The mean daily maximum and minimum temperature fluctuated between $31.6^{0}C$-$39.7^{0}C$ and $18.1^{0}C$-$29.5^{0}C$, respectively and crop received 227.2 mm of rainfall with 15 rainy days during growing season. The average daily relative humidity fluctuated between 13.6% to 90% during the experimental season.

3.3 Soil characteristics of the experimental field

The soil samples from 0-30 cm depth were drawn randomly from different spots of the experimental field to know the soil properties. The physico-chemical properties of the soil were analyzed by using a representative composite sample of the soil. The conclusive results revealed that the soil of the experimental field was loamy sand in texture, slightly alkaline in pH reaction, poor in organic carbon (0.13%), low in available nitrogen (174 kg ha^{-1}) and phosphorus (22.2 kg ha^{-1}) but medium in available potassium (325 kg ha^{-1}).

3.4 Experimental material

The experimental material used in present investigation comprised of 28 genotypes of sesame obtained from Bhabha Atomic Research Centre (BARC), Mumbai, and ARS, Mandor, Jodhpur. The details of genotypes of the investigated test material are furnished in Table 3.1.

Table 3.1: List of sesame genotypes used for present investigation

S. No.	Genotype	Source	S. No.	Genotype	Source
1.	TBS2	BARC, Mumbai	15.	NIC7909	BARC, Mumbai
2.	TBS4	BARC, Mumbai	16.	NIC7921	BARC, Mumbai
3.	TBS5	BARC, Mumbai	17.	NIC8167	BARC, Mumbai
4.	TBS6	BARC, Mumbai	18.	NIC8478	BARC, Mumbai
5.	TBS7	BARC, Mumbai	19.	NIC205312	BARC, Mumbai
6.	TBS9	BARC, Mumbai	20.	PT49-3	BARC, Mumbai
7.	TBS10	BARC, Mumbai	21.	Phule Til-1	BARC, Mumbai
8.	TBS11	BARC, Mumbai	22.	Octalone	BARC, Mumbai
9.	TBS12	BARC, Mumbai	23.	RT54	ARS, Mandor
10.	EC138836	BARC, Mumbai	24.	RT103	ARS, Mandor
11.	EC303311	BARC, Mumbai	25.	RT127	ARS, Mandor
12.	EC303441B	BARC, Mumbai	26.	RT346	ARS, Mandor
13.	EC334984B	BARC, Mumbai	27.	RT351	ARS, Mandor
14.	EC335003	BARC, Mumbai	28.	GT10	SDAU, Gujarat

3.5 Experimental details:-

In the present experiment, 28 sesame genotypes were grown in randomized block design with three replications during *Kharif*, 2018 under irrigated conditions at experimental field of ARS Mandor, Jodhpur. The experimental details are as follows:-

Season : *Kharif* 2018

Design : Randomized Block Design (RBD)

Replication : 3

Genotypes : 28

Plot Size : 0.6 x 4.0 m

Row Spacing : 30.0 cm

Seed Rate : 2.5 kg/ha

Nutrient Application : 40 kg N +25 kg P_2O_5/ha +250 kg Gypsum /ha

Irrigation : As per requirement

Date of Sowing : 09/07/2018

3.6 Observations recorded:-

Observations on days to 50% flowering and days to maturity were recorded on whole plot basis while remaining all the observations were recorded by randomly taking 10 plants from each genotype. Recorded data of each replication was averaged and mean values were subjected to statistical analysis. Procedure adopted for recording the observations for each character is described below:-

(i) Days to 50% flowering

The number of days taken from the date of sowing to the date of appearance of flowers in 50% plants in a plot was recorded.

(ii) Days to maturity

The number of days taken from date of sowing to the date on which more than 90% plants of plot mature physiologically was recorded.

(iii) Plant height (cm)

Plant height was recorded in centimetres from the base of plant to the tip of main axis at maturity for randomly selected ten plants and averaged.

(iv) Number of primary branches per plant

Total number of fruiting branches arising from main shoot was counted at the time of maturity for randomly selected ten plants and averaged.

(v) Number of capsules per plant

The number of seed bearing capsules per plant present on randomly selected ten plants were counted at maturity and averaged.

(vi) Capsule length (cm)

Five mature capsules were taken randomly from each of ten plants and measured in centimetres and averaged.

(vii) Seed yield per plant (g)

The weight of seeds from each of the randomly taken ten plants was recorded in grams and averaged.

(viii) Test weight (g)

One sample of 1000-seeds was taken manually from each genotype and recorded their weight in grams.

(ix) Harvest index (%)

Harvest index was calculated using the formula of Donald and Hamblin (1976).

$$\text{Harvest Index (\%)} = \frac{\text{Economic Yield}}{\text{Biological Yield}} \text{ x100}$$

(x) Oil content (%)

Clean seeds with 10-12% moisture content were used for oil estimation by NMR spectroscopy at Indian Institute of Oilseed Research, Hyderabad, Telangana.

(xi) Protein content (%)

Clean seeds with 10-12% moisture content were used for protein estimation by Lowry method (Lowry *et al.* 1951).

3.7 Statistical analysis

The data collected from observations were subjected to statistical analysis with the help of standard procedures as details given below:

3.7.1 Analysis of Variance (ANOVA)
3.7.2 Variability Parameters
    3.7.2.1 Analysis of Variance Components
    3.7.2.2 Broad Sense Heritability
    3.7.2.3 Genetic Advance
3.7.3 Correlation Coefficient Analysis (Dewey and Lu, 1959)
3.7.4 Path Coefficient Analysis (Wright, 1921 Dewey and Lu, 1959)
3.7.5 Genetic Divergence (Mahalanobis, 1928)

3.7.1 Analysis of variance (ANOVA)

Analysis of variance was computed as per standard statistical procedure suggested by (Panse and Sukhatme, 1985). The significance was tested by referring to the values of 'F' table (Fisher and Yates, 1963). Statistical analysis was performed using Windo Stat version 9.1 software.

Table 3.2 Analysis of variance (ANOVA)

Source	**d.f.**	**S.S.**	**M.S.**	**Expected M.S.**
Replication	(r-1)	SSr	MS_r	$\sigma^2_e + g\sigma^2_r$
Genotypes	(g-1)	SSg	MS_g	$\sigma^2_e + r\sigma^2_g$
Error	(r-1) (g-1)	SSe	MS_e	σ^2_e

Where,

r = Number of replications

g = Number of genotypes

SSr = Replication sum of square

SSg = Genotype sum of square

SSe = Error sum of square

MS_r = Replication mean sum of squares

MS_g = Genotype mean sum of squares

MS_e = Error mean sum of squares

σ^2_r = Variance due to replication

σ^2_g = Variance due to genotypes

σ^2_e = Variance due to error

Standard error of mean was calculated as follows:

$$\mathrm{SE(m)} = \sqrt{\frac{\mathrm{MSe}}{\mathrm{r}}}$$

Standard error of differences between treatment means was calculated as

$$\mathrm{SE\,(diff.)} = \sqrt{\frac{2\mathrm{MSe}}{\mathrm{r}}}$$

Where,

MS_e = Error mean sum of squares and

r = Number of replications

Coefficient of variation was calculated as

$$\mathrm{C.V.} = \sqrt{\frac{\mathrm{MSe}}{\overline{\mathrm{X}}}}\ \mathrm{x100}$$

Where,

C.V. = Coefficient of variation and

$\overline{\mathrm{X}}$ = General Mean

$$\left[\ \overline{\mathrm{X}} = \text{Population mean} = \frac{\sum_{i=1}^{g}\sum_{j=1}^{r} \mathrm{X_{ij}}}{\mathrm{rg}}\ \right]$$

r = Number of replications

g = Number of genotypes

3.7.2 Variability parameters

3.7.2.1 Analysis of variance components

The genotypic (σ^2_g) and phenotypic (σ^2_p) variances were calculated according to the following formula:

(i) Genotypic variance

$$\text{Genotypic variance } (\sigma^2_g) = \frac{MS_g - MS_e}{r}$$

Where,

MS_g = Mean sum square due to genotypes

MS_e = Mean sum square due to error

r = Number of replication

(ii) Phenotypic variance

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

(iii) Coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated as per formula suggested by Burton (1952) and Johnson *et al.* (1955).

(a) Genotypic coefficient of variation

$$\text{GCV } (\%) = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \text{ x } 100$$

(b) Phenotypic coefficient of variation

$$\text{PCV } (\%) = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \text{ x } 100$$

Where,

$\overline{X}$ = General Mean

σ^2_g and σ^2_p = Genotypic and phenotypic variances, respectively.

PCV and GCV were classified as suggested by Sivasubramanian and Menon (1973).

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

3.7.2.2 Heritability (broad sense)

Heritability was estimated by the formula as suggested by Johnson *et al.* (1955).

$$h^2(bs)\ \% = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

As suggested by Johnson *et al.* (1955) h^2 estimates were categorized as:

Low	:	0-30%
Medium	:	30-60%
High	:	above 60%

3.7.2.3 Genetic Advance (G.A.)

The expected genetic advance (GA) expressed in percentage of mean were calculated by using the method suggested by Johnson *et al.* (1955).

$$G.A. = K.\ h^2b.\sigma_p$$

$$\text{Genetic advance as percentage of mean} = \frac{GeneticAdvance}{\overline{X}} \text{X } 100$$

Where,

K = selection intensity (constant 2.06 at 5%)

σ_p = Phenotypic standard deviation

h^2b = Heritability in broad sense

$\overline{X}$ = General mean of the character concerned

Johnson *et al.* (1955) classified genetic advance into following range:

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

3.7.2 Correlation coefficient analysis:

The phenotypic and genotypic correlation coefficients were computed from the phenotypic and genotypic variance and co-variances as according to Searle (1961).

(i) Genotypic correlation coefficients between character X and Y

$$\mathrm{rxy(g)} = \frac{\mathrm{Cov.}_{xy}(\mathrm{g})}{\sqrt{\sigma^2 \mathrm{g(x)}.\sigma^2 \mathrm{g(y)}}}$$

(ii) Phenotypiccorrelation coefficients between character X and Y

$$\mathrm{rxy(p)} = \frac{\mathrm{Cov.}_{xy}(\mathrm{p})}{\sqrt{\sigma^2 \mathrm{p(x)}.\sigma^2 \mathrm{p(y)}}}$$

(iii) Environmentalcorrelation coefficients between character X and Y

$$\mathrm{rxy(e)} = \frac{\mathrm{Cov.}_{xy}(\mathrm{e})}{\sqrt{\sigma^2 \mathrm{e(x)}.\sigma^2 \mathrm{e(y)}}}$$

Where,

$r_{xy(g)}$, $r_{xy(p)}$ and $r_{xy\,(e)}$ denote genotypic, phenotypic and environmental correlation coefficients between X and Y characters, respectively.

$Cov_{xy(g)}$, $Cov_{xy(p)}$ and $Cov_{xy(e)}$ denote genotypic, phenotypic and environmental co-variances between X and Y characters, respectively.

$V_{x(g)}$, $V_{x(p)}$ and $V_{x\,(e)}$ denote genotypic, phenotypic and environmental variances for characters X, respectively.

$V_{y(g)}$, $V_{y(p)}$ and $V_{y\,(e)}$ denote genotypic, phenotypic and environmental variances for characters Y, respectively.

3.7.3.1 Test of significance

The significance of correlation coefficient was tested using the following formula

$$t_{(n-2)} = \sqrt[r]{\frac{n-2}{1-r^2}}$$

Where,

r = Correlation coefficient

t = Students ‘t’ value, and

n = Total number of observations

Searle (1965) classified correlation coefficient into following range:

Value	**Scale**
> 0.65	very strong
0.50 to 0.64	moderately strong
0.30 to 0.49	moderately weak
< 0.30	very weak

3.7.4 Path coefficient analysis

The direct and indirect effects were estimated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The following equations were solved for estimating the various direct and indirect effects.

$$r_{1y} = P_{1y} + r_{12}P_{2y} + \ldots\ldots\ldots\ldots + r_{1p}P_{py}$$

$$r_{2y} = r_{21}P_{1y} + P_{2y} + \ldots\ldots\ldots\ldots + r_{2p}P_{py}$$

$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$

$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$

$$R_{py} = r_{p1}P_{1y} + r_{p2}P_{2y} + \ldots\ldots\ldots\ldots + P_{py}$$

Where,

P_{1y}, P_{2y}……………P_{py} are direct effects of character 1,2, ……….p on Y and r_{1y}, r_{2y}…………r_{py} denote correlation coefficient between independent characters 1,2……..p and dependent character ‘Y’.

Residual effect was calculated using the following formula:

$$1 = P^2Ry + \Sigma P_{iy}R_{iys}$$

$$P_{Ry} = \sqrt{1 - (P_{1y}r_{1y}) - (P_{2y}r_{2y}) \ldots\ldots(P_{iy}r_{iy})}$$

Where,

P_{Ry} is the residual effect

Y is the seed yield

3.7.5 Estimation of genetic divergence using Mahalanobis's D^2 analysis:

3.7.5.1 Genetic divergence:

Mahalanobis gave a measure for group distance based on multiple characters in 1928. With the help of this analysis, genetic divergence between the genotypes was estimated. With $x_1, x_2, \ldots\ldots x_p$as the multiple measurements present on each individual and $d_1, d_2, \ldots\ldots d_p$as $\overline{x_1^1} - \overline{x_1^2}, \overline{x_2^1} - \overline{x_2^2}, \ldots\ldots \overline{x_p^1} - \overline{x_p^2}$, respectively, being the difference in the mean of two populations, Mahalanobis's D^2 statistics is defined as follows:

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

Here, the bi values are to be estimated such that the ratio of variance between the populations to the variance within the population is maximized. In terms of variances and co-variances, the D2 value is obtained as follows:

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

Where,

W_{ij}= Inverse of estimated variance co-variance matrix

3.7.5.2 Steps to estimate D^2 value:

3.7.5.2.1 Collection of data:

Data were collected considering 'v' populations and 'p' characters which have been measured on each individual.

3.7.5.2.2Test of significance:

Variances and co-variances are calculated from the data using appropriate model. Using 'V' statistic which, in turn, utilizes Wilk's criteria, a simultaneous test of differences between mean values of a number of correlated variables is done (Rao, 1948).

Using pivotal condensation method, the determinant of error and error + variety matrix will be calculated.

$$\Lambda = \frac{|W|}{|S|}$$

Where,

W = Determinant of error matrix

S = Determinant of error + variety matrix

$$\text{'V'}_{(\text{stat})} = -\ m\ \log_e\Lambda = -\ (n - \frac{p+q+1}{2})\ \log_e\Lambda$$

Where,

m = n – (p+q+1)/2,

p = number of variables or characters,

q = number of varieties – 1 (or d.f. for populations)

n = d.f. for error + varieties

e = 2.7183

'V' (stat) is distributed as $x^2$with pq degree of freedom. The tabulated value of $x^2$for pq degree of freedom at 5% level is compared with the x^2 value for testing the significance.

3.7.5.2.3 Transformation of correlated variables:

The correlated variables are first transformed into uncorrelated once and D^2 values are calculated because computation of D^2 values were reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e., $\sum di^2$. Transformation is done by using pivotal consideration method.

3.7.5.2.4 Computation of D^2 values:

The D^2 value obtained for a pair of population is taken as the calculated value of x^2 and is tested against the tabulated value of x^2 at "p" degree of freedom, where "p" is the number of characters considered.

3.7.5.2.5 Testing the significance of D^2 values:

The D^2 value obtained for a pair of genotypes was taken as the calculated value of x^2 and tested against tabulated x^2 at p degrees of freedom where, ‘p’ is the number of characters considered.

3.7.5.2.6 Contribution of individual characters towards divergence:

In all the combinations, each character is ranked on the basis of $d_i = Y_{ij} - Y_{ik}$ values. Rank 1 is given to the highest mean difference and rank p to the lowest mean difference, where “p” is the total number of characters.

3.7.5.2.7 Grouping of genotypes into various clusters by Tocher’s method:

The first step in grouping the varieties into distinct clusters is to arrange these populations in order of their relative distances from each other. The two population having the least distance from each other are considered first to which a third population having the smallest D^2 value from the first two population is added, then comes the nearest fourth population and so it goes on. There is abrupt increase in the average D^2 at certain stage by adding a particular population, and then this population is not added in the cluster. Similarly, second cluster is formed. Thus the process is continued till all the populations are included into one or other cluster.

3.7.5.2.8 Average intra- cluster distances:

The formula is used for measuring the intra cluster distance is as follows:

$$\Sigma \frac{D_i^2}{n}$$

Where,

$\Sigma Di^2/n$ is the sum of distances between all possible contributions (n) of the populations included in a cluster.

3.7.5.2.9 Average inter- cluster distances:

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

Average inter-cluster distance = $\frac{D^2}{n_1 \times n_2}$ Where,

n_1 and n_2 are number of genotypes of two clusters

Category 'D'	**Values**
Closely related	Below 22
Moderately divergent	Between 22 and 30
Highly divergent	Above 30

3.7.5.2.10 Cluster diagram

Draw the diagram with the help of D^2 values between and within clusters showing the relationship between different populations.

Plate No. 1. View of experimental field

4. EXPERIMENTAL RESULTS

The present investigation entitled **"Morphological Characterization and Diversity Studies in Sesame"** was carried out to evaluate 28 genotypes of sesame in RBD with 11 yield and yield attributing traits. The morphological data recorded for different characters were used to calculate genetic variability, heritability, genetic advance, character association between yield and its attributing characters and genetic divergence.

The experimental results of the present investigation are being presented under following subheads:-

4.1 Analysis of variance (ANOVA)
4.2 Variability parameters
    4.2.1 Range and mean performance
    4.2.2 Genotypic and phenotypic coefficient of variation
    4.2.3 Heritability
    4.2.4 Genetic advance
4.3 Association analysis
    4.3.1 Correlation coefficient analysis
    4.3.2 Path coefficient analysis
4.4 Genetic divergence using Mahalanobis's D^2 analysis

4.1 Analysis of variance (ANOVA)

Statistical analysis was carried out by using numerical data collected for different quantitative characters. The mean sum of squares for all the eleven traits *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of capsules per plant, capsule length, seed yield per plant, test weight, harvest index, oil content and protein content exhibited highly significant differences among the genotypes indicating the presence of considerable genetic variability among the experimental material of the present study (Table 4.1).

4.2 Variability parameters

To initiate crop improvement programme, available adequate genetic variability and its critical analysis is required for adopting appropriate breeding procedures. The presence of greater variability in the initial breeding material facilitates better chances of selection of useful and desired genotype.

Mean, range, phenotypic and genotypic coefficient of variation (%), heritability in broad sense (%) and genetic advance as percentage of mean are the parameters of genetic variability (Table 4.3).

4.2.1 Range and mean performance

The range and mean performance of 28 genotypes for seed yield and its components traits is presented in Table 4.2 and Table 4.3. The details of the results obtained are furnished below.

4.2.1.1 Days to 50 per cent flowering

This character showed a range from 37 to 68.67 days with a general mean of 52.35 days and coefficient of variation 3.16%. Among all the genotypes, EC 138836 was earliest (37 days), while TBS 9 (69 days) was late. Exotic genotypes EC 138836, EC 303441B, and EC 334984B, EC 303311 were earlier as compared to other genotypes.

4.2.1.2 Days to maturity

The average number of days taken for maturity varies from 77 days (RT 127) to 91 days (TBS 2) with a general mean of 84.6 days and coefficient of variation 5.34%. The genotypes RT 127, EC 303441B, NIC 8167, RT 103, RT 346, NIC 205312, GT 10, Phule Til-1, EC 138836 and NIC 7921 exhibited quite early maturity (77 to 85 days).

4.2.1.3 Plant height

Plant height exhibited wide variability ranging from 67.9 cm to 109.27 cm with a general mean of 89.3 cm and coefficient of variation 7.63%. RT 54 was the shortest, while RT 127 was the tallest among all the genotypes under study.

4.2.1.4 Number of primary branches per plant

Number of primary branches per plant recorded minimum of 2.13 (PT 49-3) and maximum 6.0 (EC 303311) with mean of 3.7 and coefficient of variation 8.34%.

Table 4.1: Analysis of variance (ANOVA) for seed yield and its contributing traits

Source	DF	Day to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of capsules per plant	Capsule length (cm)	Seed yield per plant (g)	Test weight (g)	Harvest index (%)	Oil content (%)	Protein content (%)
Replication	2	7.30	3.89	129.22	0.26	9.48*	0.05	0.03	0.00	3.51	2.97	0.96
Genotype	27	271.79**	41.36*	413.09**	2.53**	391.36**	0.10*	5.09**	2.15**	470.04**	80.99**	12.00**
Error	54	2.74	20.42	46.41	0.10	2.67	0.05	0.03	0.01	6.30	0.98	0.38

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

Table 4.2: Mean performance of 28 genotypes of sesame for seed yield and its contributing traits

S. No.	Genotype	Day to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of capsules per plant	Capsule length (cm)	Seed yield per plant (g)	Test weight (g)	Harvest index (%)	Oil content (%)	Protein content (%)
1	TBS 2	59	91	105.4	4.6	46.6	2.8	1.9	4.5	8.1	36.5	20.1
2	TBS 4	58	88	105.7	4.7	24.4	2.8	2.1	4.3	15.8	33.5	20.1
3	TBS 5	60	89	102.8	4.5	31.3	2.5	1.8	3.7	10.6	33.7	19.0
4	TBS 6	65	90	99.8	2.5	17.4	2.6	1.8	4.6	19.8	31.7	18.2
5	TBS 7	66	86	108.4	3.3	20.7	2.6	1.8	3.9	16.6	28.4	19.1
6	TBS 9	69	82	90.1	2.2	12.5	1.9	1.4	3.1	16.2	30.6	19.2
7	TBS 10	68	86	84.3	3.4	31.9	2.6	2.0	4.7	10.1	31.8	19.0
8	TBS 11	64	86	86.7	3.6	27.4	2.5	2.1	4.4	16.6	35.0	20.5
9	TBS 12	61	86	80.3	3.5	24.1	2.3	1.4	4.3	18.2	26.0	20.3
10	EC 138836	37	85	69.1	4.0	13.8	2.6	2.8	2.4	42.0	37.8	17.0
11	EC303311	47	84	83.1	6.0	43.6	2.6	1.6	3.0	15.6	31.4	20.0
12	EC303441B	38	78	82.7	3.9	27.4	2.5	1.6	2.7	27.4	38.0	18.2
13	EC334984B	42	87	86.1	4.0	24.4	2.5	2.5	2.0	30.6	26.4	13.4
14	EC335003	53	89	83.9	4.2	37.3	2.7	3.2	3.6	39.2	38.1	19.3
15	NIC7909	49	88	93.7	4.5	40.3	2.7	4.6	2.9	40.6	36.9	20.0
16	NIC7921	49	85	100.7	3.7	35.6	2.4	3.5	3.5	34.8	37.3	20.0
17	NIC8167	47	78	102.3	4.3	55.6	2.3	2.7	1.9	21.7	27.4	17.7
18	NIC 8478	50	85	78.8	4.5	25.1	2.3	2.1	3.3	31.9	35.1	20.3
19	NIC205312	53	83	80.7	2.6	12.5	2.4	2.2	2.9	32.1	41.2	16.1
20	PT 49-3	63	88	80.4	2.1	7.6	2.5	1.9	4.1	36.9	34.2	20.7
21	Phule Til-1	58	85	87.8	4.0	17.8	2.5	1.6	2.2	25.1	36.6	19.8
22	Octalone	46	82	92.0	4.6	32.5	2.4	2.9	2.4	34.5	35.2	17.4
23	RT 54	40	82	67.9	3.5	31.6	2.5	2.8	2.0	29.9	26.8	15.3
24	RT 103	46	79	76.9	2.7	30.2	2.5	1.6	2.6	16.1	43.9	13.4
25	RT 127	42	77	109.3	2.8	37.5	2.6	4.4	3.7	34.8	41.4	18.7
26	RT 346	46	81	101.0	2.8	34.1	2.6	4.3	3.2	44.6	43.2	18.9
27	RT 351	46	87	78.6	3.2	35.6	2.7	5.3	3.5	30.6	42.4	20.4
28	GT 10	44	84	82.7	5.0	44.3	2.4	2.8	3.5	19.5	40.0	20.0
Trial Mean		52.3	84.6	89.3	3.7	29.4	2.5	2.5	3.3	25.7	35.0	18.6
SEM		0.96	2.61	3.93	0.18	0.94	0.13	0.10	0.06	1.50	0.57	0.36
CD5 %		2.71	7.40	11.15	0.51	2.67	0.38	0.30	0.16	4.25	1.62	1.01
CV%		3.16	5.34	7.63	8.34	5.55	9.19	7.13	3.01	10.09	2.82	3.31

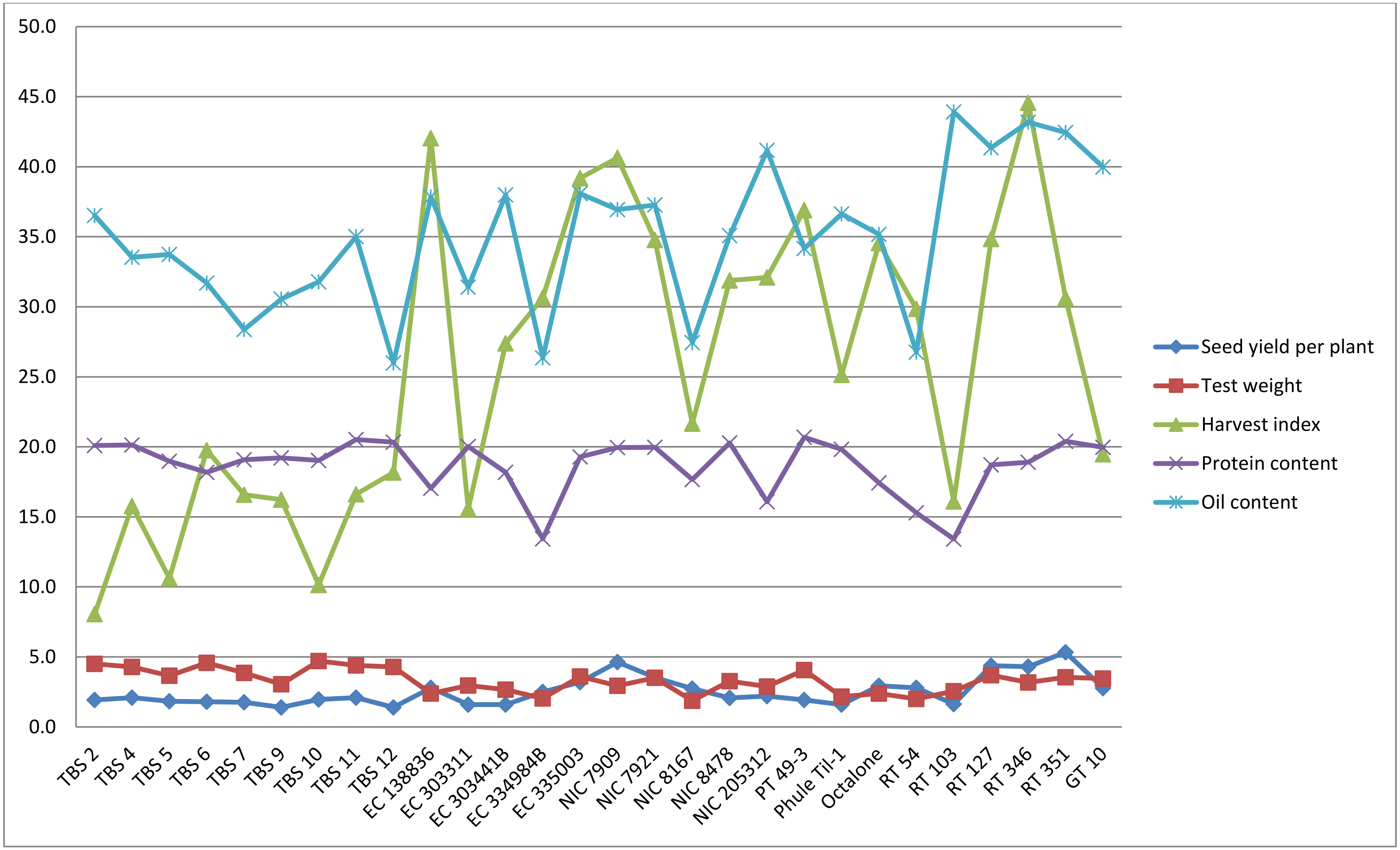

Fig. 4.1: Mean performance of different sesame genotypes for seed yield and some yield attributing trait

4.2.1.5 Number of capsules per plant

Number of capsules per plant varied between 7.6 (PT 49-3) to 55.6 (NIC 8167) with mean value of 29.4 and coefficient of variation 5.55%.

4.2.1.6 Capsule length

Capsule length ranged from 1.93 cm (TBS 9) to 2.83 cm (TBS 2 & TBS 4) with a mean of 2.5 cm and coefficient of variation 9.19%.

4.2.1.7 Seed yield per plant

Seed yield per plant ranged from 1.4 g (TBS 9 & TBS 12) to 5.33 g (RT 351) with a general mean of 5 g and coefficient of variation 7.13%. The genotypes RT 351, NIC 7909, RT 127, RT 346 and EC 335003 exhibited high seed yield per plant as compare to other genotypes.

4.2.1.8 Test Weight

The mean value for this trait ranged from 1.87g (NIC 8167) to 4.71g (TBS 10) with a general mean of 3.3g and coefficient of variation 3.01%.

4.2.1.9 Harvest Index

The mean value for this trait ranged from 8.06 (TBS 2) to 44.56 (RT 346) with a general mean of 25.7 and coefficient of variance 10.09%.

4.2.1.10 Oil Content

Oil content varied between 25.99% (TBS 12) to 43.92% (RT 103) with a mean of 35% and coefficient of variation 2.82%.

4.2.1.11 Protein Content

Protein content varies from 13.42% (EC 334984B & RT 103) to 20.68 % (PT 49-3) with a mean of 18.65% and coefficient of variation 3.31%.

4.2.2 Genotypic and phenotypic coefficient of variation

The phenotypic coefficient of variation (PCV) was comparatively higher in magnitude than that of genotypic coefficient of variation (GCV) for all the characters under study which indicates the presence of environmental influence. Seed yield per plant recorded highest PCV (42.02%) and GCV (41.41%) followed by harvest index (41.96%, 40.73%), number of capsules per plant (39.11%, 38.72%), test weight (25.72%, 25.55%) and number of primary branches per plant (25.51%, 24.11%). Moderate PCV and GCV were recorded for days to 50% flowering (18.37%, 18.09%), oil content (15.02%, 14.75%), plant height (14.54%, 12.38%), protein content (11.06%, 10.55%). Low PCV and GCV were recorded for days to maturity (6.18%, 3.12%) and capsule length (10.35%, 4.78%) (Table 4.3).

4.2.3 Heritability in broad sense (%)

Heritability in broad sense is the ratio of the genetic variation present in the population to the total observed variance. The magnitude of heritable variation present in relation to observed variation decides performance of selection in succeeding generations and is prerequisite measure for planning any breeding programme.

Heritability was estimated for all the eleven characters under study. Most of the characters showed high estimates of heritability. The highest heritability was exhibited by test weight (98.63%) followed by number of capsules per plant (97.98%), seed yield per plant (97.12%), day to 50% flowering (97.03%), oil content (96.47%), harvest index (94.22%), protein content (91.04%), number of primary branches per plant (89.32%) and plant height (72.48%). The traits *viz*., days to maturity (25.46%) and capsule length (21.28%) exhibited low heritability (Table 4.3).

4.2.4 Genetic advance as per cent of mean

Genetic advance is the measure of genetic gain under selection which refers to the improvement in mean genotypic value of the selected plants over the parental population**.** The estimate of genetic advance as percentage of mean is given in Table 4.3. The highest genetic advance as percentage of mean (at 5% selection intensity) was recorded for seed yield per plant (84.07%) followed by harvest index (81.45%), number of capsules per plant (78.95%), test weight (52.27%), number of primary branches per plant (46.93%), days to 50% flowering (36.71%), oil content (29.84%), plant height (21.71%) and protein content (20.75%). Low genetic advance was exhibited by capsule length (4.54%) and days to maturity (3.24%).

Table 4.3: Mean, range, variability, heritability (broad sense), genetic advance and genetic advance as per cent of mean for seed yield and its contributing traits

Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance at 5%	Genetic advance as per cent mean at 5%
		Min	Max	Genotypic	Phenotypic			
Day to 50% flowering	52.35	37.00	68.67	18.09	18.37	97.03	19.22	36.71
Days to maturity	84.64	77.33	90.67	3.12	6.18	25.46	2.75	3.24
Plant height (cm)	89.33	67.93	109.27	12.38	14.54	72.48	19.39	21.71
Number of primary branches	3.74	2.13	6.00	24.11	25.51	89.32	1.75	46.93
Number of capsules per plant	29.40	7.63	55.60	38.72	39.11	97.98	23.21	78.95
Capsule length (cm)	2.51	1.93	2.83	4.78	10.35	21.28	0.11	4.54
Seed yield per plant (g)	2.53	1.40	5.33	41.41	42.02	97.12	2.13	84.07
Test weight (g)	3.30	1.87	4.71	25.55	25.72	98.63	1.73	52.27
Harvest index (%)	25.71	8.06	44.56	40.73	41.96	94.22	20.94	81.45
Oil content (%)	35.01	25.99	43.92	14.75	15.02	96.47	10.45	29.84
Protein content (%)	18.65	13.42	20.68	10.55	11.06	91.04	3.87	20.75

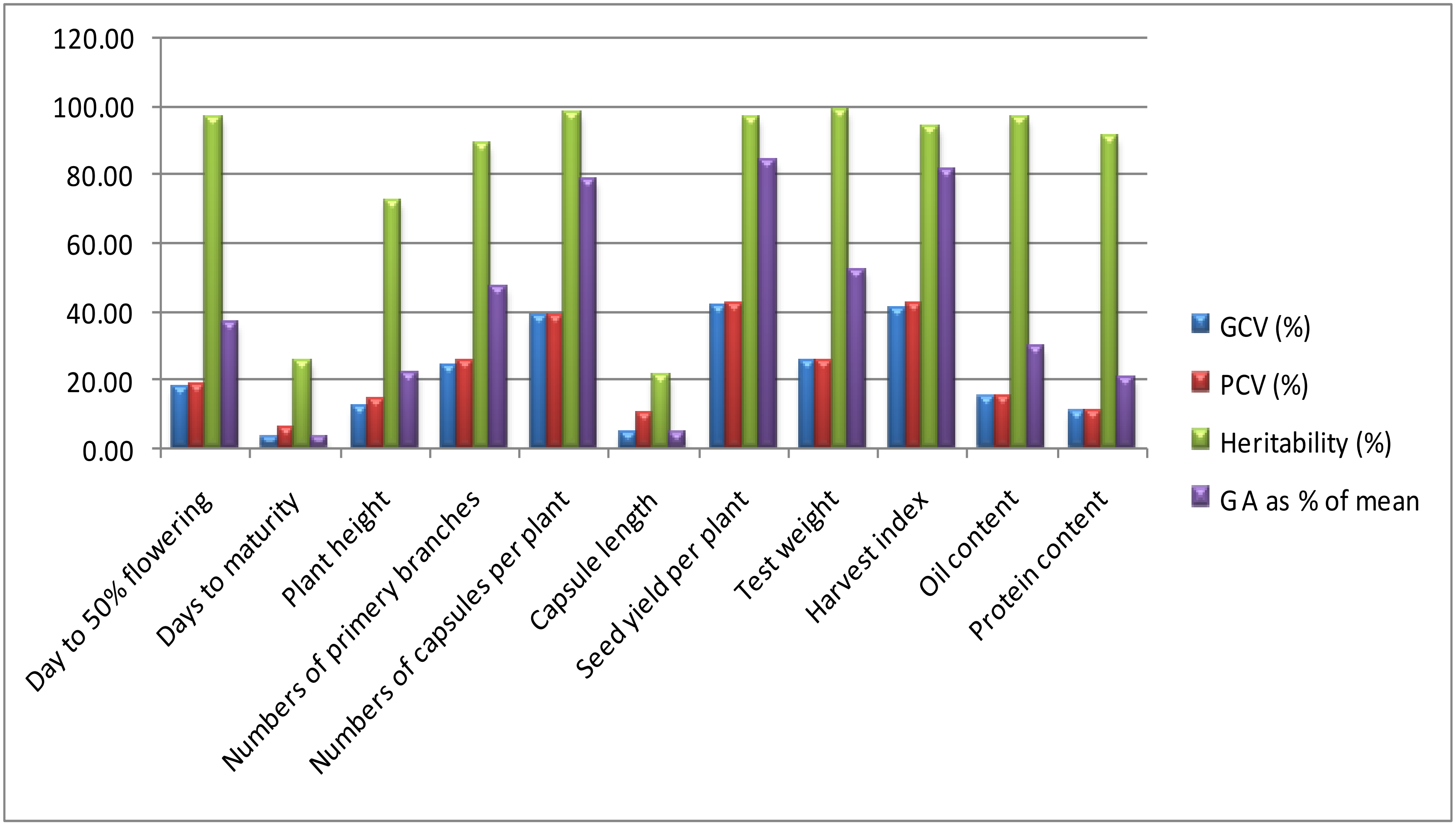

Fig. 4.2 GCV, PCV, heritability (broad sense) and genetic advance as per cent of mean for various characters in sesame

Heritability estimates along with genetic advance as percentage of mean presents an indication about nature of gene action operative in inheritance of various traits. The study exhibited that test weight (98.63%, 52.27%) followed by number of capsules per plant (97.98%, 78.95%), seed yield per plant (97.12%, 84.07%), days to 50% flowering (97.03%, 36.71%), oil content (96.47%, 29.84%), harvest index (94.22%, 81.45%), protein content (91.04%, 20.75%), number of primary branches (89.32%, 46.93%) and plant height (72.48%, 21.71%) had high heritability coupled with high genetic advance, hence these characters might be governed by additive genes and direct selection would be effective from these genotypes. Low heritability coupled with low genetic advance was recorded for days to maturity (25.46%, 3.24%) and capsule length (21.28%, 4.54%); hence these characters might be governed by non-additive gene action indicating that direct selection would not be effective for these characters.

4.3 Association Analysis

4.3.1 Correlation Coefficient Analysis

Phenotypic and genotypic correlations between seed yield per plant and various yield component traits *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of capsules per plant, capsule length, test weight, harvest index (%), oil content (%) and protein content (%) are presented in Table 4.4. The results showed that the estimates of genotypic correlation coefficients were higher than the phenotypic correlation coefficients. Study exhibited that seed yield per plant had positive significant genotypic and phenotypic correlation with harvest index (0.644**, 0.646**) followed by oil content (0.468**, 0.456**), capsule length (0.455**, 0.252*) and number of capsules per plant (0.407**, 0.400**), while, significant negative genotypic and phenotypic correlation was exhibited with days to 50% flowering (-0.491**, -0.478**).

4.3.1.1 Days to 50% flowering

The trait recorded positive significant genotypic and phenotypic correlation with days to maturity (0.719**, 0.346**), test weight (0.675**, 0.659**), plant height (0.344**, 0.279**) and protein content (0.442**, 0.423**). Harvest index (-0568**, -0.540**), seed yield per plant (-0.491**, -0. 478**), number of primary branches per plant (-0.304**, -

0.282**), number of capsules per plant (-0.351*, -0.354*) and oil content (-0.342**, -0.324**) recorded negative significant association at both the levels, while capsule length (-0.228*) showed negative significant correlation at only genotypic level.

4.3.1.2 Days to maturity

Days to maturity exhibited positive significant association at genotypic and phenotypic level with test weight (0.787**, 0.392**) and protein content (0.589**, 0.258**). The traits *viz.,* number of primary branches per plant (0.272*) and capsule length (0.838**) exhibited positive significant association at genotypic level only. This trait showed negative significant association *via,* number of capsules per plant (-0.274*), harvest index (-0.226*) and oil content (-0.252*) at genotypic level only.

4.3.1.3 Plant height

Plant height exhibited high positive significant association with number of capsules per plant (0.304**, 0.255*) and test weight (0.362**, 0.303**) at genotypic and phenotypic both levels. Capsule length (0.254*) had positive significant association at genotypic level while protein content (0.238*) had positive significant association at phenotypic levels only. Harvest index (-0.232*) showed negative significant correlation at genotypic level only.

4.3.1.4 Numbers of primary branches per plant

Positive significant correlation of this trait was observed with number of capsules per plant (0.585**, 0.551**) and capsule length (0.380**, 0.225*) at genotypic and phenotypic level, respectively. Negative significant correlation was exhibited with days to 50% flowering (-0.304**, -0.282**).

4.3.1.5 Number of capsules per plant

Positive significant correlation of this trait was observed with seed yield per plant (0.407**, 0.400*), plant height (0.304**, 0.255*) and number of primary branches per plant (0.585**, 0.551**) at genotypic and phenotypic levels. Capsule length showed high positive significant association (0.440**) at genotypic level only. This trait exhibited

Table 4.4: Phenotypic and genotypic correlation coefficients among yield attributes in 28 sesame genotypes

Character		Day to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of capsules per plant	Capsule length (cm)	Seed yield per plant (g)	Test weight (g)	Harvest index (%)	Oil content (%)	Protein content (%)
Day to 50% flowering	G	1.000	0.719**	0.344**	-0.304**	-0.351**	-0.228*	-0.491**	0.675**	-0.568**	-0.342**	0.442**
	P	1.000	0.346**	0.279*	-0.282**	-0.354*	-0.116	-0.478**	0.659**	-0.540**	-0.324**	0.423**
Days to maturity	G		1.000	0.146	0.272*	-0.274*	0.838**	-0.131	0.787**	-0.226*	-0.252*	0.589**
	P		1.000	0.065	0.133	-0.094	0.175	-0.065	0.392**	-0.126	-0.158	0.258*
Plant height (cm)	G			1.000	0.024	0.304**	0.254*	0.118	0.362**	-0.232*	-0.045	0.305**
	P			1.000	0.038	0.255*	0.169	0.105	0.303**	-0.209	-0.028	0.238*
Number of primary branches	G				1.000	0.585**	0.380**	-0.038	-0.159	-0.188	-0.142	0.214
	P				1.000	0.551**	0.225*	-0.024	-0.162	-0.156	-0.143	0.182
Number of capsules per plant	G					1.000	0.440**	0.407**	-0.077	-0.124	0.091	0.113
	P					1.000	0.199	0.400**	-0.075	-0.117	0.081	0.100
Capsule length (cm)	G						1.000	0.455**	0.418**	0.044	0.409**	0.154
	P						1.000	0.252*	0.189	0.057	0.175	0.061
Seed yield per plant (g)	G							1.000	-0.118	0.644**	0.468**	0.087
	P							1.000	-0.117	0.646**	0.456**	0.076
Test weight (g)	G								1.000	-0.404**	0.014	0.613**
	P								1.000	-0.392**	0.013	0.587**
Harvest index (%)	G									1.000	0.373**	-0.114
	P									1.000	0.352**	-0.103
Oil content (%)	G										1.000	0.056
	P										1.000	0.057
Protein content (%)	G											1.000
	P											1.000

negative non-significant correlation with days to 50% flowering (-0.351**, -0.354*) at both the levels, while days to maturity exhibited negative significant association (-0.274*) only at genotypic level.

4.3.1.6 Capsule length

The capsule length had positive significant association with number of primary branches per plant (0.380**, 0.225*) and seed yield per plant (0.455**, 0.252*) at genotypic and phenotypic both levels. This trait showed positive significant genotypic correlation with days to maturity (0.838**), plant height (0.254*), number of capsules per plant (0.440**), test weight (0.418**) and oil content (0.409**). Negative significant association was shown with days to 50% flowering (-0.228*) at genotypic level only.

4.4.1.7 Seed yield per plant

Seed yield per plant exhibited positive significant genotypic and phenotypic correlation with harvest index (0.644**, 0.646**) followed by oil content (0.468**, 0.456**), capsule length (0.455**, 0.252*) and number of capsules per plant (0.407**, 0.400*) while, significant negative genotypic and phenotypic correlation was exhibited with days to 50% flowering (-0.491**, -0.478**).

4.3.1.8 Test Weight

Test weight exhibited significant positive genotypic and phenotypic correlation with days to 50% flowering (0.675**, 0.659**), days to maturity (0.787**, 0.392**), plant height (0.362**, 0.303**) and protein content (0.613**, 0.587**), while, capsule length (0.418**) exhibited significant positive association at genotypic level only. This trait exhibited negative significant correlation with harvest index (-0.404**, -0.392**) at both the levels.

4.3.1.9 Harvest index

Harvest index had positive significant correlation with seed yield per plant (0.644**, 0.646**) and oil content (0.373**, 0.352**), while significant negative genotypic and phenotypic correlation with days to 50% flowering (-0.568**,-0.540**) and test weight (-0.404**, -0.392**) at both levels. Days to maturity (-0.226*) and plant height (-0.232*) were exhibited negative significant association at genotypic level.

4.3.1.10 Oil content

This trait had positive significant association with seed yield per plant (0.468**, 0.456**) and harvest index (0.373**, 0.352**), while significant negative genotypic and phenotypic correlation with days to 50% flowering (-0.342**, -0.324**). Capsule length exhibited positive significant correlation at genotypic level only (0.409**).

4.3.1.11 Protein content

The character, protein content had significant positive correlation with test weight (0.613**, 0.587**), days to maturity (0.589**, 0.258*), plant height (0.305**, 0.238*) and days to 50% flowering (0.442**, 0.423**) at genotypic and phenotypic level.

4.3.2 Path Coefficient Analysis

Seed yield is a complex character and associated with number of component traits which are inter-related; among themselves interdependence often affects their relationship with yield, thereby making correlation in effective. Path coefficient analysis estimates direct and indirect effect of various independent characters on the dependent characters. It reveals the relationship of these independent characters with yield, whether the dependent character is due to its direct effect on yield or is consequence of their indirect effects *via* other component characters. This method was developed by Sewall Wright in 1921 and Dewey and Lu (1959) employed this method for the first time in plants to disentangle the direct and indirect influences of components of seed yield.

The direct and indirect effects of different yield attributing characters on yield were recorded using genotypic and phenotypic correlation coefficients and are presented in Table 4.5. The cause-effect relationships at phenotypic and genotypic levels are diagrammatically presented in Figure 4.3 and Figure 4.4, respectively. The results of both phenotypic and genotypic path coefficient analysis of yield and its attributing traits are described here under.

4.3.2.1 Days to 50% flowering

The direct contribution of this trait was negative on seed yield per plant (-0.299, -0.132) both at genotypic and phenotypic both levels.

Table 4.5: Phenotypic and genotypic path coefficients among yield attributes in 28 sesame genotypes

Character		Days to 50% flowering	Days to maturity	Plant height (cm)	Numbers of primary branches	Numbers of capsules per plant	Capsule length (cm)	Test weight (g)	Harvest index (%)	Oil content (%)	Protein content (%)	Seed yield per plant (g)
Days to 50% flowering	G	**-0.299**	0.131	-0.000	0.315	-0.192	-0.156	-0.562	-0.090	0.052	0.312	-0.491**
	P	**-0.132**	0.031	0.022	0.083	-0.192	-0.010	0.043	-0.332	-0.033	0.043	-0.478**
Days to maturity	G	-0.215	**0.182**	-0.000	-0.282	-0.150	0.572	-0.655	-0.035	0.038	0.415	-0.131
	P	-0.045	**0.091**	0.005	-0.039	-0.051	0.016	0.026	-0.077	-0.016	0.026	-0.065
Plant height (cm)	G	-0.103	0.026	**-0.002**	-0.025	0.166	0.173	-0.301	-0.036	0.007	0.214	0.118
	P	-0.037	0.005	**0.080**	-0.011	0.139	0.015	0.020	-0.128	-0.002	0.024	0.105
Number of primary branches	G	0.091	0.049	-0.000	**-1.035**	0.321	0.259	0.132	-0.029	0.021	0.150	-0.038
	P	0.037	0.012	0.003	**-0.294**	0.299	0.020	-0.010	-0.096	-0.014	0.018	-0.024
Numbers of capsules/plant	G	0.105	-0.050	-0.000	-0.607	**0.548**	0.300	0.064	-0.019	-0.014	0.080	0.407**
	P	0.047	-0.008	0.020	-0.162	**0.543**	0.018	-0.005	-0.072	0.008	0.010	0.400**
Capsule length (cm)	G	0.068	0.153	-0.000	-0.394	0.241	**0.682**	-0.348	0.007	-0.062	0.108	0.455**
	P	0.015	0.015	0.013	-0.066	0.108	**0.092**	0.012	0.035	0.018	0.006	0.252*
Test weight (g)	G	-0.202	0.143	-0.000	0.164	-0.042	0.285	**-0.832**	-0.064	-0.002	0.432	-0.118
	P	-0.087	0.035	0.024	0.047	-0.041	0.017	**0.066**	-0.241	0.001	0.059	-0.117
Harvest index (%)	G	0.170	-0.041	0.000	0.194	-0.068	0.030	0.336	**0.158**	-0.057	-0.080	0.644**
	P	0.071	-0.011	-0.016	0.046	-0.064	0.005	-0.026	**0.615**	0.036	-0.010	0.646**
Oil content (%)	G	0.102	-0.046	0.001	0.147	0.050	0.279	-0.012	0.059	**-0.153**	0.039	0.468**
	P	0.043	-0.014	-0.002	0.042	0.044	0.016	0.001	0.216	**0.103**	0.005	0.456**
Protein content (%)	G	-0.132	0.107	-0.007	-0.221	0.062	0.105	-0.510	-0.018	-0.008	**0.704**	-0.087
	P	-0.056	0.023	0.019	-0.053	0.054	0.005	0.038	-0.063	0.005	**0.101**	0.076

Residual effect (G) = 0.33, (P) = 0.49 Bold values represents direct effects,
P =Phenotypic path coefficient and G = Genotypic path coefficient

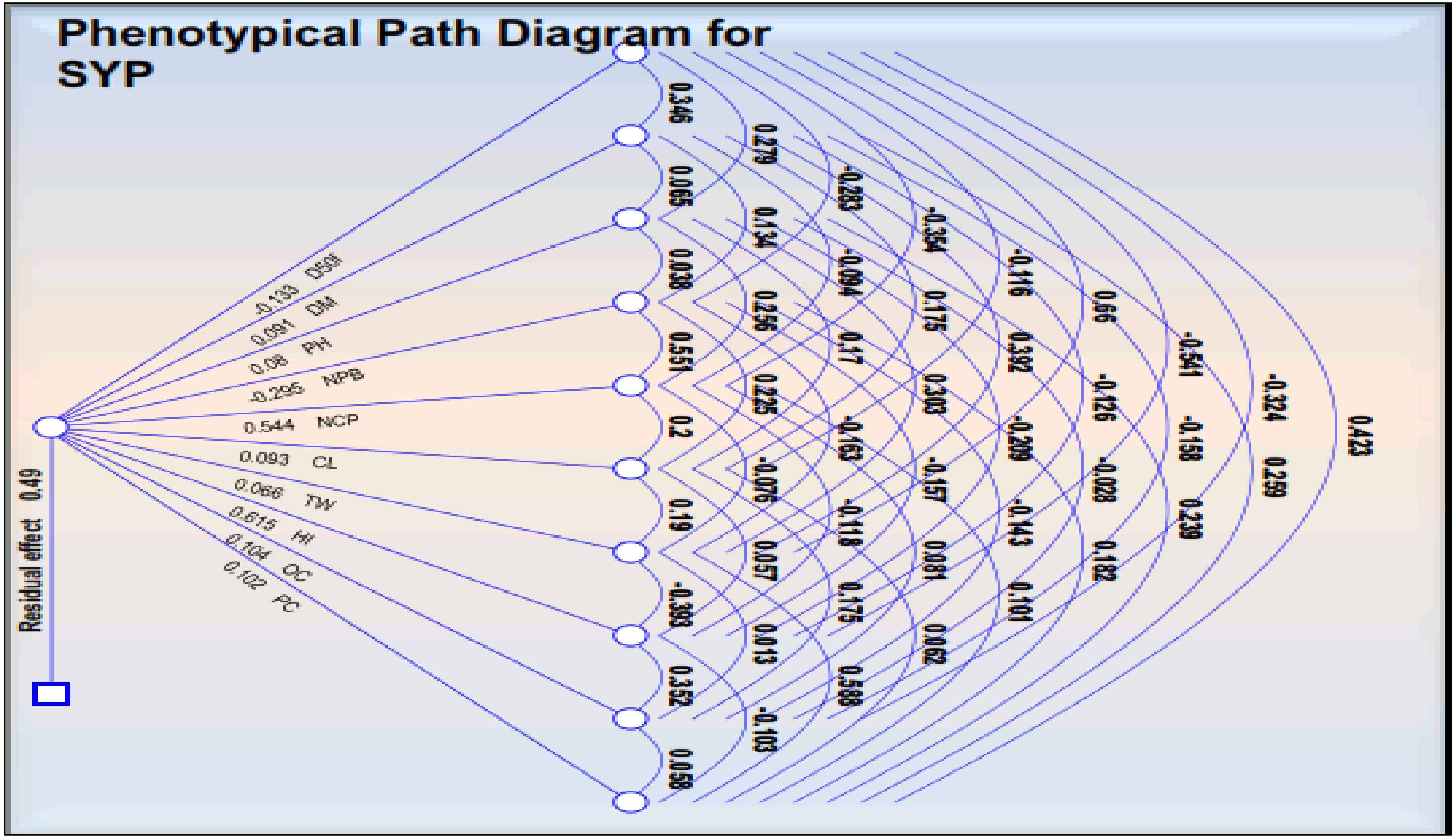

Plate No 2: Phenotypic path diagram for yield in sesame

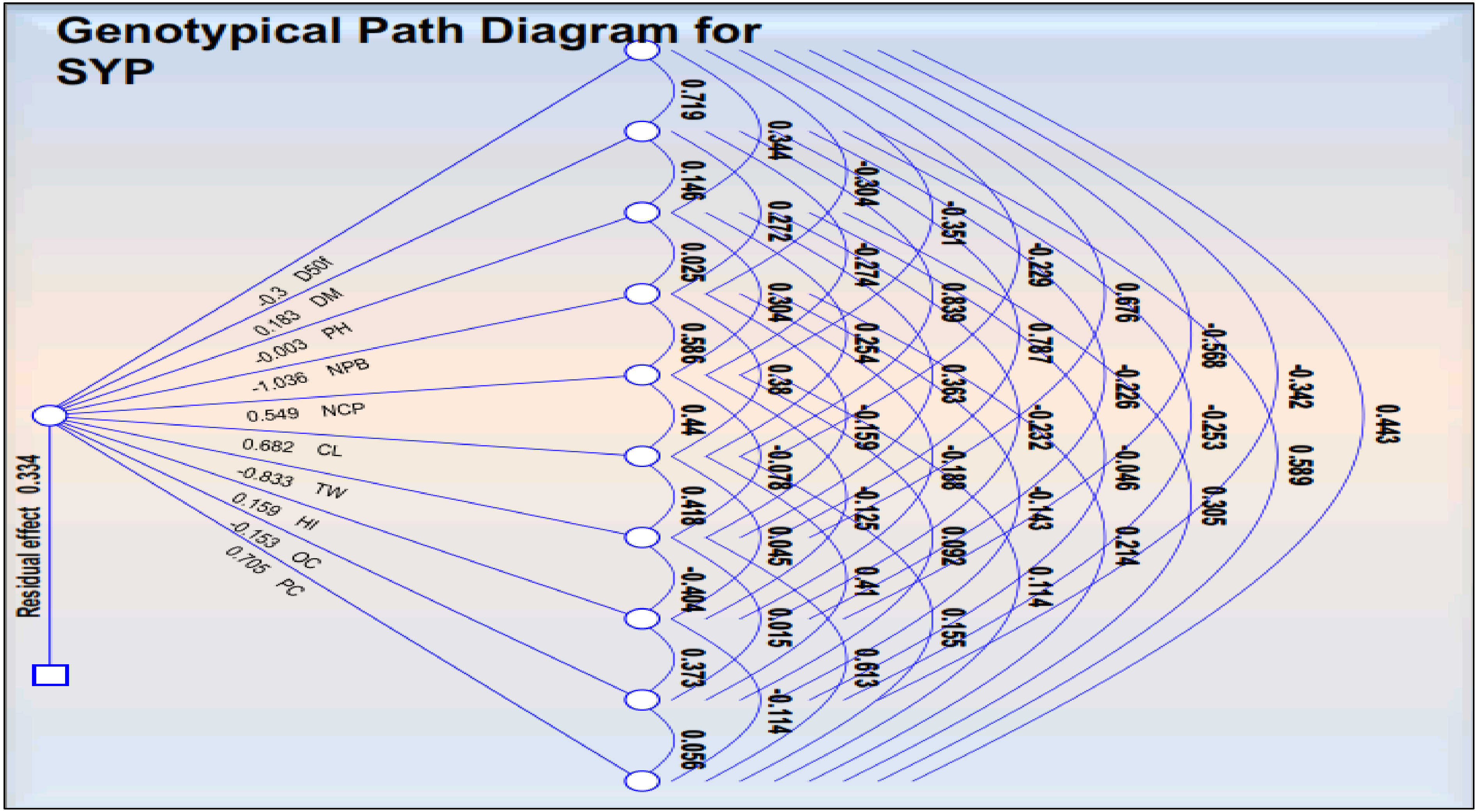

Plate No. 3: Genotypic path diagram for yield in sesame

This trait exhibited positive indirect effects on seed yield per plant through days to maturity (0.131, 0.031), number of primary branches per plant (0.315, 0.083) and protein content (0.312, 0.043) at genotypic and phenotypic both levels. The trait showed positive indirect effect on seed yield per plant through plant height (0.022) and test weight (0.043) at phenotypic level only and genotypic effect through oil content (0.052). The negative significant correlation (-0.491**, -0.478**) of this trait with seed yield per plant was mainly due to the negative indirect effects *via* number of capsules per plant (-0.192, -0.192), capsule length (-0.156, -0.010) and harvest index (-0.090, -0.332) at both the genotypic and phenotypic levels and oil content (-0.033) at phenotypic levels, while plant height (-0.0008) and test weight (-0.562) at genotypic level..

4.3.2.2 Days to maturity

The trait, days to maturity showed positive direct effect (0.182, 0.091) on seed yield per plant at genotypic and phenotypic levels.

This trait exhibited indirect negative non-significant correlation (-0.131, -0.065) with seed yield per plant. It was mainly due to negative indirect effects through days to 50% flowering (-0.215, -0.045), number of primary branches per plant (-0.282, -0.039), number of capsules per plant (-0.150, -0.051) and harvest index (-0.035, -0.077) at both the levels and oil content (-0.016) at phenotypic level and negative indirect effect of plant height (-0.003) and test weight (-0.655) at genotypic level. The positive indirect effects of days to maturity was observed through capsule length (0.572, 0.016) and protein content (0.415, 0.026) at both the levels, while plant height (0.005) and test weight (0.026) at phenotypic level and oil content (0.038) at genotypic level only.

4.3.2.3 Plant height

The direct contribution of this character towards seed yield per plant was negative (-0.002) at genotypic level, while it was positive at phenotypic level (0.080).

Plant height showed positive non-significant indirect effect (0.118, 0.105) via days to maturity (0.026, 0.005), number of capsules per plant (0.166, 0.139), capsule length (0.173, 0.015) and protein content (0.214, 0.024) at genotypic and phenotypic both levels. Negative indirect effect was exhibited *via* days to 50% flowering (-0.103, -0.037), number of primary branches (-0.025, -0.011) and harvest index (-0.036, -0.128).

4.3.2.4 Number of primary branches per plant

The direct contribution of this character to seed yield per plant was negative (-1.035, -0.294) at genotypic and phenotypic both levels.

The trait, number of primary branches per plant showed negative indirect effect *via* harvest index (-0.029, -0.096) at both levels, while positive indirect effect was shown *via* days to 50% flowering (0.091, 0.037), days to maturity (0.049, 0.012), number of capsules per plant (0.321, 0.299), capsule length (0.259, 0.020) and protein content (0.150, 0.018) at genotypic and phenotypic both levels.

4.3.2.5 Number of capsules per plant

The direct contribution of this character to seed yield per plant was positive (0.548, 0.543) at genotypic and phenotypic both levels.

The positive significant effect of number of capsules per plant with seed yield per plant (0.407**, 0.400**) was mainly due to indirect positive effects of this trait *via* capsule length (0.300, 0.018), days to 50% flowering (0.105, 0.047) and protein content (0.080, 0.010) at both the levels and plant height (0.020) and oil content (0.008) expressed indirect positive phenotypic effect, while positive genotypic indirect effects were reported through test weight (0.064). This trait showed negative indirect effects on seed yield per plant through days to maturity (-0.050, -0.008), plant height (-0.005, -0.039), number of primary branches per plant (-0.607, -0.162) and harvest index (-0.019, -0.072) at both the levels.

4.3.2.6 Capsule length

Capsule length had positive direct effect (0.682, 0.092) at genotypic and phenotypic level, respectively.

Positive significant indirect effects (0.455**, 0.252**) of this trait on seed yield per plant was recorded through days to 50% flowering (0.068, 0.015), days to maturity (0.153, 0.015), number of capsules per plant (0.241, 0.108), harvest index (0.007, 0.035) and protein content (0.108, 0.006) at both the levels and plant height (0.013), test weight (0.012) and oil content (0.018) expressed indirect positive phenotypic effect.

This trait exhibited negative indirect effects on seed yield per plant through number of primary branches per plant (-0.394, -0.066) at both the levels and plant height (-0.006), test weight (-0.348) and oil content (-0.062) expressed indirect negative genotypic effect.

4.3.2.7 Test Weight

Test weight had negative (-0.832) and positive (0.066) direct effect at genotypic and phenotypic levels, respectively.

This trait showed negative non-significant association (-0.118, -0.117) with seed yield per plant at genotypic level and phenotypic levels. Indirect negative effects of this trait were showed *via* days to 50% flowering (0.-0.202, -0.087), number of capsules per plant (-0.042, -0.041) and harvest index (-0.064, -0.241) at both levels. However, plant height (-0.001) and oil content (-0.002) expressed genotypic negative indirect effect. This trait exhibited positive indirect effects on seed yield per plant through days to maturity (0.143, 0.035), number of primary branches per plant (0.164, 0.047), capsule length (0.285, 0.017) and protein content (0.432, 0.059) at both the levels.

4.3.2.8 Harvest index

The trait, harvest index exhibited positive direct effect on seed yield per plant (0.159, 0.615) at genotypic and phenotypic level, respectively.

The positive significant correlation of harvest index with seed yield per plant (0.644**, 0.646**) was mainly due to indirect positive effects on seed yield per plant manifested through days to 50% flowering (0.170, 0.071), number of primary branches per plant (0.194, 0.046) and capsule length (0.030, 0.005) at both the levels and plant height (0.001) and test weight (0.336) at genotypic level only. This trait recorded negative indirect effects on seed yield per plant through days to maturity (-0.041, -0.011), number of capsules per plant (-0.068, -0.064) and protein content (-0.080, -0.010) at both the levels.

4.3.2.9 Oil content

The direct contribution of oil content to seed yield per plant was positive (0.103) at phenotypic and negative (-0.153) at genotypic level.

This trait had shown positive significant indirect effect (0.468**, 0.456**) *via* days to 50% flowering (0.102, 0.043), number of primary branches per plant (0.1478, 0.042), number of capsules per plant (0.050, 0.044), capsule length (0.279, 0.016), harvest index (0.059, 0.216) and protein content (0.039, 0.005) at both the levels and plant height (0.001) expressed indirect positive genotypic effect. Negative indirect effect was shown *via* days to maturity (-0.046, -0.014) at both the levels and test weight (-0.012) expressed negative indirect effect at genotypic level only.

4.3.2.10 Protein content

Protein content had positive direct effect (0.704, 0.101) at genotypic and phenotypic levels, respectively.

This trait exhibited positive non-significant association (0.076) with seed yield per plant at phenotypic level and negative non-significant (-0.087) at genotypic level. Indirect positive effects of this trait were showed *via* days to maturity (0.107, 0.023), number of capsules per plant (0.062, 0.054) and capsule length (0.105, 0.005) at genotypic and phenotypic both levels, while plant height (0.019), test weight (0.005) and oil content (0.005) expressed phenotypic positive indirect effect only.

This trait exhibited negative indirect effects on seed yield per plant through days to 50% flowering (-0.132, -0.056), number of primary branches per plant (-0.221, -0.053) and harvest index (-0.018, -0.063) at both the levels.

4.4 Genetic divergence using Mahalanobis's D^2 analysis

Characterization and quantification of genetic diversity has long been a predominant goal in crop improvement programs. Information on genetic diversity within and among closely related crop germplasm is essential for economic use of genetic resources. Parents selected for hybridization on the basis of such study would help in obtaining higher amount of heterotic expression in F_1 and broad spectrum of variability in subsequent segregating generations for various quantitative characters. The quantitative assessment of genetic divergence was made by adopting Mahalanobis's D^2 statistic for yield and its component traits. The results obtained from the study are furnished below.

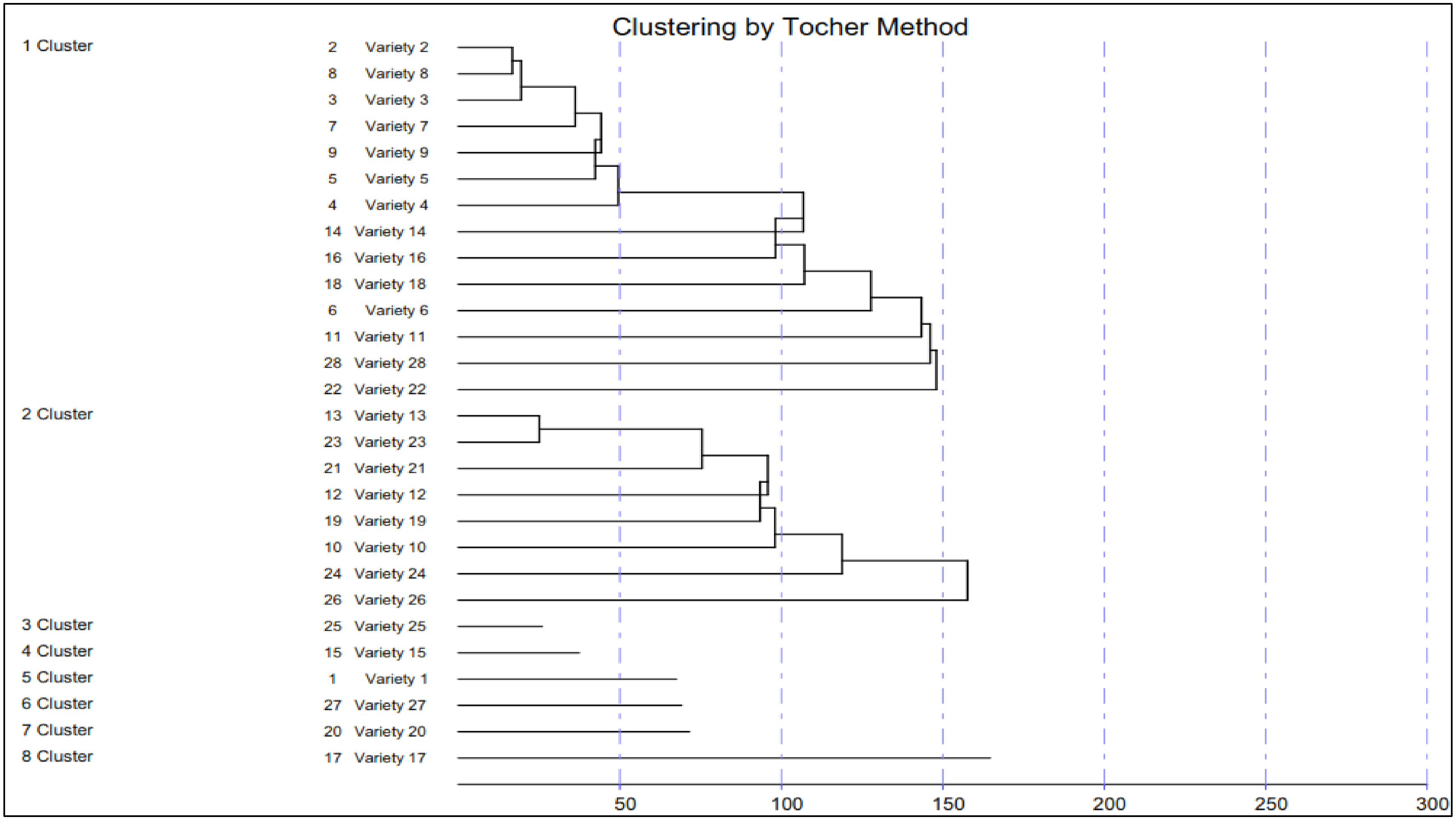

Fig. 4.3: Clustering pattern of 28 genotypes in sesame by (Tocher's method)

4.4.1 Wilk’s ‘V’ criterion test

Wilk's 'V’ (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V’ (statistic) value was tested by % at 610 degrees of freedom. The 'V’ statistic value was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously.

The significance of twenty eight genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

4.4.2 Mahalanobis’s generalized distance D^2 values

In order to study the genetic diversity among 28 genotypes, D^2 statistic was used following the procedure given by Rao (1952), since the entire 11 yield component traits were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method.

4.4.3 Grouping of genotypes into various clusters

In the present study, 28 genotypes were grouped into eight clusters based on D^2 values using Tocher's method (Rao, 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The

Table 4.6: Clustering pattern among 28 genotypes of sesame (Tocher’smethod)

Cluster Number	Number of genotypes	Genotypes
I	14	TBS 4, TBS 11, TBS 5, TBS 10, TBS 12, TBS 7, TBS 6, EC 335003, NIC 7921, NIC 8478, TBS 9, EC 303311, GT 10, Octalone
II	8	EC 334984B, RT 54, PhuleTil-1, EC 303441B, NIC 205312, EC 138836, RT 103, RT 346,
III	1	RT 127
IV	1	NIC 7909
V	1	TBS 2
VI	1	RT 351
VII	1	PT 49-3
VIII	1	NIC 8167

distribution of genotypes into various clusters has been presented in Table 4.6 and Fig 4.3. Out of eight clusters, cluster I was the largest comprising of fourteen genotypes followed by clusters II with eight genotypes, clusters III, IV, V, VI, VII and VIII were mono-genotypic clusters, suggesting the existence of high degree of heterogeneity among the genotypes. Grouping of genotypes was not related with the geographical distribution and were mainly grouped due to their morphological differences.

4.4.4 Contribution of individual character towards genetic divergence

The percentage of contribution towards genetic divergence by all the characters is presented in Table 4.7. The trait test weight (36.24%) contributed maximum to genetic divergence by taking 137 times first rank followed by number of capsules/plant (20.9%) by 79 times, seed yield per plant (15.08%) by 57 times, oil content (12.17%) by 46 times, harvest index (7.41%) by 28 times, days to 50% flowering (6.08%) by 23 times, protein content (1.85%) by seven times and numbers of primary branches per plant (0.26%) by one times. There was no contribution of days to maturity, plant height and capsule length in genetic divergence.

Table 4.7: Contribution of different characters towards genetic divergence in 28 sesame genotypes

S. No.	Source	Contribution %	Times ranked 1st
1.	Days to 50 % flowering	06.08	23
2.	Days to maturity	-	
3.	Plant height (cm)	-	
4.	Numbers of primary branches per plant	00.26	1
5.	Numbers of capsules per plant	20.09	79
6.	Capsule length (cm)	-	
7.	Seed yield per plant (g)	15.08	57
8.	Test weight (g)	36.24	137
9.	Harvest index (%)	07.41	28
10.	Oil content (%)	12.17	46
11.	Protein content (%)	01.85	7

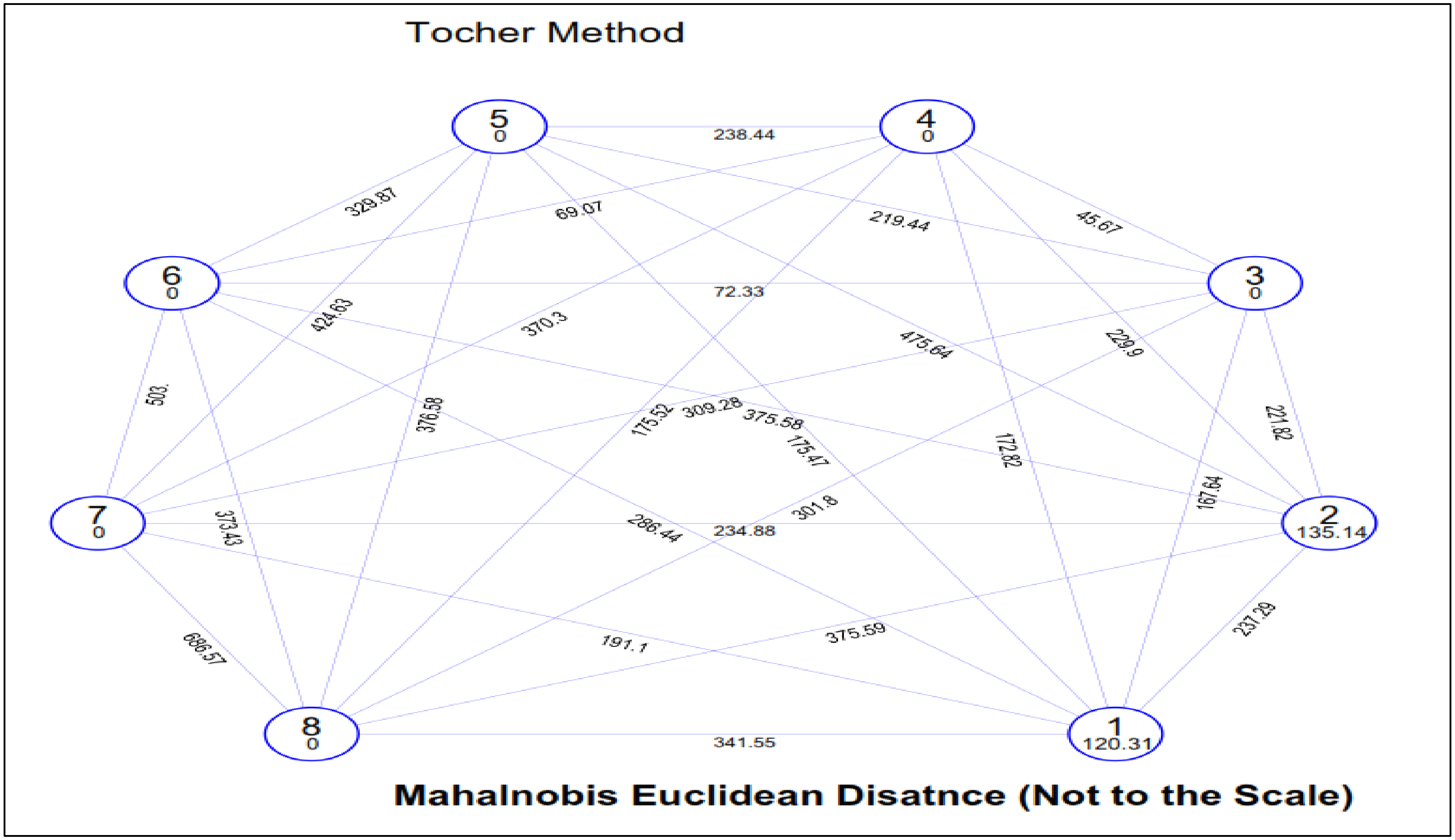

Plate No 4: Diagram showing inter and intra cluster distances

4.4.5 Average inter and intra cluster distances

D^2 statistics measures the forces of differentiation at two levels namely, intra cluster and inter cluster levels. The average intra and inter cluster D^2 values are presented in Table 4.8 and statistical distance among 28 genotypes. Intra cluster D^2 values ranged from zero (cluster III, IV, V, VI, VII and VIII) to 135.14 (cluster II). Maximum intra cluster distance was observed in cluster II (135.14), followed by cluster I (120.31).

Table 4.8: Intra (diagonal) and inter-cluster average of D^2 values of 28 sesame genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	120.31	237.29	167.64	172.82	175.47	282.44	191.10	341.55
Cluster II		135.14	221.82	229.90	475.64	375.58	234.88	375.59
Cluster III			0.00	45.67	219.44	72.33	309.28	301.80
Cluster IV				0.00	238.44	69.07	370.30	175.52
Cluster V					0.00	329.87	424.63	376.58
Cluster VI						0.00	503.00	373.43
Cluster VII							0.00	686.57
Cluster VIII								0.00

The inter cluster distance was greater than intra cluster distance (Table 4.8), indicating the presence of wide genetic diversity among the different genotypes under investigation. Maximum inter cluster distance was recorded between cluster VII and VIII (686.57) having genotypes PT 49-3 and NIC 8167 followed by cluster VI and VII (503.00) having genotypes RT 351 and PT 49-3, cluster II and V (475.64) having genotypes EC 334984B, RT 54, Phule Til-1, EC 303441B, NIC 205312, EC 138836, RT 103, RT 346 and TBS 2, cluster V and VII (424.63) having genotypes TBS 2 and PT 49-3, cluster V and VIII (376.58) having genotypes TBS 2 and NIC 8167, cluster II and VIII (375.59) having genotypes EC 334984B, RT 54, Phule Til-1, EC 303441B, NIC 205312, EC 138836, RT 103, RT 346 and NIC 8167, cluster II and VI (375.58) having genotypes EC 334984B, RT 54, Phule Til-1, EC 303441B, NIC 205312, EC 138836, RT 103, RT 346 and RT 351, cluster VI and VIII having genotypes RT 351 and NIC 8167, cluster IV and VII having genotypes NIC 7909 and PT 49-3. Distance is directly proportional to the wider genetic diversity between two clusters. Highly divergent genotypes would be of great use in recombination breeding programme in order to make highly desirable recombinants. The lowest inter cluster divergence was recorded between cluster III and IV (45.67) having genotypes RT 127 and NIC 7909, followed by cluster IV and VI (69.07) having genotypes NIC 7909 and RT 351, cluster III and VI (72.33) having genotypes RT 127 and RT 351 indicating that the genotypes included in these clusters were closely related. Selection should be performed in genetically heterogeneous clusters to maintain relatively broad genetic base.

4.4.6 Cluster mean values of different characters

The data indicated that the cluster mean for days to 50% flowering was highest in cluster VII (63.00) having the genotype PT 49-3 and the lowest in cluster III (42.33) having the genotype RT 127. Days to maturity were exhibited highest and lowest means in cluster V (90.67) (TBS 2) and cluster III (77.33) (RT 127), respectively. Cluster III exhibited highest mean for plant height (109.27 cm) having the genotype RT 127, while lowest was in cluster VI (78.60 cm) having the genotype RT 351. Cluster V recorded the highest number of branches per plant (4.60) having the genotype TBS 2 and the lowest was recorded in cluster VII (2.13) having the genotype PT 49-3. The number of capsules per plant was highest in cluster VIII (55.60) having the genotype NIC 8167 and lowest in cluster VII (27.27) having the genotype PT 49-3. Cluster V exhibited highest capsule length (2.83 cm) having the genotype TBS 2 while in cluster VIII it was lowest (2.33 cm) having the genotype NIC 8167. Highest seed yield per plant was recorded in cluster VI (5.33 g) having the genotype RT 351, while lowest in cluster V and VII (1.93 g) having the genotypes TBS 2 and PT 49-3. Highest test weight was recorded in cluster V (4.51 g) having the genotype TBS 2 and lowest in cluster VIII (1.87 g) having the genotype NIC 8167 and cluster IV exhibited the highest harvest index (40.63%) having the genotype NIC 7909 and the lowest was recorded in cluster V (8.06%) having the genotype TBS 2. Cluster VI showed highest oil content (42.45%) having the genotype RT 351 while in cluster VIII it was lowest (27.44) having the genotype NIC 8167. The protein content was highest in cluster VII (20.68) having the genotype PT 49-3 and lowest in cluster II (16.52) having the genotype EC 334984B, RT 54, Phule Til, EC 303441B, NIC 205312, EC 138836, RT 103, RT 346 (Table 4.9).

Table 4.9: Cluster means for seed yield and yield attributing characters in 28 sesame genotypes

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Days to 50% flowering	57.07	45.04	42.33^{L}	48.67	59.33	45.67	63.00^{H}	47.33
Days to maturity	85.86	82.38	77.33^{L}	82.67	90.67^{H}	86.67	88.33	78.33
Plant height (cm)	91.38	81.54	109.27^{H}	93.67	105.40	78.60^{L}	80.40	102.27
Number of primary branches	3.97	3.44	2.80	4.47	4.60^{H}	3.23	2.13^{L}	4.30
Number of capsules per plant	29.15	23.99	37.53	40.33	46.60	35.57	7.63^{L}	55.60^{H}
Capsule length (cm)	2.46	2.51	2.60	2.73	2.83^{H}	2.70	2.50	2.33^{L}
Seed yield per plant (g)	2.18	2.43	4.37	4.63	1.93^{L}	5.33^{H}	1.93^{L}	2.73
Test weight (g)	3.71	2.48	3.69	2.94	4.51^{H}	3.54	4.07	1.87^{L}
Harvest index (%)	21.38	30.98	34.85	40.63^{H}	8.06^{L}	30.61	36.91	21.67
Oil content (%)	33.40	36.73	41.35	36.94	36.51	42.45^{H}	34.16	27.44^{L}
Protein content (%)	19.46	16.52^{L}	18.72	19.95	20.10	20.40	20.68^{H}	17.66

H= High, L= Low

5. DISCUSSION

Sesame is an important ancient oilseed crop having medicinal and nutritional values and commonly known as "Queen of oilseeds" due to its resistance to oxidation and rancidity. In spite of an important oilseed crop in India, its large scale production continues to be hindered due to the unavailability of high yielding, non-shattering, synchronous maturity and phyllody tolerant varieties.

The knowledge of magnitude and nature of genetic variability is important to develop a successful breeding programme. Applications of systematic breeding efforts are compulsory and the key to create high yielding in any crop. Genetic diversity in a crop germplasm is the basis of any crop improvement programme and useful in selecting the high yielding and desirable genotypes.

Hence, the present investigation was undertaken to study the different genetic parameters *viz.,* genetic variability, heritability (broad sense), genetic advance character association and genetic divergence (D^2 statistics). On the basis of these studies, ranking of genotypes can be done and superior genotypes can be used in further breeding programmes. The experimental findings of the present investigation are being discussed under following sub heads.

5.1 Analysis of variance
5.2 Variability parameters
    5.2.1 Range and mean performance
    5.2.2 Genotypic and phenotypic coefficient of variation
    5.2.3 Heritability and genetic advance as per cent of mean
5.3 Association analysis
    5.3.1 Correlation coefficient analysis
    5.3.2 Path coefficient analysis
5.4 Genetic divergence using Mahalanobis's D^2 analysis

5.1 Analysis of variance

Results of analysis of variance (ANOVA) revealed significant differences among the twenty-eight genotypes for all the characters studied in sesame indicating that all these traits are amicable to exploitation. This indicates the presence of sufficient variability for all the traits among different genotypes. In general, it was observed that the phenotypic variances were invariably higher than corresponding genotypic variances.

Present results showed similar trend with earlier reports published by Chandra Mohan (2014), Abate *et al.* (2015), Prithviraj and Parameshwarappa (2017), Singh *et al.* (2018). They also reported significant differences among most of the traits studied under the research work.

5.2 Variability parameters

5.2.1 Range and mean performance

The mean performance of the genotypes (Table 4.2) exhibited a wide range of variability for all the eleven traits. The range of variability was recorded for the character days to 50 % flowering (37-68.67), days to maturity (77.33-90.67), plant height (67.93-109.27 cm), number of primary branches per plant (2.13-6.00), number of capsules per plant (7.63-55.60), capsule length (1.93-2.83 cm), seed yield per plant (1.40-5.33 g), test weight (1.87-4.71 g), harvest index (8.06-44.56%), oil content (25.99-43.92%) and protein content (13.42-20.68%).

Mean performance of genotypes revealed that among 28 genotypes evaluated, EC138836 was earliest for days to 50% flowering while RT 127 was earliest for days to maturity. RT 127 showed maximum plant height. Genotype EC 303311 and NIC 8167 revealed maximum number of primary branches per plant and number of capsules per plant, respectively. TBS 2 and TBS 4 showed maximum capsule length, while RT 351 revealed maximum seed yield per plant. TBS 10 and RT 346 showed maximum test weight and harvest index, respectively. Maximum oil and protein content were observed in the genotypes RT 103 and PT 49-3, respectively.

These findings were similar to those reported by Bharathi *et al.* (2014) for the characters *viz*, days to maturity, plant height, number of primary branches per plant, capsule length and test weight. Prithviraj and Parameshwarappa (2017) also observed a wide range of variability for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length, test weight and oil content while Teklu *et al*. (2017) reported high range for days to 50% flowering, days to maturity, number of capsules per plant, number of primary branches per plant, capsule length and test weight. Singh *et al*. (2018) also reported similar results for days to 50% flowering, plant height, number of primary branches per plant, capsule length, days to maturity and test weight. Variation for important yield contributing traits indicated great scope to make selections for desirable types.

5.2.2 Genotypic and phenotypic coefficient of variation

Coefficient of variation measures the amount of genetic variation present in a population. Genotypic coefficient of variation (GCV) indicates the extent of genetic variability available in a crop species at gene level whereas phenotypic coefficient of variation (PCV) of a character is the manifestation of genotypes, environment and interaction between the genotypes and environment. Therefore, to know the true breeding nature of the particular character, the total variation should be partitioned into heritable and non-heritable components. Lesser difference between magnitude of GCV and PCV indicates the presence of substantial amount of genetic variability in the population and indicates the little effect of the environment on the expression of the character. In all the characters studied in present investigation, the PCV was slightly higher in magnitude than the corresponding GCV.

High magnitudes of PCV and GCV were observed for the traits *viz.,* seed yield per followed by harvest index (41.96%, 40.73%), number of capsules per plant (39.11%, 38.72%), test weight (25.72%, 25.55%) and number of primary branches per plant (25.51%, 24.11%). These results indicated greater scope for selection of these characters for further improvement programme because of substantial variability present in germplasm lines for these traits. This finding is substantiated by similar results reported by Chandra Mohan (2014) and Tripathy *et al*. for number of primary branches per plant; Chandra Mohan (2014), Saxena and Bisen (2016), Teklu *et al.(*2017), Prithviraj and Parameshwarappa (2017) for number of capsules per plant and seed yield per plant. However results reported by Saxena and Bisen (2016), Tripathy *et al*. (2016), Prithviraj and Parameshwarappa (2017) and Singh *et al.* (2018) for oil content, Saxena and Bisen

(2016), Tripathy *et al*. (2016), Prithviraj and Parameshwarappa (2017) for days to 50% flowering and Saxena and Bisen (2016) for harvest index were contradictory to present findings.

Moderate values of PCV and GCV were noticed for characters *viz*., days to 50% flowering, plant height, oil content and protein content indicating that there is little role of environmental component in the observed variation. Similar results have been reported by Singh *et al*. (2018) for days to 50 flowering; Chandra Mohan (2014), Saxena and Bisen (2016), Teklu *et al.(*2017) for plant height. Results contradictory to present findings reported by Saxena and Bisen (2016), Tripathy *et al*. (2016), Prithviraj and Parameshwarappa (2017) and Singh *et al.* (2018) for oil content and Saxena and Bisen (2016), Tripathy *et al*. (2016), Prithviraj and Parameshwarappa (2017) for days to 50% flowering.

Low value of GCV and moderate value of PCV for capsule length were also reported by Abate *et al*. (2015) and Prithviraj and Parameshwarappa (2017). PCV and GCV were low for days to maturity and which is in conformity to earlier findings of Chandra Mohan (2014), Saxena and Bisen (2016), Tripathy *et al*. (2016), Teklu *et al.* *(*2017) and Singh *et al*. (2018). Low values of PCV and GCV for capsule length and days to maturity indicated there is lesser variability and selection of these traits will be comparatively less effective.

5.2.3 Heritability and genetic advance as per cent of mean

Genetic coefficient of variation represents the total genetic variation whereas, heritability measures the proportion to which the variability of a character is transmitted to off-springs. Burton (1952) suggested that GCV along with heritability estimates would give a better idea about the efficiency of selection. Thus a character having higher GCV with more heritability will be more valuable in a selection programme. Shift in gene frequency towards superior side under selection pressure is termed as genetic advance and is generally expressed as percent of mean (genetic gain). Johnson *et al.* (1955) found it more useful to estimate heritability values together with genetic advance in predicting the ultimate choice of the best individuals by selection.

If high or moderate heritability is coupled with high or moderate genetic advance indicates preponderance of additive gene action involved in the inheritance of particular traits and selection of the traits may be useful in this case, while high or moderate heritability is involved with low genetic advance or vice versa it indicates preponderance of non additive gene action.

In the present study, high heritability coupled with high genetic advance as per cent of mean were observed for days to 50% flowering, plant height, number of primary branches per plant, number of capsules per plant, seed yield per plant, test weight, harvest index, oil content and protein content indicating lesser influence of environment in expression of these characters and may be governed by additive gene action, hence effective for simple selection.

Similar results were reported by Bindu *et al*. (2014), Saxena and Bisen (2016) and Teklu *et al.* (2017) for plant height; Bindu *et al*. (2014), Hika *et al.* (2015), Tripathy *et al.* (2016) and Singh *et al.* (2018) for number of branches per plant; Bindu *et al*. (2014), Hika *et al.* (2015), Saxena and Bisen (2016), Teklu *et al.* (2017), Prithviraj and Parameshwarappa (2017) and Singh *et al.* (2018) for number of capsules per plant; Bindu *et al*. (2014), Tripathy *et al.* (2016), Saxena and Bisen (2016), Teklu *et al.* (2017), Prithviraj and Parameshwarappa (2017) and Singh *et al.* (2018) for seed yield per plant; Hika *et al.* (2015) for harvest index and Haibru *et al.* (2018) for test weight. Contradictory results have also been shown by Tripathi *et al.* (2013) and Saxena and Bisen (2016) for oil content.

Low heritability with low genetic advance as percent of mean was recorded for the characters *viz*, days to maturity and capsule length. This indicates the presence of non additive gene action and hence selection would be ineffective for these traits.

These findings are in conformity with the results of Abate *et al*. (2015) for days to maturity and Tripathi *et al.* (2014), Teklu *et al.* (2017) and Singh *et al.* (2018) for capsule length.

5.3 Association analysis

Complete knowledge on interrelationship of plant characters is of paramount importance to the researcher for useful and effective selection. Hence, association analysis was undertaken to determine the direction of selection and number of characters to be involved in improving seed yield.

5.3.1 Correlation coefficient analysis

Correlation coefficient is a statistical procedure which measures the degree and direction of association between two or more characters. It helps in direct selection of related characters for the improvement of desirable characters.

A positive correlation between desirable characters is useful because it helps in simultaneous improvement of both the characters. Negative correlation on the other hand, will hinder the simultaneous selection of both characters.

In the present investigation, the estimates of genotypic correlation coefficients were higher than the phenotypic correlation coefficients. The genotypic and phenotypic correlation of seed yield per plant exhibited significant positive correlation with harvest index, oil content, capsule length and number of capsules per plant suggesting that selection of these traits may be helpful in improvement of seed yield and breeder should be kept in mind for successful crop improvement programme.

The results are in agreement with reports of Patil and Lokesha (2018) and Abhijatha *et al.* (2017) for number of capsules per plant and capsule length; Abate (2018) for harvest index; Sabiel *et al.* (2015) and Hika *et* al. (2014) for days to 50% flowering; Sopundharrya *et al.* for days to 50% flowering and number of capsules per plant; Kindeya *et al.* (2017) for days to 50% flowering and number of capsules per plant and oil yield. Conflicting results have been given by Ramprasad *et al.* (2019) for capsule length; Hika *et* al. (2014) and Abhijatha *et al.* (2017) for days to 50% flowering.

The association analysis exhibited that number of number of capsules per plant, capsule length, harvest index and oil content were the important characters and may be selected to increase the seed yield. Results in present investigation also revealed that by making selection for a particular trait, simultaneous improvement in the associated trait(s) may be achieved.

The association of days to 50% flowering with seed yield was significantly negative. In such cases it would be difficult to exercise simultaneous selection for the particular trait in a breeding programme. Hence under such situations, judicious and effective selection programme might be formulated for simultaneous improvement of such important developmental and component traits.

5.3.2 Path coefficient analysis

The correlations alone do not provide true association of the characters with each other, when other characters are held constant. The mutual relationship among different traits, which may be positive or negative, is more complex and do not lead to meaningful interpretations. In such situation path coefficient analysis, devised by Wright (1921), had been found useful in partitioning direct and indirect causes of association. Path coefficient estimates direct and indirect effect of various independent characters on the dependent character and reveals the relationship of these independent characters with dependent character (yield) indicating that occurrence of association is due to their direct effect on yield or is consequence due to their indirect effect *via* other component characters.

As yield is influenced by many factors, selection based on simple correlation without taking into consideration the interactions between the component characters may sometimes prove misleading the aim of this analysis in the present investigation was to compare the obtained results of correlation coefficient with path coefficient analysis and to demonstrate the significance of path coefficient analysis in determining the true nature of characters association. For example oil content showed high positive significant correlation with seed yield but the path analysis revealed that its direct contribution to seed yield was negative (genotypic) or positive but lower value (phenotypic level).

The result of the preset investigation showed that the characters like capsule length, number of capsules per plant, days to maturity and harvest index had direct and positive effect on seed yield per plant. Protein content also had positive direct effect on seed yield but it had negative correlation at genotypic level due to indirect negative effect through days to 50% flowering, number of primary branches per plant, plant height, test weight and oil content. The trait, days to maturity had direct positive effect on seed yield but it had negative non-significant correlation due to negative indirect effect of days to 50% flowering, number of primary branches, number of capsules per plant and harvest index. Besides this, number of primary branches per plant and test weight had negative direct effect as well as negative correlation with seed yield per plant.

These results are in agreement with the reports of Abate (2018) for number of capsules per plant, capsule length and harvest index; Ramprasad *et al*. (2019) for days to maturity, number of capsules per plant and capsule length; Singh *et* al. (2018) for capsule length, number of capsules per plant and harvest index. Contradictory reports have been given by Ramprasad *et al*. (2019) for plant height and numbers of primary branches per plant; Abate (2018) for test weight; Singh *et al.* (2018) for days to maturity, plant height, oil content; Lalpantluangi *et al*. (2018) for number of capsules per plant and capsule length. Negative direct as well as negative significant correlation of days to 50% flowering with seed yield per plant was reported earlier by Sabiel *et al.* (2015), Sopundharrya *et al.* (2017) and Singh *et al*. (2018).

The residual effect determines how much the independent characters account for the variability of the dependent character (yield). Their estimates are 0.33 and 0.49 for genotypic and phenotypic levels, respectively. The low residual effect signifies that the traits chosen for the present investigation are appropriate.

Out of ten independent characters studied in path coefficient analysis only three characters *viz,* number of capsules per plant, capsule length and harvest index showed maximum direct as well as indirect contributions through other characters on seed yield. Hence, these characters may be considered as important quantitative traits in sesame improvement programme and direct selection for these traits will be useful.

5.4 Genetic divergence using Mahalanobis's D^2

Larger genetic distance between two genotypes indicates the presence of wider diversity which facilitates selection of best parents for hybridization. Mahalanobis's D^2 is a potent technique of measuring genetic divergence among the different genotypes which helps to select genetically divergent parents and determines relative proportion of each component trait.

In the present investigation, eight clusters have formed by using Tocher's method for grouping of genotypes into clusters. Varieties RT 103, RT 346, RT 127, RT 351 and RT 54 developed at Mandor, Jodhpur spread into three clusters *viz.*, cluster II (RT 103, RT 346), cluster III (RT 127) and cluster VI (RT 351). Similarly mutants received from BARC, Mumbai were grouped into three different clusters indicating that clustering of genotypes was not associated with the geographical distribution but they grouped in different clusters due to their morphological differences. Thus, indicating evidence that geographical isolation is not responsible for causing genetic diversity in sesame genotypes. Similar results were given by Singh *et al.* (2018) and Tanwar and Bisen (2018). The pattern of cluster formation was random and independent, and cluster I was largest with 21 genotypes, followed by cluster II with 8 genotypes.

Maximum intra cluster distance was shown by cluster II (135.14), followed by cluster I (120.31) indicated that some genetic divergence still existed among the genotypes within the clusters. Selection within such clusters might be conducted based on maximum mean value for the desired character. Similar results have been also obtained by Gogoi *et al.* (2018) for all the eight clusters, while contradictory reports to the present study have been given by Jadhav and Mohrir (2013); Tanwar and Bisen (2018) and Soundharya *et al.* (2017).

The maximum inter cluster distance was shown by cluster VII and VIII (686.57) followed by cluster VI and VII (503.00) and cluster II and V (475.64) indicated the presence of wide diversity between the genotypes of the clusters. Selection of parents from these groups may be useful to obtain greater variability in segregating generations. The wide range of D^2 values revealed that enormous diversity could be created through inter-cluster hybridization.

The mean values of different characters in the eight clusters revealed that the different clusters were superior in respect of different traits. The entry TBS 2 in cluster V had more number of primary branches, longer capsule with bold seed size but matured too late. The genotypes grouped in cluster III (RT 127) took least days to flower, earliest in maturity with tallest height while the entries RT 351 (Cluster VI), PT 49-3 (Cluster VII) and NIC 8167 (Cluster VIII) had high oil content, protein content and more number of capsules per plant, respectively. Therefore, the genotypes from these clusters may be selected as a parent in future crossing programme to incorporate the characters for which these have showed superiority. Lower cluster mean values were reported in cluster V for seed yield per plant and harvest index (TBS 2), cluster VII for number of primary branches per plant, number of capsules per plant and seed yield per plant (PT 49-3), cluster VIII for capsule length, test weight and oil content (NIC 8167), cluster III for days to 50% flowering and days to maturity (RT 127), cluster II for protein content (EC 334984B, RT 54, Phule Til-1, EC 303441B, NIC 205312, EC 138836, RT 103, RT 346) and cluster VI for plant height (RT 351). Therefore, the above genotypes from these clusters should be avoid to use as parents in hybridization programme as these genotypes contain less diversity.

The highest contribution for genetic diversity was due to test weight (36.24%) followed by number of capsule per plant (20.09%), seed yield per plant (15.08%) and oil content (12.17%) indicated that these attributes could be offered ample scope for selecting desired genotypes. Jadhav and Mohrir (2013) also found that seed yield per plant contributed grater in diversity, however, contradictory to the present investigation, Chandra Mohan (2014), Gogoi *et al* (2018) and Swathy *et al* (2018) reported the importance of other characters for contribution to the diversity in sesame.

Thus, the promising genotypes which contains maximum inter cluster distance (PT 49-3, NIC 8167 and RT 351, PT 49-3) and higher cluster mean (RT 127 and NIC 7909) values from these clusters may be used directly according to the objective of the hybridization programme for adaptation or may be used as parent in the future breeding programme, to obtain superior heterotic segregants.

6. SUMMARY AND CONCLUSION

The present investigation entitled "Morphological Characterization and Diversity Studies in Sesame" was conducted at Agricultural Research Station, Mandor (Jodhpur) during *kharif* season of 2018. This investigation was carried out with 28 genotypes of sesame in Randomized Block Design with three replications.

Two observations *viz.,* days to 50% flowering and days to maturity were recorded on plot basis while characters *viz.,* plant height (cm), number of primary branches per plant, number of capsules per plant, capsule length (cm), seed yield per plant (g), test weight (g), harvest index (%), oil content (%) and protein content (%) were recorded by randomly selecting ten plants.

The objective of this study was to assess genotypic and phenotypic variance, heritability, genetic advance, genotypic and phenotypic correlation and direct and indirect effects of yield components on seed yield as well as to estimate genetic divergence.

Analysis of variance exhibited the presence of significant differences among genotypes indicated the availability of considerable variability among the germplasm for all the eleven traits studied. High genetic variability in the genotypes facilitates the scope of selection for crop improvement programme including these particular genotypes.

The genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV) for all the traits under study which exhibited that there was less influence of environment on the characters so direct selection for these traits may be effective. Further, seed yield per plant revealed highest PCV and GCV values followed by harvest index, number of capsules per plant, test weight and numbers of primary branches per plant while days to 50% flowering, oil content, plant height and protein content exhibited moderate PCV and GCV whereas, moderate PCV and low GCV values were reported for capsule length. Low PCV and GCV values were reported for days to maturity.

Broad sense heritability and genetic advance are two important parameters for the selection in crop improvement. High estimates of heritability were depicted by test weight, number of capsules per plant, seed yield per plant, days to 50% flowering, oil content, harvest index, protein content, number of primary branches per plant and plant height while low heritability was recorded for days to maturity and capsule length.

Likewise, the high genetic advance as percentage of mean was shown by seed yield per plant followed by harvest index, number of capsules per plant, test weight, number of primary branches per plant, days to 50% flowering, oil content, plant height and protein content while low genetic advance was recorded for days to maturity and capsule length.

High heritability coupled with high genetic advance as per cent of mean were recorded for test weight, number of capsules per plant, seed yield per plant, days to 50% flowering, oil content, harvest index, protein content, number of primary branches per plant and plant height while low heritability with low genetic advance as per cent of mean was recorded for days to maturity and capsule length, indicating greater influence of environment in expression of these two characters.

Phenotypic and genotypic correlations between seed yield per plant and various yield contributing traits was studied. The results exhibited that the estimates of genotypic correlation coefficients were greater than the phenotypic correlation coefficients. Study revealed that seed yield plant showed highly positive significant correlation with harvest index followed by oil content, capsule length and number of capsules per plant, while, significant negative correlation was exhibited with days to 50% flowering.

Path coefficient analysis measures the cause of association between two characters. It also measures direct and indirect effect of various independent traits on the dependent trait. In the present investigation, results revealed that substantial positive direct effect on seed yield was executed by protein content, capsule length, number of capsules per plant, days to maturity and harvest index.

Wide range of inter-cluster distances indicated the presence of substantial diversity among the genotypes under study. The 28 sesame genotypes under investigation were grouped into eight divergent clusters based on D^2 values using Tocher's method such that the genotypes belonging to same cluster had revealed an average smaller D^2 values than those belonging to different clusters. Out of eight clusters, cluster I was the largest comprising of fourteen genotypes, followed by cluster II with eight genotypes, clusters III, IV, V, VI, VII and VIII were represented by single genotype.

Maximum intra cluster distance was observed in cluster I, followed by cluster II indicated that some genetic divergence still existed among the genotypes within each of these clusters while maximum inter cluster distance was exhibited between cluster VII and VIII, followed by cluster VI and VII, cluster II and V, cluster V and VII, cluster V and VIII, cluster II and VIII, cluster II and VI, cluster VI and VIII and cluster IV and VII. The greater distance between two clusters indicates the presence of wider genetic diversity among the genotypes of those clusters.

The highest cluster mean values were recorded for plant height in cluster III, harvest index in cluster IV, days to maturity, number of primary branches per plant, capsule length and test weight in cluster V, seed yield per plant and oil content in cluster VI, days to 50% flowering and protein content in cluster VII and number of capsules per plant in cluster VIII.

Among the eleven traits studied, the maximum genetic divergence was contributed by test weight (36.24%) followed by number of capsules0 per plant (20.9%), seed yield per plant (15.08%), oil content (12.17%), harvest index (7.41%), days to 50% flowering (6.08%), protein content (1.85%) and number of primary branches per plant (0.26%). There was no contribution of days to maturity, plant height and capsule length in genetic divergence.

Thus, it is suggested that these characters should be given importance during hybridization and selection of segregating populations, in this particular set of sesame genotypes to develop high yielding varieties.

Conclusions

1. Substantial variability was recorded for all the characters under study which indicates that the genotypes have sufficient exploitable level of genetic variability to develop potential future pre-breeding lines/cultivars of sesame.
2. The estimates of phenotypic coefficient of variation were significantly greater in magnitude than that of genotypic coefficient of variation for all the traits under study indicating little influence of environment for their expression. High genotypic and phenotypic coefficient of variation for seed yield per plant followed by harvest index, number of capsules per plant, test weight and number of primary branches per plant indicated availability of adequate variability in the existing germplasm.
3. High heritability coupled with high genetic advance as per cent of mean were recorded for the traits *viz.,* days to 50% flowering, plant height, number of primary branches per plant, number of capsules per plant, seed yield per plant, test weight, harvest index, oil content and protein content indicated lesser influence of

environment in expression of the trait and may be governed by additive gene action, hence effective for simple selection.

4. Correlation and path analysis concluded that the characters *viz.*, number of capsules per plant, capsule length, harvest index and oil content exhibited positive direct association along with high significant positive correlation with seed yield. Thus, these characters may be used as a criterion for improving seed yield in crop improvement programme of sesame.
5. The percentage contribution towards genetic divergence was found high for test weight followed by number of capsules per plant, seed yield per plant, oil content, harvest index, days to 50% flowering, protein content and number of primary branches per plant.
6. Maximum inter cluster divergence was observed between cluster VII and VIII followed by cluster VI and VII indicated that good recombinants can be realized by mating between the genotypes PT 49-3 X NIC 8167 and RT 351 X PT 49-3 in a definite fashion.

Suggestions for Future Work:

- In order to confirm the results, the analysis of these germplasm should be repeated over the years in multilocational trials to validate the results and adaptation of the characters.
- Characters revealing high heritability coupled with high genetic advance should be exploited to construct better crop ideotype using results of correlation analysis, path analysis and genetic divergence studies.
- Molecular characterization should be done in further investigation of above identified sesame genotypes to provide more accurate estimates of genetic diversity.
- The promising genotypes belonging to distant clusters should be used in hybridization programmes to exploit the heterotic effect, desirable genes and to obtain potential segregants.

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Morphological Characterization and Diversity Studies in Sesame

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ABSTRACT

An experiment entitled “Morphological Characterization and Diversity Studies in Sesame” was carried out during *Kharif* 2018 at the Research Farm of Agricultural Research Station, Mandor, Jodhpur (Rajasthan). The experiment was laid out in Randomized Block Design (RBD) with 28 genotypes and three replications to estimate the extent of genetic variability, heritability, genetic advance, correlation coefficient, path coefficient analysis and genetic divergence among all the genotypes.

Analysis of variance exhibited significant difference for all the characters suggested the presence of great inherent genetic variations among all the genotypes investigated. The phenotypic coefficient of variation (PCV) was slightly higher than the respective genotypic coefficient of variation (GCV) for all the characters under study indicated less influence of environmental on the genotypes. Highest magnitudes of PCV and GCV were observed for seed yield per plant whereas, the lowest for days to maturity.

Almost all the traits showed high estimates of heritability except days to maturity and capsule length. High heritability and high genetic advance as per cent of mean altogether were observed for the traits like seed yield per plant, harvest index, number of capsule per plant, test weight, days to 50% maturity, number of primary branches, oil content, protein content and plant height suggested additive gene action for expression of these characters. Hence, these characters may be proved as effective criteria for selection to improve seed yield in sesame.

Correlation studies among the characters revealed that seed yield per plant has a strong positive and significant association with characters like number of capsules per plant, capsule length, harvest index and oil content both at phenotypic and genotypic levels depicting that these are important yield contributing traits. Path coefficient analysis of various quantitative traits indicated that protein content had the maximum positive direct effect followed by capsule length, number of capsules per plant, days to maturity and harvest index while, test weight exhibited the maximum negative direct effect on seed yield per plant in sesame.

Based on the relative magnitude of D^2 values, Tocher’s method resulted in formation of eight clusters. Out of eight clusters, cluster I was the largest comprising of fourteen genotypes followed by cluster II with eight genotypes, clusters III, IV, V, VI, VII, VIII were monogenotypic suggested the existence of high degree of heterogeneity among the genotypes. The trait test weight contributed maximum towards genetic divergence. The highest intra cluster distance was recorded in cluster II followed by cluster I. The inter cluster distance was highest between cluster VII and VIII followed by cluster VI and VII indicated that superior recombinants can be achieved by mating between the lines of the clusters i.e. PT 49-3, NIC 8167 and RT 351, PT 49-3 in a definite fashion.

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तिल में लक्षणात्मक निरूपण और विविधता का अध्ययन

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अनुक्षेपण

कृषि अनुसंधान केन्द्र, मण्डोर, जोधपुर (राजस्थान) के अनुसंधान प्रक्षेत्र पर खरीफ 2018 के दौरान ''तिल में लक्षणात्मक निरूपण और विविधता का अध्ययन'' हेतु एक प्रयोग लगाया गया। यह प्रयोग तिल के 28 जीन प्रारूपों को तीन पुनरावृतियों के साथ यादृच्छिक खण्ड अभिकल्पना में आनुवांशिक विभिन्नता, वंशानुगति, आनुवांशिक प्रगति, उपज व अन्य लक्षणो में सहसंबंध, उपज में सहायक लक्षणों का प्रत्यक्ष एवं अप्रत्यक्ष प्रभाव (पाथ गुणांक विश्लेषण माध्यम से) और सभी जीनप्रारूपों में आनुवांशिक विधिधता D^2 महालेनोबिस विधि द्वारा निर्धारण के लिए आयोजित किया गया।

विभिन्नता के विश्लेषण ने सभी लक्षणों के लिए सार्थक अंतर को दर्शाया जिसने सुझाया कि सभी विश्लेषित जीनप्रारूपों के मध्य अत्यधिक वंशानुगत आनुवांशिक विविधता थी। अध्ययन में सम्मिलित सभी लक्षणों के लिए विभिन्नता का लक्षण प्रारूप गुणांक, जीनप्रारूप गुणांक की तुलना में थोडा ज्यादा था, जिसनें जीन प्रारूप पर वातावरण के प्रभाव को दर्शाया। बीज उपज के लिए लक्षण व जीन प्रारूप गुणांक का परिमाण सर्वाधिक था, जबकि परिपक्वता दिनों के लिए सबसे कम था।

परिक्वता के लिए दिनों की संख्या तथा बीजकोश की लंबाई के अलावा लगभग सभी लक्षणों ने वंशानुगति के उच्च निर्धारक दर्शाये। बीज उपज प्रति पौधा, कटाई सूचकांक, प्रति पौधा बीजकोशो की संख्या, हजार दानों का वजन, परिपक्वता के लिए दिनों की संख्या, प्राथमिक शाखाओं की संख्या, तेल की मात्रा, प्रोटीन की मात्रा और पौधे की ऊंचाई के लिए उच्च वंशानुगति के साथ उच्च आनुवांशिक प्रगति प्रेक्षित की गई जिसने इन लक्षणों की अभिव्यक्ति के लिए योज्य जीन प्रभाव को सुझाया। अतः ये लक्षण तिल में उपज सुधार हेतु चयन के प्रभावी मापदण्ड के रूप में प्रमाणित किये जा सकते हैं।

लक्षणों के मध्य सहसंबंध के अध्ययन ने दर्शाया कि बीज उपज प्रति पौधा, अन्य लक्षणों जैसे प्रतिपौधा बीजकोश की संख्या, बीजकोशों की लंबाई, कटाई सूचकांक और तेल की मात्रा के साथ जीन प्रारूपी और लक्षण प्रारूपी दोनों स्तरों पर सकारात्मक और सार्थक सहचार्य था, जिसने सुझाया कि ये सभी मुख्य उपज सहायक लक्षण थे। विभिन्न मात्रात्मक लक्षणों के पाथ गुणांक विश्लेषण ने दर्शाया कि तिल में प्रोटीन की मात्रा का बीज उपज प्रति पौधा पर सर्वाधिक सकारात्मक प्रत्यक्ष प्रभाव था उसके पश्चात बीजकोश की लंबाई, प्रतिपौधा बीजकोशों की संख्या परिपक्वता के लिये दिनों की संख्या और कटाई सूचकांक थे। जबकि हजार दानों के वजन ने सर्वाधिक नकारात्मक प्रत्यक्ष प्रभाव दर्शाया।

D^2 मान के संबधित परिमाण के आधार पर, टॉचर विधि से आठ समूहों को निर्माण हुआ। आठ समूहों में से, समूह –I चौदह जीन प्रारूपों के साथ सबसे बड़ा था। उसके पश्चात समूह-II में आठ जीन प्रारूप थे। समूह III, IV,V, VI, VII, और VIII में एक–एक जीन प्रारूप थें। इस परिणाम ने दर्शाया कि जीन प्रारूपों के मध्य उच्च कोटि की विजातियता थी। आनुवांशिक विविधता में सर्वाधिक प्रतिशत योगदान हजार दानों के वजन ने दिया। सर्वाधिक समूह के अंदर दूरी समूह II व समूह I के लिये दर्ज की गयी। जबकि समूहों के बीज सर्वाधिक दूरी समूह VII व समूह टप्प् के मध्य पायी गयी। जिसने दर्शाया की दो समूहों के बीच अधिक दूरी वाले जीनप्रारूपों जो कि PT 49-3, NIC 8167 और RT 351, PT 49-3 थे, के मध्य एवं निश्चित प्रारूप में संकरण से उत्कृष्ट पुनःसंयोजक प्राप्त किये जा सकते है।

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**शोधग्रंथ स्नातकोत्तर कृषि आनुवांशिकी और पादन प्रजनन डिग्री की आंशिक आवश्यकता पूर्ति के लिए डॉ. बी. आर. चौधरी, विभाग प्रमुख और आचार्य, आनुवांशिकी और पादप प्रजनन विभाग, कृषि विश्वविद्यालय, जोधपुर की देखरेख में जमा किया गया।

APPENDIX-I

Mean weekly parameters and total rainfall during pending dependency of crop growth (*Kharif*, 2018)

S.M. W.N.	Period	Temp. (°C)		Rainfall (mm)	Rainy Days (No.)	R.H. (%)	
		Max.	Min.			Max. (%)	Min. (%)
26.	Jun. 25-Jul.1	36.4	27.3	31.1	3	74.9	52.3
27.	Jul. 2-Jul. 8	37.9	29.5	0.0	0	65.9	37.6
28.	Jul.9- Jul.15	39.7	29.2	9.8	1	68.7	44.6
29.	Jul. 16-Jul. 22	33.6	26.2	105.3	4	90.0	69.9
30.	Jul. 23-Jul. 29	31.6	26.8	0.0	0	79.0	59.6
31.	Jul. 30- Aug. 5	35.3	26.9	0.0	0	69.3	42.9
32.	Aug. 6-Aug. 12	33.9	26.8	26.5	1	75.3	54.6
33.	Aug. 13-Aug. 19	34.7	27.4	31.8	1	78.7	60.4
34.	Aug. 20-Aug. 26	32.0	25.7	6.5	2	82.7	64.6
35.	Aug. 27- Sep.2	33.6	25.1	8.6	1	82.9	54.6
36.	Sep.3-Sep. 9	33.7	25.1	5.2	1	78.7	50.6
37.	Sep. 10-Sep. 16	33.6	23.9	2.4	1	77.9	43.9
38.	Sep. 17-Sep. 23	37.2	24.9	0.0	0	63.7	33.3
39.	Sep. 24-Sep. 30	37.3	23.6	0.0	0	58.9	20.9
40.	Oct. 1-Oct. 7	39.4	23.5	0.0	0	51.9	16.7
41.	Oct. 8-Oct. 14	38.1	23.1	0.0	0	43.1	15.1
42.	Oct. 15-Oct. 21	37.4	20.9	0.0	0	49.4	13.6
43.	Oct. 22-Oct. 28	36.0	19.0	0.0	0	48.4	16.6
44.	Oct. 29-Nov. 4	35.2	18.1	0.0	0	57.1	17.4

Note: M. W. – Meteorological week