“STUDIES ON GENETIC DIVERSITY, PATH ANALYIS AND CORRELATION IN SESAME (*Sesamum indicum* L.)”

By

KANTE SRIKANTH

B.Sc. (Horti.)

MASTER OF SCIENCE

(AGRICULTURE)

IN

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY

COLLEGE OF AGRICULTURE, LATUR

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DISSERTATION

Submitted To

The Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. In Partial Fulfilment Of The Requirements For The Degree Of

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CANDIDATE'S DECLARATION

I hereby declare that the dissertation

or part thereof, has not been

previously submitted by

me for a degree of

any University or

Institution

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CERTIFICATE-I

This is to certify that dissertation entitled "**STUDIES ON GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS IN SESAME (*Sesamum indicum* L.)"** submitted by **Shri. KANTE SRIKANTH to the Vasantrao Naik Maratwada Krishi Vidyapeeth, Parbhani** in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **GENETICS AND PLANT BREEDING** is record of original and bonafide research work carried out by him under my guidance and supervision. It is of sufficiently high standard to warrant the presentation for the award of the said degree.

I also certify that the dissertation or part thereof has not been previously submitted by him for a degree of any university.

Place: Latur **M.K. GHODKE**

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CERTIFICATE – II

This is to certify that the dissertation entitled **"STUDIES ON GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS IN SESAME (*Sesamum indicum* L.)"** submitted by **Shri. KANTE SRIKANTH** to the **Vasantrao Naik Maratwada Krishi Vidyapeeth, Parbhani** in partial fulfilment of the requirements of the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **GENETICS AND PLANT BREEDING** has been approved by the student's advisory committee after viva-voce examination in collaboration with the external examiner.

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With the blessings of my parents and teachers that I could accomplish and bring to light this humble piece of work

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Date:

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LIST OF ILLUTRATIONS

LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
*	:	Significance at 5% level
**	:	Significance at 1% level
ORS	:	Oilseeds Research Station
X	:	Mean Value
/	:	Per
CV	:	Coefficient of Variation
CD	:	Critical Difference
Cm	:	Centimeter
d.f	:	Degree of freedom
ECV	:	Environment Coefficient of Variation
et al.,	:	and others
Fig	:	Figure
G	:	gram
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Coefficient of Variation
Ha	:	Hectare
h^2 (b)	:	Heritability (broad sense)
i.e.,	:	That is
MSL	:	Mean Sea Level
PCV	:	Phenotypic Coefficient of Variation
SEd	:	Standard Error of Difference
Viz.,	:	Namely
Via	:	Through

Chapter I

INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the world's oldest spice and oilseed crop and it is native to tropic and sub-tropic regions. It's known with various names such as sesamum, til, gingelly, simsim, gergelim etc. It belongs to Pedaliaceae family having chromosome number as (2n=26) and is an annual, self-pollinated oil seed crop. It is under cultivation in Asia for over 5000 years (Bisht *et al.*, 1999). The crop has its early origins in East Africa and India (Bedigian and Harlan 1986). Today, India and China are the world's largest producers of sesame, followed by Myanmar, Sudan, Uganda, Nigeria, Pakistan, Tanzania, Ethiopia, Guatemala and Turkey.

Sesame is the sixth most important oilseed crop in the world after soybean, rapeseed, cottonseed, sunflower and groundnut. India is the world leader in the area and production of sesame. In India, Sesamum is cultivated in an area of 1.78 million hectares, with a production of 0.81 million tons with productivity of 456 kg (2014-15). It is grown in marginal and sub-marginal lands to an altitude of 1200 meters, about 500 mm rainfall and with temperature requirement about 25-27° C. It is grown as rain fed crop mainly in the states of Gujarat, West Bengal, Uttar Pradesh, Rajasthan, Madhya Pradesh, Andhra Pradesh, Maharastra, Tamilnadu, Odisha and Karnataka, which account for more than 96% of the total area and production. In Maharastra it is cultivated in an area of 30.4 thousand hectares, with a production of 5.6 thousand tones with average productivity of 184 kg ha^{-1} (Oilseeds statistics A Compendium- 2015 and Indian Institute of Oilseeds Research, Hyd.).

Sesame is grown mainly for its seeds that contain approximately 50% oil and 25% protein (Burden, 2005). The presence of antioxidants (sesamolin and sesamol) makes the oil to be one of the most stable vegetable oils in the world. Sesamum oil is highly resistant to oxidative deterioration even though oleic and linoleic acids are the predominant fatty acids (about 80% of its total) of sesame oil, (Uzun *et al.*, 2007). The high level of unsaturated fat increases the quality of sesame oil for human consumption. Due to high stability of its oil with distinct sweet flavor, sesamum is regarded as the 'Queen of Oilseeds'.

Sesame oil comprising 50% of the dry seed weight has been preferentially consumed in oriental food because of its distinctive flavor and the stabilizing antioxidant properties. The oil extracted from sesame seeds is of very high medicinal quality. The great medical authority of ancient India, Charak, has said that of all the oils, the gingelly or sesame-oil is the best. It has the finest flavor and a high boiling point. This latter quality is important from the health point of view, for it indicates that less molecular restructuring takes place in sesame oil than any other seed oil. Aside it's being antioxidative, antihypertensive, hypocholesteremic, anticancer and immunoregulatory properties, sesame oil finds use in cosmetic, pharmaceutical, paint, detergent and pesticide industries. Sesame secured its position in various civilizations across the world and it's continuing still today. No "burger" in any famous bakery or confectionary across the world comes without sesame seeds topped on it. Indian Hindus believe that lilting light "deepa" with sesame oil is sacred, no meal in northern Europe completes without "Margoreta" an edible sweet made from sesame. A highly valued confectionary commodity, besides being the much sought after edible oil source world over, sesame has all the potential to emerge as an important commodity in International trade. This important

oilseed crop has been grown for centuries for its oil and high energy content.

In spite of being the first oilseed crop known to man and its long history, sesame is a typically neglected crop or an “Orphan crop” or “Underutilized crop” because of lack of appreciable research efforts, in India and abroad.

The crop is highly drought tolerant, grows well in most kinds of soils, regions and is well suited to different crop rotations. In reality, sesame is mostly grown under moisture stress with low management input by small holders (Cagirgan, 2006). However, the sesame production is below expectation, as it has not contributed its best to the current bright oilseed scenario. The low production is due to a number of reasons such as low inputs and poor management (e.g low or non-fertilization, irrigation, pest control etc.,) occurrence of biotic and abiotic stresses and more importantly, lack of an organized breeding program. Major factors that limit its productivity besides narrow genetic base are extreme susceptibility to biotic and abiotic stresses.

The success of any crop improvement programme essentially depend on the nature and magnitude of genetic variability present in the crop & in-depth understanding of the underlying gene action & genetic architecture of traits related to yield. Sesame is plant breeder’s dream because of its great variability. The knowledge of nature and magnitude of genetic variability is of immense value for planning efficient breeding programme to improve the yield potential of the genotypes. Improvement in yield is normally attained through exploitation of the genetically diverse parents in breeding programmes. Genetic divergence among parents is essential since the

crossing programme involving genetically diverse parents is likely to produce high heterotic effects and also more variability could be expected in the segregating generations. Genetic diversity between populations/genotypes indicate the differences in gene frequencies. For identifying such diverse parents for crossing, multivariate analysis using Mahalanobis D^2 statistic (1936) has been used in several crops. This is a valuable tool to study genetic divergence at inter varietal and sub-species level in classifying the crop plants.

Assessment of variability forms the basis for any crop improvement programme. A study of the manner in which a particular character behaves in relation to others contributing to seed yield will be great significance in planning successful breeding strategies in any crop improvement programme. Yield being a complex character is influenced by various component characters, which are polygenetically inherited and highly subjected to environmental variation. More emphasis, therefore, needs to be placed on the selection of yield attributes which are less influenced by the environment. Besides, genotypic and phenotypic coefficient of variation, heritability and genetic advance, a study of correlation among yield and its components and their relative contribution to yield is of great value in the breeding programmes.

With this available background information, the present studies have been initiated with the following objectives**.**

1. To study the extent of genetic variability for yield and yield contributing characters.
2. To estimate the genetic diversity among the sesame genotypes using Mahalanobis D^2 statistics.
3. To study character association for yield and yield contributing characters.

Chapter II

REVIEW OF LITERATURE

A brief review of literature in consonance with the objectives of present investigation in sesame (*Sesamum indicum* L.) is presented under the following heads.

1) Genetic parameters
   i) Genetic variation
   ii) Heritability and genetic advance
2) Character association
   i) Path analysis
   ii) Correlation
3) Genetic Divergence

2.1 Genetic variation

i) Genetic variability.

The genetic variability is important in all plant breeding programs. Greater the genetic variability in the crop, wider will be the scope for selection in crop breeding program. Fisher (1918) for the first time studied the genetic variability in relation to environmental variability. Later on several workers have also derived different techniques for the estimation of components of variance (Wright, 1921, Johnson *et al.*, 1955).

Patil and Sheriff (1996) reported high heritability estimates for seed yield, oil yield per plant, days to 50% flowering and capsule length. They further reported high GCV, heritability estimates and genetic advance for seed yield, oil yield and number of capsules.

Subrata and Mait (1997) found high estimates of broad sense heritability, genetic advance and genotypic coefficient of variation indicating the importance of seed yield, number of branches and 1000-seed

weight. They opined that simple selection would help in improving these characters.

Joel and Thangavelu (1997) while studying 95 diverse genotypes reported high GCV and PCV for 1000-seed weight, capsules length, capsule breadth, oil content, days to 50% flowering, days to maturity and seeds per capsule along with high heritability estimates.

Variability studies in segregating populations by Backiyarani *et al.* (1997) revealed moderate to high heritability estimates for primary branches, capsules number, seed number, percentage of oil and yield per plant.

Reports of Singh *et al.* (1997) suggested scope for improvement of productive capsules per plant and seed yield per plant through simple selection. High heritability coupled with high genetic advance was recorded for days to maturity, productive capsules per plant and seed yield per plant.

Motilal (2000) reported high heritability estimates for plant height, length of fruiting stem, number of capsules and seed yield in sesame. He also reported high genetic advance for seed yield and number of capsules indicating additive gene action.

Low estimates of heritability for primary and secondary branches, seeds per capsule and total dry matter produced at 75 days after sowing and maturity were reported by Singh *et al.* (2000).

Sharma and Mandal (2001) reported high heritability estimates for capsules per plant followed by days to 50% flowering, plant height and mean capsule weight. They reported maximum PCV for number of branches per plant followed by harvest index.

Reddy *et al.* (2001) performed Analysis of genetic parameters for 44 genotypes of sesame revealed high heritability and genetic advance as per cent of mean for seed yield per plant, capsules per plant, capsules on main

stem, capsules on primary branches, capsule length, plant height and dry matter production.

Babu *et al.* (2004) assessed eighteen white seeded genotypes of sesame. Wide range of variability is recorded for twelve traits studied, high heritability coupled with high genetic advance observed for number of primaries, number of capsules per plant, seed yield per plant, and oil yield indicating these characters governed by additive gene action.

Singh and Singh (2004) studied the thirty diverse lines and 0 varieties of sesame and observed wide range of variations for all characters except capsule length, plant height, capsules per plant, seeds per capsules and grain yield.

Babu *et al.* (2005) studied the analysis of variance of 4 lines, 3 testers and 12 hybrids obtained from line x tester mating indicated significant variation among all nineteen sesame genotypes for all characters studied. Estimates of heritability were high for all characters, while high genetic advance as percent mean observed for seed yield per plant, number of seeds per capsules, number of primaries, number of capsules per plant and 1000-seed weight.

Raghuwanshi (2005) assessed genetic variability for eight characters in 100 sesame genotypes. A wide range of variability was observed for yield and its components in all environments. However, high was observed for observed for all characters except for 1000-seed weight which showed low to moderate variability.

Iwo *et al.* (2007) estimated genetic variability of seven yield and related traits including broad sense heritability for nineteen genotypes of sesame. All characters investigated showed high estimates of high heritability except capsule length and high genetic advance for number of branches, number of capsules per plant and seed yield is observed.

Gawali *et al.* (2007) observed wide range of variability for all the nine characters studied except for number of branches per plant. Higher

heritability coupled with genetic advance as percentage of mean was noticed in seed yield per plant, number of capsules per plant, seeds per capsules and 1000-seed weight indicating the presence of additive gene action.

Manjunatha *et al.* (2008) evaluated sixty sesame genotypes and studied variability parameters, phenotypic and genotypic variances, heritability and genetic advance, correlation and path coefficient analysis. Based on studies they suggested that plant type with the characters *viz.*, long duration, tallness, more plant height up to first branch, more number of nodes up to first branch, high number of primary branches and capsules, long and wide capsules can be considered as essential in achieving improvement in seed yield under late *kharif* conditions.

Suvarna *et al.* (2008) evaluated fifty sesame entries in an augmented design. Genetic variability parameters, phenotypic and genotypic variances, heritability and genetic advance, correlations and path coefficients were studied. Based on their studies they suggested that plant type with the characters viz., long duration, tallness, more plant height up to first branch, more number of nodes up to first branch, high number of primary branches and capsules, long and wide capsules can be considered as essential in achieving improvement in seed yield under late *kharif* conditions.

Kumhar and Solanki (2009) studied genetic diversity and variability in 82 sesame genotypes. Their results showed that mean sum of squares were significant for all the characters studied except oil content, indicating the presence of variability. Characters like seed yield, primary branches/plant, capsules/plant and plant height to first capsule exhibited heritability coupled with high genetic advance revealing that these characters were controlled by additive gene action.

Sumathi and Muralidharan (2010) observed that number of branches per plant, number of capsules per plant and seed yield per plant showed high PCV and GCV estimates. High heritability combined with high

genetic advance as per cent of mean observed for plant height, number of branches, number of capsules and seed yield per plant these characters might be controlled by additive gene effects and phenotypic selection for these characters would likely to be effective.

Gangadhara *et al.* (2012) studied that genetic divergence, genetic advance and heritability in 81 indigenous sesame accessions based on eleven characters. The ANOVA revealed significant difference among genotypes for all characters except seed weight per capsule. High GCV and PCV estimates were observed for seed yield per plant, capsules per plant and plant height, while the branches per plant, capsule length, 1000-seed weight and seeds per capsule recorded moderate values, while low GCV and PCV values were observed for oil content, days to maturity and days to 50 per cent flowering. High heritability and genetic advance was observed for seed yield per plant, capsules per plant, plant height, and number of branches per plant, capsule length, seeds per capsule and 1000-seed weight. High heritability coupled with moderate genetic advance was recorded for days to 50 per cent flowering, days to maturity and oil content. Seed weight per capsule recorded low heritability and genetic advance as per cent mean.

Revathi *et al.* (2012) observed high genotypic coefficient of variability and phenotypic coefficient of variability for number of branches per plant, number of capsules per plant and seed yield per plant. High heritability along with high genetic advance as per cent of mean was observed for number of branches per plant, number of capsules per plant and seed yield per plant.

Jadhav *et al.* (2012) studied genetic variability for quantitative traits in 31 germplasm accessions of sesame. Analysis of variance revealed significant differences for all characters except days to flower initiation. Characters *viz*., seed yield per plant, number of capsules per plant, number of capsules on main stem and plant height for first capsule, had high GCV

and PCV values and hence improvement through selection could be possible. High GCV, heritability and genetic advance as per cent of mean were recorded for seed yield per plant, number of capsules on main stem, number of capsules per plant, number of nodes on main stem and plant height for first capsule indicating that selection could be effective for improvement of these characters.

Salah *et al.* (2012) studied the variability of yield and some morphological traits in some sesame genotypes in two seasons under rain-fed conditions. A wide range of variability was detected among the genotypes for all characters in both seasons. High heritability coupled with low genetic advance was recorded for days to 50% flowering, days to maturity and plant height which indicated dominant and epistatic gene action while low to moderate heritability with high genetic advance was recorded for the yield and its components which indicated the additive nature of inheritance. Therefore, direct simple selection might improve the morphological traits of the crop, whereas, other mechanisms may be needed to improve the seed yield and its components.

Siva *et al.* (2013) recorded high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for number of branches/plant followed by seed oil content (%) and seed yield/plant (g). PCV values were magnitudinally higher than GCV for all the characters indicating the environment effect on character expression.

Vanishree *et al.* (2013) evaluated one hundred and twenty four F4 families of sesame and reported high GCV and PCV for branches/plant, capsules/plant and seed yield/plant.

Tripathi *et al.* (2013) revealed significant difference among genotypes for all the nine characters studied. The traits seed yield/plant followed by number of secondary branches/plant, 1000 seed weight and number of primary branches/plant estimated high PCV and GCV.

Gidey *et al.* (2013) observed high GCV and PCV for harvest index, seed yield/ha, height to the first capsule, number of capsules/ha, number of primary branches/ha, number of seed/capsule and plant height in 81 sesame genotypes.

Narayan and Murugan (2013) evaluated fifty sesame genotypes to estimate the phenotypic variability. Analysis of variance revealed that there was highly significant difference among the genotypes for all the characters studied. High Phenotypic Coefficient of Variation (PCV) was recorded for days to 50 per cent flowering, plant height, number of capsules plant per plant, capsule length, number of branches per plant, number of seeds capsule per plant and seed yield per plant.

Bharathi *et al.* (2014) studied fifty genotypes of sesame. The variation of different traits under this study revealed that the Phenotypic coefficient of variation (PCV) were higher than Genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. The traits seed yield per plant followed by number of capsules per plant and number of branches per plant showed high PCV and GCV estimates. High coefficient of variation for number of branches per plant and seed yield per plant has also been reported.

Chandra Mohan (2014) revealed high values of genotypic and phenotypic coefficient of variation for primary branches per plant followed by capsules per plant and seed yield per plant, whereas lower values for days to maturity and days to 50% flowering.

Ismaila and Usman (2014) reported high estimates of GCV than PCV for characters number of capsules per plant, number of branches per plant and seed yield.

A study on 64 Ethiopian sesame genotypes by Hika *et al.* (2015) revealed high estimates of GCV and PCV for characters number of primary

branches, number of branches per plant, seed yield, biological yield and harvest index.

Saxena *et al.* (2016) studied variability in twenty six sesame genotypes and reported slightly higher amount of PCV than GCV. High GCV and PCV values are observed for number of capsules per plant and seed yield per plant and high PCV values were observed for number of primary branches and number of secondary branches.

ii) Heritability and genetic advance

Heritability is the proportion of phenotypic variation in a population that is attributable to genetic variation among individuals. The parameter H2 is the broad-sense heritability and reflects all possible genetic contributions to a population's phenotypic variance. It is the good index of transmission of characters from parents to their offspring (Falconer, 1981).

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance (GA) was calculated by the method of Johnson *et al.* (1955).

Solanki and Gupta (2004) reported high heritability for seed yield/plant, plant height, number of branches/plant, number of capsules/plant and 1000-seed weight in 48 sesame genotypes. High heritability coupled with high genetic advance was recorded for seed yield/plant and number of branches/plant.

Babu *et al.* (2005) estimated high heritability for all the characters studied, while genetic advance was high for seed yield/plant, number of seeds/capsule, number of primaries/plant, number of capsules/plant and 1000-seed weight. Medium genetic advance was recorded for days to 50% flowering and plant height. Oil content and days to maturity had a low genetic advance as percent of mean. This indicated that simple selection

could be effective for improving majority of characters including seed yield/plant.

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

Gawali *et al.* (2007) studied heritability and genetic advance in 50 sesame genotypes. Higher heritability coupled with genetic advance as percentage of mean was noticed in seed yield/plant, number of capsules/plant, seeds/capsule and 1000-seed weight indicating the presence of additive gene action and direct selection may be effective.

Kumhar and Solanki (2009) reported that characters like seed yield, primary branches/plant, capsules/plant and plant height to first capsule exhibited heritability coupled with high genetic advance revealing that these characters were controlled by additive gene action.

Gangarde *et al.* (2009) reported that capsule length, number of capsules/plant showed high heritability estimates accompanied with high genetic advance as a per cent of mean in sesame. It suggests that most likely the heritability is due to additive gene effects and selection may be effective.

Parameshwarappa *et al.* (2009) evaluated one hundred fifty one sesame genotypes and observed high heritability and genetic advance as per cent mean for seed yield, number of primary branches/plant, number capsules/plant, number of seeds/capsule, plant height and days to 50% flowering.

Alake *et al.* (2010a) observed high heritability for height of first capsule, final plant height, number of seeds per capsule and seed yield per hectare, capsule weight per plant, 1000-seed weight, height of flowering

and number of capsule per plant. The highest genetic advance was recorded for number of seeds per capsule followed by height of first capsule and seed yield per hectare. Highest heritability coupled with high genetic advance was observed for capsule weight per plant, height of first capsule and seed yield per hectare. Thus, these traits could be used as selection criteria for yield improvement in sesame.

Sumathi and Muralidharan (2010) reported high heritability combined with high genetic advance for plant height, number of branches/plant, number of capsules/plant and seed yield/plant indicating that these characters were controlled by additive gene effects and phenotypic selection for these characters would likely to be effective.

Boranayaka *et al.* (2011) reported high heritability and genetic advance for number of seeds/capsule and number of capsules/plant in sesame genotypes.

Aremu *et al.* (2011) evaluated fifteen indigenous sesame genotypes and reported that in improving indigenous sesame seed yield, there is reliability in selecting number of capsule and seed per capsule as these traits recorded highest selection index using heritability and genetic advance parameters.

Gangadhara *et al.* (2012) observed high heritability and genetic advance for seed yield/plant, capsules/plant, plant height, number of branches/ plant, capsule length, seeds/capsule and 1000 seed weight in sesame.

Shekhawat *et al.* (2013a) evaluated fifty five genotypes of sesame for seed yield and reported that heritability ranged from 10.20% (branches per plant) to 97.10% (days to flowering), confirming that genotypic variance has contributed substantially to the total variance.

Vanishree *et al.* (2013) observed high heritability coupled with high genetic advance as per cent mean for plant height, branches/plant, capsules/plant, capsule length, distance from ground to first capsule, seeds/capsule, 1000 seed weight and seed yield/plant.

Tripathi *et al.* (2013) recorded high heritability for days to 50% flowering, seed yield/plant, number of secondary branches/plant and days to maturity. High genetic advance were recorded for seed yield/plant followed by number of secondary branches/plant and low for oil content and capsule length in 100 sesame accessions. High heritability coupled with high genetic advance was recorded for seed yield/plant, number of secondary branches/plant and 1000 seed weight indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

Gidey *et al.* (2013) observed high heritability coupled with high genetic advance was observed for number of primary branches/plant, height to first capsule and harvest index.

Narayan and Murugan (2013) evaluated fifty sesame genotypes and reported that high heritability value was observed for all the characters studied.

Bharathi *et al.* (2014) studied fifty genotypes of sesame and reported high heritability for characters days to maturity, days to 50% flowering, seed yield per plant, number of capsules per plant and number of branches per plant.

Hika *et al.* (2015) observed high heritability coupled with high genetic advance estimates for characters seed yield, primary branches per plant, number of branches per plant, biological yield and moderate heritability and harvest index observed for test weight.

Ismaila and Usman (2014) reported high heritability coupled with high genetic gain for number of capsules per plant, number of branches per

plant, and yield per hectare which indicated the additive nature of inheritance.

2.2 Association analysis

i) Correlation analysis

Correlation analysis is a statistical measure used to measure the degree and direction of relationship between two or more variables. It includes both genotypic and environmental effects. Correlation studies provide better pathway for yield improvement during selection (Robinson *et al.*, 1951 and Johnson *et al.* 1955).

Yingzhong and Yishou (2002) reported that seed yield per plant was positively and significantly correlated with number of capsules per plant and plant height. Plant height had significantly positive correlations with days to flowering, height to first capsule and number of capsules per plant and significantly negative with capsule width and 1000-seed weight. Capsule width and 1000-seed weight were negatively and significantly correlated with number of capsules per plant.

Begum and Dasgupta (2003) observed that plant height, number of branches/plant, number of capsules/plant, capsule length and number of seeds/capsule were significantly and positively correlated both at genotypic and phenotypic levels. On the other hand, 1000-seed weight was negatively correlated with seed yield in 23 sesame cultivars.

Mothilal (2005) revealed that plant height and number of capsules exhibited high positive association with seed yield indicating its true relationship. Other characters such as number of branches, fruiting stem length, number of seed/capsule and 1000-seed weight showed positive association with seed yield.

Sudhakar *et al.* (2007) revealed that seed yield showed significant and positive association with plant height, number of capsules/plant, capsule length, number of seeds/capsule and number of primary branches in sesame genotypes.

Parameshwarappa *et al.* (2009) observed that seed/plant showed significant and positive association with number of primary branches/plant, number of seeds/capsule and capsule length in sesame.

Kordestani *et al.* (2009) recorded that seed yield showed highly significant, positive correlation with plant height, pod length, number of seeds/pod, 1000-seed weight, number of stems, biological yield and number of pods/plant in sesame.

Sumathi and Muralidharan (2010) revealed that seed yield/plant showed significantly positive correlation with plant height, number of branches/plant, number of capsules/plant, days to 50% flowering, days to maturity and 100 seed weight. Capsule breadth showed significantly negative association with seed yield/plant.

Yol *et al.* (2010) indicated that plant height, number of branches/plant, number of capsules/plant and 1000 seed weight had the significant positive effect on seed yield. The characters related to maturity, days to first flowering and 50% flowering showed negative correlation with seed yield in sesame.

Alake *et al.* (2010a) observed that most characters showed significant positive correlation with grain yield except 1000-seed weight which showed negative correlation with seed yield.

Alake *et al.* (2010b) indicated that sesame seed yield was significantly and positively correlated with number of days to flowering, height of first capsule, capsule weight per plant, and capsule number/plant in thirteen sesame genotypes.

Akbar *et al.* (2011) evaluated the correlation coefficient analysis indicating that plant height, capsules/plant, capsule length and 1000 seed weight had the significant positive effect on seed yield. The characters related to maturity, days to flower initiation and days to 50% flowering showed negative correlation with seed yield.

Goudappagoudra *et al.* (2011) reported that seed yield/plant showed significant positive association with number of capsules, number of seeds, number of branches/plant, plant height and 1000 seed weight. Selection for these characters may be useful in increasing seed yield in sesame.

Vanishree *et al.* (2011) studied the character association and contribution of yield related traits to seed yield in segregating generation (F4 Families) of sesame. The results indicated that days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length and number of seeds per capsule had positive and significant association with seed yield per plant. The magnitude of correlation was the highest in case of number of capsules per plant with seed yield per plant. Number of capsules per plant had the highest positive direct effect followed by equal contribution by number of seeds per capsule and 1000-seed weight. Selection for capsules per plant should improve seed yield in sesame.

Gangadhara *et al.* (2012) studied eleven characters in 81 genotypes of sesame. Seed yield per plant had significant positive association with capsules per plant, capsule length, plant height, days to maturity, branches per plant and seeds per capsule.

Ibrahim and Khidir (2012) revealed highly significant positive genotypic correlations for seed yield/plant with seed yield/ha and for each of them with plant height, number of capsules/plant, number of primary branches/plant, height to first capsule, days to 50% flowering and days to maturity. They also reported that number of capsules/plant, number of

seeds/capsule and 1000-seed weight are the principal yield components, and selection for these traits may be useful in improving seed yield in sesame.

Shekhawat *et al.* (2013) reported that genotypic correlation coefficients were higher than the respective phenotypic correlation coefficients for all the characters. The association analysis revealed that capsules/plant, seeds/capsule, oil content and plant height were the important characters and may be selected to increase the seed yield ability.

Vanishree *et al.* (2013) studied correlation and path coefficient analysis of yield and yield attributing traits in F2 generation of sesame. They found that maximum positive direct effect of capsules per plant on seed yield per plant followed by number of seeds per capsule and 1000-seed weight. Selection for capsules per plant should improve seed yield in sesame.

Ismaila and Usman (2014) revealed that number of branches per plant, number of capsules per plant, days to maturity, capsule length, weight of seeds per capsule and 1000-grain weight shown positive significant correlation with seed yield per hectare.

Abate and Mekbib (2015) studied forty nine sesame genotypes and reported positive significant correlation of characters plant height, number of capsules per plant, number of seeds per capsule and harvest index on seed yield and positive but non-significant correlation exerted by character capsule length on seed yield.

Bharathi *et al.* (2015) reported positive significant correlation of seed yield with characters number of capsules per plant, number of seeds per capsule, test weight and plant height.

Bamrotiya *et al.* (2016) studied correlation and path analysis in forty genotypes of sesame and revealed that number of seeds per capsule

followed by number of branches per plant and number of capsules per plant exhibited high and positive direct effect on seed yield per plant.

Saxena *et al.* (2016) reported positive correlation of characters days to flower initiation, days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, number of capsules per plant, capsule length, seeds per capsule, 1000-seed weight, oil content and harvest index with seed yield whereas plant height negatively correlated with seed yield.

ii) Path analysis

The path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measure of direct and indirect effects. The concept of path coefficient was developed by Wright (1921). Path coefficient analysis is applied for assessment by Dewey and Lu (1959) in crested wheat grass. The literatures available on path analysis in sesame are listed below:

Parimala and Mathur (2006) recorded that the highest direct effect on seed yield was exerted by the number of capsules/plant in sesame.

Sudhakar *et al.* (2007) revealed maximum positive direct effect of capsule on seed yield followed by capsule length and plant height in sixty two sesame genotypes.

Parameshwarappa *et al.* (2009) observed maximum positive direct effect of number of capsules on seed yield followed by capsule length and plant height in sesame.

Kordestani *et al.* (2009) revealed that number of seeds/pod had the highest positive direct effect on plant yield indicating that this trait can be considered as a criterion for improving seed yield in sesame breeding programs.

Muhamman *et al.* (2010) reported that number of branches and plant height showed positive direct association with seed yield/plant. Hence, these two may serve as a basis for selection in sesame crop improvement.

Yol *et al.* (2010) implicated that plant height had the highest positive direct effect on seed yield. This character was followed by days to first flowering, number of capsules and 1000 seed weight. Number of branches and number of capsules per plant had indirect effect over plant height on seed yield.

Alake *et al.* (2010b) revealed that capsule weight per plant had the highest positive direct effect on seed yield relative to other variables.

Aremu *et al.* (2011) evaluated fifteen indigenous sesame genotypes and reported that number of capsules per plant and seed per capsule contributed highest direct effect to seed yield of sesame.

Kurdistani *et al.* (2011) reported that seeds number/capsule had the highest positive direct effect on seed yield and can be considered as a criterion for improving seed yield in breeding programs in sesame.

Goudappagoudra *et al.* (2011) reported that number of capsules /plant, number of seeds/capsule and 1000 seed weight had high and positive direct effect on seed yield. The indirect effect of number of capsules/plant via days to 50% flowering, plant height, number of branches/plant on seed yield was high and positive. Selection for these characters may be useful in increasing seed yield in sesame.

Renuka *et al.* (2011) reported significant positive association of seed yield per plant with number of capsules, number of seeds, number of branches per plant, plant height and 1000-seed weight. The magnitude of correlation was the highest in case of number of capsules per plant. Number of capsules per plant, number of seeds per capsule and 1000-seed weight had high and positive direct effect on seed yield. The indirect effect

of number of capsules per plant *via* days to 50% flowering, plant height, number of branches per plant on seed yield was high and positive. Selection for these characters might be useful in increasing seed yield in sesame.

Vanishree *et al.* (2011) studied the character association and contribution of yield related traits to seed yield in segregating generation (F_4 Families) of sesame. The results indicated that days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length and number of seeds per capsule had positive and significant association with seed yield per plant. The magnitude of correlation was the highest in case of number of capsules per plant with seed yield per plant. Number of capsules per plant had the highest positive direct effect followed by equal contribution by number of seeds per capsule and 1000-seed weight. Selection for capsules per plant should improve seed yield in sesame.

Azeez and Morakinyo (2011) revealed that number of seeds/plant and 1000-seed weight had the highest direct influence on single plant seed yield while the number of pods/plant had the highest indirect effect through the number of seeds/plant.

Ibrahim and Khidir (2012) observed that number of capsules/plant, 1000-seed weight and number of seeds/capsule had the highest positive direct effect on seed yield/plant. Number of primary branches/plant via number of capsules/plant gave the highest positive indirect effect on seed yield/plant in sesame.

Gangadhara *et al.* (2012) 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. Selection for the traits will be useful for the improvement in sesame.

Shekhawat *et al.* (2013) revealed that capsules per plant, seeds per capsule, oil content and plant height were the important characters and may be selected to increase the seed yield ability in sesame.

Vanishree *et al.* (2013) studied correlation and path coefficient analysis of yield and yield attributing traits in F_2 generation of sesame. They found that maximum positive direct effect of capsules per plant on seed yield per plant followed by number of seeds per capsule and 1000-seed weight. Selection for capsules per plant should improve seed yield in sesame.

Abate and Mekbib (2015) revealed positive direct effects on seed yield by characters days to 50% flowering, plant height, number of capsules per plant, 1000-seed weight and 1000-seed weight and negative direct effects on seed yield by number of seeds per capsule, capsule length and days to maturity.

Bharathi *et al.* (2015) revealed positive significant direct effect of characters plant height, number of capsules per plant, number of seeds per capsule and test weight with seed yield.

Bamrotiya *et al.* (2016) reveled positive significant direct effects of characters days to flowering, days to maturity, plant height, height to first capsule, capsule length, number of seeds per capsule and harvest index.

Saxena *et al.* (2016) revealed that number of capsules per plant had maximum direct effect on seed yield per plant followed by number of secondary branches and number of primary branches. Negative direct effects were recorded for days to flower initiation, days to maturity, number of seeds per capsule and harvest index. Other character days to 50 per cent flowering had positive direct effect.

Tripathy *et al.* (2016) observed significant positive direct effects of number of capsule, period of flowering and height to first capsule and positive directs of 500 seed weight and capsule breadth on seed yield.

2.3 Genetic Divergence

Morphological similarity, eco-geographic diversity, phylogenetic relationships *etc.* were the few earlier methods used for discriminating divergent populations, which are reinstated by more scientific and advanced biometrical technique viz., multivariate analysis based on Mahalanobis's D^2 statistic. Estimation of degree of divergence between biological populations and computation of relevant contributions of different components to total divergence is done completely by Mahalanobis's generalized distance estimated by D^2 statistic (Maurya and Singh, 1977). Selection of parents for hybridization programme based on Mahalanobis's D^2 statistic is more reliable method as the requisite knowledge of parents in respect of number of characters is available prior to crossing programme.

Available literature on Mahalanobis D^2 analysis is presented.

Ganesh and Thangavelu (1995) by using Mahalanobis D^2 analysis studied 50sesame genotypes and grouped into four clusters. The clustering pattern indicated that geographic diversity need not necessarily be related to the genetic diversity.

Manivannan and Nadarajan (1996) reported that the plant height was the highest contributor towards the genetic divergence followed by number of primary branches, seed yield and number of capsules per plant.

Swain and Dikshit (1997) by using Mahalanobis D^2 statistics in sesame revealed no linear relationship between geographic and genetic divergence. Seed oil content, 1000 seed weight and days to flowering contributed maximum towards genetic divergence.

Dikshit and Swain (2000) by using Mahalanobis D^2 statistics in sesame revealed no relationship between geographic origin and genetic

divergence. Seed oil content contributed maximum (76.6%) towards the divergence.

Manivannan and Ganeshan (2000) evaluated 67 genotypes and reported that the plant height is highest contributor towards the genetic divergence followed by number of branches and 1000 seed weight.

A study was undertaken by Gupta *et al.* (2001) by using Mahalanobis D^2 analysis for evaluating 50 genotypes of sesame and was grouped into 16 clusters.

Navale *et al.* (2001) evaluated the genetic diversity of 50 germplasm lines of sesame (*Sesamum indicum L.*) including exotic and indigenous lines using multivariate analysis and were grouped into six clusters. Number of seeds per plant, capsule diameter, capsule length contributed considerably to divergence.

Ujjainkar *et al.* (2002) studied 50 genotypes of sesame by using D^2 statistics. Cluster analysis showed the absence of significant relationship between genetic and geographical diversity.

Ashokvardhan Reddy *et al.* (2002) performed multivariate analysis among 44 genotypes of sesame and grouped into nine clusters. No relationship was observed between geographic origin and genetic diversity. Total dry matter production per plant contributed maximum for 43.13 percent of the total divergence.

Solanki and Deepak Gupta (2002) studied 50 genotypes of sesame and grouped into eight clusters. They revealed that grouping of genotypes into different clusters was not related to their geographic origin. Among the eight characters studied for genetic divergence capsules per plant contributed maximum, accounting for 39.02 per cent of total divergence followed by total divergence followed by seed yield per plant (28.65%).

Priti Rodge *et al.* (2003) studied 36 genotypes of sesame and grouped into seven clusters. The clustering pattern indicated that there was no relationship between genetic diversity and geographic diversity.

Forty eight sesame (Sesamum indicum L.) genotypes were evaluated by Solanki and Deepak Gupta (2004) and were grouped into 10 clusters based on their diversity. Seed yield per plant, plant height, number of branches per plant, number of capsules per plant and 1000 seed weight contributed maximum towards genetic divergence.

Ved Narain Gupta and Singh (2004) evaluated 72 genotypes of sesame through D^2 statistics and grouped them into 10 clusters. They reported that capsules per plant followed by days to maturity, 1000 seed weight and seed yield contributed maximum towards divergence in sesame.

Gangadhara Rao (2004) evaluated 72 sesame genotypes and observed that the capsules per plant followed by days to maturity, 1000-seed weight and seed yield contributed maximum towards genetic divergence.

Anuradha and Laxmikantha Reddy (2005) estimated genetic divergence among 71 divergent lines of sesame by using Mahalanobis D^2 technique. They observed that characters viz., days to maturity followed by 1000 seed eight, seeds per capsule and capsule length contributed maximum towards genetic divergence.

Raghuwanshi (2005) studied genetic diversity of 100 genotypes of sesame using D^2 analysis. They revealed that oil content and days to 50 percent flowering contribute maximum towards the divergence followed by 1000 seed weight and seed yield.

Gawali *et al.* (2006) estimated genetic divergence in a set of 50 sesame genotypes using Mahalanobis D^2 statistics and grouped into seven clusters.

Sudhakar *et al.* (2006) evaluated 62 genotypes of sesame by using Mahalanobis D^2statistics. They observed that the number of capsules per plant contributed maximum towards genetic divergence.

Fifty three genotypes of sesame (Sesamum indicum L.) were evaluated and grouped into eight clusters by Gangadhara Rao (2006). It is observed that there is no relationship between geographic origin and genetic diversity. Seed yield per plant contributed maximum towards divergence followed by days to initial flowering and capsules per plant.

An investigation was carried out by Ranjith *et al.* (2008) in 93 sesame (Sesamum indicum L.) genotypes by using Mahalanobis D^2 analysis. The results revealed that the genotypes exhibited wide variation and were grouped into 12 clusters. Cluster analysis indicates clustering pattern did not reflect geographic origin.

Patel *et al.* (2008) assessed 60 genotypes of sesame by Mahalanobis D^2 statistics and grouped into 11 clusters. Branches per plant contributed maximum towards total divergence followed by plant height, seed yield per plant and 1000 seed weight.

Swapna *et al.* (2008) evaluated sixty genotypes of sesame (Sesamum indicum L) by using Mahalanobis D^2 statistics, cluster analysis and principal component analysis. Based on the clustering methods, seven and eight clusters were formed in D^2 statistic and cluster analysis, respectively. Thousand seed weight contributed maximum towards the genetic divergence.

Kumhar and Solanki 2009) studied 82 genotypes of sesamum. The genotypes were groups into eight clusters and seed yield contributed maximum accounting for 38.9 percent of the total divergence.

Gangadhara Rao *et al.* (2011) studied genetic diversity for 76 genotypes of sesame using Mahalanobis D^2 analysis. The genotypes were

grouped into nine clusters and clustering pattern indicates that there was no relationship between geographic origin and genetic divergence.

Kumhar and Solanki (2009) found that presence of genetic diversity in eighty two genotypes of sesame for eight characters using Wards minimum variance method. The genotypes were grouped into eight clusters. The inter-cluster Euclidean distance was maximum between cluster V and VIII. Among the eight characters studied seed yield contributed the most (38.9%) towards the divergence of genotypes.

Murugan *et al.* (2011) assessed the genetic diversity in forty two sesame genotypes for eight characters using Mahalanobis D^2 statistics and grouped them into six clusters. The relative divergence of each cluster from other clusters indicated high order of divergence between cluster II and V followed by I and V. Days to maturity contributed maximum towards the divergence.

Venkatesh *et al.* (2011) conducted an experiment on genetic divergence using D^2 analysis among fifty three sesame genotypes for thirteen characters and grouped into eight clusters. Grouping of genotypes into different clusters was not related to their geographic origin. The maximum inter cluster distance was recorded between cluster II and VIII while; it was least between cluster IV and V.

Gangadhara *et al.* (2012) studied genetic diversity in eighty one sesame genotypes using Mahalanobis D statistics and grouped them into seven for eleven characters using clusters. The study revealed that the D values from 25.05 to 1525.16, indicating significant divergence in the genotypes.

Parameshwarappa *et al.* (2012) studied genetic diversity in one hundred and thirty one genotypes of sesame for six characters using Mahalanobis D^2 statistics. Seed yield, plant height and seeds per capsule were observed to be the major contributors towards the genetic divergence.

Grouping of genotypes into clusters using Tocher's method resulted in formation of eight clusters. Seed yield contributed maximum towards the diversity.

Jadhav et al (2013) studied thirty one germplasm lines of sesame for genetic divergence using Mahalanobis D^2 analysis. Thirty one genotypes were grouped into seven clusters and oil content contributed maximum towards genetic divergence.

Kumhar *et al.* (2013) studied genetic diversity in thirty six genotypes of sesame for ten characters. The genotypes were grouped into seven clusters using Ward's minimum variance method. The inter cluster Euclidean distance was maximum between cluster III and VII and followed by cluster VI and VII and cluster II and VII. Number of primary branches per plant contributed the most towards the divergence of genotypes.

Narayanan and Murugan (2013) evaluated the genetic diversity in sixteen sesame genotypes for eight characters using Mahalanobis D^2 statistics. The genotypes were grouped into 8 clusters. 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.

Shekawat *et al.* (2013) studied the genetic divergence using D^2 analysis in fifty five sesame genotypes and grouped them into fourteen clusters. No relationship between geographic origin and genetic diversity was observed.

Tripathi *et al.* (2013) studied genetic diversity in hundred sesame genotypes for nine characters using Mahalanobis D^2 analysis. The genotypes were grouped into eleven different clusters. Clustering was not associated with the geographical distribution instead accessions were mainly grouped due to their morphological differences.

Chandramohan (2014) studied genetic diversity in two hundred and eighty sesame genotypes for seven characters using Mahalanobis's

D^2 statistic and grouped them into twelve clusters. Among the traits studied capsule per plant and plant height contributed maximum for studying divergence while no contribution from capsule length.

Abate and Mekbib (2015) studied genetic diversity in forty nine sesame genotypes for fourteen quantitative traits using Mahalanobis's D^2 statistic and based on D^2 values, the genotypes were grouped into seven clusters. The clustering pattern suggested the absence of relationship between geographic diversity and genetic diversity. Harvest index, seed yield, biomass yield and plant height had highest contribution towards genetic divergence.

Hemalatha *et al.* (2015) studied genetic diversity in sixty sesame genotypes for ten characters using Mahalanobis D^2 statistics and grouped genotypes into six clusters. Six characters *viz.*, number of capsules per plant, harvest index, number of branches per plant, 1000 seed weight, number of seeds per capsule and plant height together contributed 87.44% towards the divergence in total.

Chapter III

MATERIAL AND METHODS

The experiment was laid out in *kharif* 2016 at Oil seed Research Station, Latur. The Research station is located on the South-East to Latur city at an altitude of 636 m above mean sea level and its geographical bearing is 73° 25' East longitude and 18° 70' North latitude.

3.1 Material

Sixty five diverse genotypes of sesame including four check varieties Swetha, JLT-408, G-1 and Madhuri were included in the present study. The details of genotypes are furnished in Table 3.1.

3.2 Methods

The 65 sesame genotypes were sown on 1st July, 2016 in a Randomized Block Design with two replications. Each genotype in each replication was sown by dibbling the seeds in one row plot of 9.0 m length, adopting a spacing of 45 cm between rows and 10 cm between the hills. Thinning of seedlings was carried out after 10 days of sowing by keeping one seedling per hill. The recommended cultural practices were adopted in respect of irrigation, weeding and fertilization. Plant protection measures were taken up as and when required. The genotypes were harvested as and when they attained physiological maturity.

3.2.1 Data recording

Observations pertaining to 12 characters as detailed below were recorded on five randomly tagged plants in each genotype in each replication. The mean of five plants for all the characters, except days to 50 per cent flowering and maturity was utilized for carrying out statistical analysis. For days to 50 per cent flowering and maturity the data was recorded on plot basis.

Table 3.1 Details of 65 genotypes of sesame.

	Genotype	Source	S.No	Genotype	Source
1	SI-413-A	P.C. Unit, Jabalpur.	34	IC-42200	P.C. Unit, Jabalpur.
2	SI-205-61	P.C. Unit, Jabalpur.	35	IC-23233	P.C. Unit, Jabalpur.
3	SI-199-2-84	P.C. Unit, Jabalpur.	36	NIC-16220	P.C. Unit, Jabalpur.
4	SI-1147	P.C. Unit, Jabalpur.	37	EC-231-2-84	P.C. Unit, Jabalpur.
5	IS-299A	P.C. Unit, Jabalpur.	38	EC-370840	P.C. Unit, Jabalpur.
6	ES-44	P.C. Unit, Jabalpur.	39	EC-209	P.C. Unit, Jabalpur.
7	ES-146-1-84	P.C. Unit, Jabalpur.	40	EC-89111	P.C. Unit, Jabalpur.
8	ES-113-18-84	P.C. Unit, Jabalpur.	41	EC-377015	P.C. Unit, Jabalpur.
9	EC-370936	P.C. Unit, Jabalpur.	42	SI-983	P.C. Unit, Jabalpur.
10	IC-204001	P.C. Unit, Jabalpur.	43	OSC-3209	P.C. Unit, Jabalpur.
11	GM-NIC- 7909	P.C. Unit, Jabalpur.	44	DS-21	P.C. Unit, Jabalpur.
12	GM-NIC- 7913	P.C. Unit, Jabalpur.	45	EC-101396	P.C. Unit, Jabalpur.
13	GM-NIC- 8202	P.C. Unit, Jabalpur.	46	SI-5354	P.C. Unit, Jabalpur.
14	GM-NIC- 8631	P.C. Unit, Jabalpur.	47	IS-424	ORS, Latur.
15	GM-NIC- 8934	P.C. Unit, Jabalpur.	48	SI-3168	ORS, Latur.
16	GM-NIC-16146	P.C. Unit, Jabalpur.	49	KMR-69	ORS, Latur.
17	GM-NIC-16226	P.C. Unit, Jabalpur.	50	KMR-114	ORS, Latur.
18	GM-NIC-16330	P.C. Unit, Jabalpur.	51	GT-3	ORS, Latur.
19	GM-NIC-16332	P.C. Unit, Jabalpur.	52	SI-1003	ORS, Latur.
20	GM-NIC- 8254	P.C. Unit, Jabalpur.	53	YLM-17	ORS, Latur.

21	NIC-7855	P.C. Unit, Jabalpur.	54	EC-303423	ORS, Latur.
22	NIC-7903	P.C. Unit, Jabalpur.	55	PKDS-8	ORS, Latur.
23	NIC-10621	P.C. Unit, Jabalpur.	56	JLT-07	ORS, Latur.
24	NIC-16114	P.C. Unit, Jabalpur.	57	TKG-22	ORS, Latur.
25	NIC-16324	P.C. Unit, Jabalpur.	58	EC-S-0523A	ORS, Latur.
26	NIC-16104	P.C. Unit, Jabalpur.	59	EC-S-0223	ORS, Latur.
27	NIC-8263	P.C. Unit, Jabalpur.	60	TKG-306	ORS, Latur.
28	EC-310439	P.C. Unit, Jabalpur.	61	IS-207	ORS, Latur.
29	ES-42-2-84	P.C. Unit, Jabalpur.	62	JLT-408	ORS, Latur.
30	K-5170	P.C. Unit, Jabalpur.	63	MADURI	ORS, Latur.
31	UKNM-1067	P.C. Unit, Jabalpur.	64	G-1	ORS, Latur.
32	UKNM-2386	P.C. Unit, Jabalpur.	65	SWETA	Local selection from Telangana
33	IC-41962	P.C. Unit, Jabalpur.			

3.2.1.1 Number of days to fifty per cent flowering

Number of days taken from sowing to the attainment of 50 per cent flowering of plants in each plot and in each replication was recorded.

3.2.1.2 Number of days to maturity

Yellowing of capsules and withering of bottom leaves on the plant was taken as the index of physiological maturity. The number of days to maturity of each genotype was calculated from date of sowing to physiological maturity of about 50 per cent of plants in each entry.

3.2.1.3 Number of primary branches per plant

The number of branches that arose from main stem and were bearing capsules for each plant were counted.

3.2.1.4 Plant height (cm)

Plant height was measured with meter scale from the cotyledonary node up to the tip of plant at the time of maturity.

3.2.1.5 Number of capsules per plant

The capsules that were present on the main stem, primary branches and secondary branches of a plant were taken and recorded as the total number of capsules per plant.

3.2.1.6 Number of seeds per capsule

Three capsules were randomly selected from each of the five sampled plants and the number of seeds per capsule were counted and the mean number of seeds per capsule were recorded.

3.2.1.7 Capsule length (cm)

Five capsules were randomly selected from each plant at harvest and the length of capsules from base to tip was measured in centimeters with Vernier Callipers and the mean length of capsule was recorded.

3.2.1.8 Capsule width (cm)

Five capsules were randomly selected from each plant at harvest and the distance across the widest point of same capsule used for length was measured in centimeters with Vernier Callipers and mean length of capsule was recorded.

3.2.1.9 1000-seed weight (g)

The weight of one thousand randomly selected seeds from each plant was recorded in grams with the help of Electronic top pan balance (precision of 0.001 g).

3.2.1.10 Seed yield per plant (g)

Weight of seeds obtained from each individual plant was recorded, in grams with the help of Electronic top pan balance (precision of 0.001 g).

3.2.2.11 Oil content (%)

Oil content was recorded with NMR spectrometer at Oilseed Research Station, Akola.

3.2.2.12Phyllody Count.

The Plants affected by Phyllody were noticed and noted in each replication

3.3 STATISTICAL ANALYSIS

The data for all the characters was analysed using Indostat Services, Hyderabad.

3.3.1 Analysis of variance (ANOVA)

Differences among 59 genotypes for different characters were tested for significance by using Analysis of Variance technique on the basis of model proposed by Panse and Sukhatme (1978).

$Y_{ij} = \mu + g_i + r_j + e_{ij}$

Y_{ij} = Phenotypic observation in 'i^{th}' genotype and 'j^{th}' replication μ = General mean

g_i = True effect of 'i^{th}' genotype

r_j = True effect of 'j^{th}' replication

e_{ij} = Random error associated with 'i^{th}', genotype and 'j^{th}', replication.

The analysis of variance for each character was carried out as indicated

Source of Variation	Df	MS	F-ratio
Replications	(r-1)	Mr	*Mr/Me*
Treatments	(t-1)	Mt	*Mt/Me*
Error	(r-1) (t-1)	Me	
Total	(rt-1)		

Where r = number of replications

t = number of treatments (genotypes)

Mr, Mt and Me stand for mean squares due to replications, treatments and error, respectively. The significance was carried out as per Fisher and Yates (1967).

3.3.2 Genetic diversity

The genetic diversity in 59 genotypes for 10 characters was estimated using Mahalanobis's (1936) D^2 statistic technique.

The D^2 value between 'i^{th}' and 'j^{th}' genotypes for 'p' characters were calculated as

$$D^2ij = \sum_{t=1}^{P} (Y_{it} - Y_{jt})$$

Where

Y_{it} = Uncorrelated mean value of 'i^{th}' genotype for't' characters.

Y_{jt} = Uncorrelated mean value of 'j^{th}' genotype for't' characters and

D^2_{ij} = D^2 between' i^{th}' and 'j^{th}' genotypes.

The steps involved are

3.3.2.1 Test of Significance

Variances were calculated for all 10 characters investigated and test of significance was carried. Analysis of Covariance (ANCOVA) for the character pairs was estimated on the basis of mean values. From these estimates, a dispersion table was prepared. After testing the differences between genotypes for each of the characters, a simultaneous test of significance of differences between the mean values of a number of correlated variables was done, by using 'V' statistic, which in turn utilizes Wilk's Criterion (Rao, 1952).

Wilk's Criterion 'A' = $| E | / | E + V |$

$| E |$ = Determinant of error matrix and

$| E + V |$ = Determinant of (genotypes + error) sum of squares and sum of product matrix.

Then the value of 'V' statistic was worked out using Wilk's Lambda Criterion.

$$'V'_{(stat)} = -m\ 11\&\ 'A'$$

Where,

$m=n-(p+q+1)/2$

p = number of characters

q = number of genotypes-1 (or df for genotypes)

n = degrees of freedom for error + genotypes and

e = 2.7183

'V' (stat) is distributed as X^2 with pq degrees of freedom.

3.3.2.2 Transformation of correlation variables

In the present model, computation of D^2 values was reduced to simple summation of differences in mean values of various characters of two genotypes i.e.

Σd^2_i, therefore, transformation of correlated variables into standardized uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

3.3.2.3 Computation of D^2 values

For five combinations of 'i' and 'j' genotypes, the mean deviation *i.e.*, $Y_{it} - Y_{jt}$ for t = 1, 2.... p variables are computed and the D^2 values were calculated as sum of deviations.

$$\text{i.e., } = \sum_{t=1}^{P} (y_{it} - y_{jt})^2$$

3.3.2.4 Testing and 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 was tested against tabulated value of X^2 for 'p' degrees of freedom where 'p' is the number of variables (or) characters considered.

3.3.2.5 Contribution of individual characters towards divergence

In all the combinations, each character was ranked on the basis of their contribution towards divergence between two entries $d_j = (Y_{it} - Y_{jt})$. Rank '1' was given to the highest mean difference and rank 'p' to the lowest mean difference, where 'p' is the total number of characters considered. Percentage contribution of each character towards the divergence was calculated by using the formula.

$$X = \frac{N}{M} \times 100$$

Where

X = Per cent contribution of character

N = Number of genotype combinations where the character was ranked first

M = All possible combinations of the genotypes concerned

3.3.2.6 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done by using Tocher's method as described by Rao (1952). The criterion used in clustering by this method was that any two genotypes belonging to same cluster should at least on an average show an average of smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose D^2 value of all the combinations in each genotype was arranged in the increasing order of their magnitude in the tabular form as described by Singh and Chaudhary (1977). To start with, the two genotypes having the smallest distance from each other were considered first to which a third population having smallest average D^2 value from the first two genotypes was added. Then comes the nearest fourth genotype and so it goes on. At certain stage when it was felt that after adding a particular variety, there was an abrupt increase in the average D^2 value, then that variety was not considered for inclusion in that cluster. Similarly, a second cluster was formed. Then the process was continued till all the genotypes were included in one or other cluster.

3.3.2.7 Inter and intracluster distance

3.3.2.7.1 Average intracluster distance

For the measure of intracluster distance, the formula used was ΣD^2_i /n whereΣD^2_i was the sum of distances between all possible combinations (n) of the genotypes included in a cluster.

3.3.2.7.2 Average intercluster distance

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

3.3.2 Variance

The genotypic and phenotypic variances were calculated as per the formulae given by Burton and Devane (1953).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{Mean sum of squares due to treatments} - \text{Mean sum of squares due to error}}{\text{Number of replications}}$$

Phenotypic variance $(\sigma^2 p) = \sigma^2 p + \sigma^2 e$

$\sigma^2 e$ = Error variance

3.3.4.1 Genotypic and phenotypic coefficients of variation

The genotypic (GCV) and phenotypic (PCV) coefficients of variation were calculated as per the formulae given by Burton (1952).

$GCV = \sigma_g / X \times 100$

$PCV = \sigma_p / X \times 100$

Where σ_g and σ_p are genotypic and phenotypic standard deviations, respectively. X is grand mean.

3.3.4.2 Heritability (Broad Sense)

Heritability in broad sense was estimated by using the formula given by Allard (1960).

Broad sense heritability $(h^2_{bs}) = \sigma^2_g / \sigma^2_p \times 100$

Where

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.3.4.3 Genetic advance (GA)

It was calculated as per the formula proposed by Burton (1952).

$$GA = (K)\ (\sigma^2_p)\ (h^2_{bs})$$

Where

GA = Expected genetic advance under selection

K = Selection differential (2.06) at 5 per cent intensity of selection

σ_p = Phenotypic standard deviation

h^2bs = Heritability coefficient

3.3.4.4 Genetic advance as per cent of mean (GA as % of mean)

Genetic advance as per cent of mean was calculated as per the formula.

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

GA = Genetic advance

X = Grand mean of the character

3.3.5 Character Association

The correlation coefficients were calculated to determine the degree of association of the yield components with seed yield and also among themselves.

Phenotypic and genotypic correlation coefficients were compared against 'r' values given in Fisher and Yates (1967) tables for (n-2) degrees of freedom at probability level of 0.05 and 0.01 to test their significance.

3.3.5.1 Phenotypic correlation coefficients

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

Where

r_p (xy) = Phenotypic correlation between 'x' and 'y'

Cov_p (xy) = Phenotypic covariance between character 'x' and 'y'

σ^2 p(x) = Phenotypic variance of 'x'

σ^2 p(y) = Phenotypic variance of 'y'

3.3.5.2 Genotypic correlation coefficients

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

Where,

r_g (xy) = Genotypic correlation between 'x' and 'y'

Cov_g (xy) = Genotypic covariance between character 'x' and 'y'

σ^2 g(x) = Genotypic variance of 'x'

σ^2 g(y) = Genotypic variance of 'y'

3.3.6 Path coefficient analysis

Path coefficient analysis was carried out by using the phenotypic and genotypic correlation coefficients, to know the direct and indirect effects of the yield components on yield as suggested by Wright (1921) and as illustrated by Dewey and Lu (1959).

The path coefficients were obtained by solving the 'P' normal equations following the matrix method given by Singh and Chaudhary (1977).

Correlations among all the variables were utilized to set up the simultaneous equations.

$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots\ldots\ldots + r_1 Y_1 P_{iy}$

$r_{2y} = r_{21}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots\ldots\ldots + r_2 Y_1 P_{iy}$

:
:
:

$r_{iy} = r_{i1}P_{1y} + ri_2P_{2y} + r_{i3}P_{3y} + \ldots\ldots\ldots + P_{iy}$

Where,

r_{1y} to r_{iy} = Coefficients of correlation between causal factors 1 to 'i' and dependent character '1'.

r_{12} to r_{i-1} = Coefficients of correlation among causal factors.

P_{1y} to p_{iy} = Direct effects of characters '1' to 'i' on character 'y'.

The above equations were written in matrix form as under

$$A \quad \begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ \vdots \\ r_{iy} \end{pmatrix} \qquad C \quad \begin{pmatrix} 1 & r_{12} & r_{13} & \cdots\cdots & r_{1i} \\ r_{21} & 1 & r_{23} & \cdots\cdots & r_{2i} \\ r_{31} & 1 & 1 & \cdots\cdots & r_{3i} \\ \vdots & \vdots & \vdots & & \vdots \\ r_{i1} & r_{i2} & r_{i3} & \cdots\cdots & 1 \end{pmatrix} \qquad B \quad \begin{pmatrix} p_{1y} \\ p_{2y} \\ p_{3y} \\ \vdots \\ p_{iy} \end{pmatrix}$$

Then $B = [C]^{-1} A$

Where,

$$[C]^{-1} \begin{pmatrix} C_{11} & C_{12} & C_{13} & \cdots\cdots & C_{1i} \\ C_{21} & C_{22} & C_{23} & \cdots\cdots & C_{2i} \\ \vdots & \vdots & \vdots & & \vdots \\ C_{i1} & C_{i2} & C_{i3} & \cdots\cdots & C_{ii} \end{pmatrix}$$

Then, direct effects were calculated as follows:

$$P_{1y} = \sum_{i=1}^{I} C_{1i}\, r_{1y}$$

$$P_{2y} = \sum_{i=1}^{I} C_{2i}\, r_{2y}$$

$$P_{iy} = \sum_{i=1}^{I} C_{ij}\, r_{iy}$$

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

Residual effect (PR_y) = $[1 – (Pr_{1y} + P_{2y}\, r_{2y} + \ldots\ldots + P_{iy}\, r_{iy})]^{½}$

Where

PR_y = Residual effect

P_{iy} = Direct effect of 'x_i' on 'y'

r_{iy} = Correlation coefficient of 'xi' and 'y'.

Chapter IV

RESULTS

The present investigation entitled “Studies on genetic diversity, path analysis and correlation in sesame (*Sesamum indicum* L.) was conducted to evaluate sixty five genotypes of sesame using eleven yield and yield contributing traits in order to reveal the amount of variability, genetic diversity present in the experimental material and also to know the correlation between yield and its contributing traits. The experimental findings obtained from the present study are furnished under the following heads and the available information on various aspects of the investigation has been discussed subsequently.

4.1 Analysis of variance

4.2 Mean performance of genotypes

4.3 Genetic Variability, Heritability and Genetic Advance

4.4 Genetic divergence

4.5 Character association

4.6 Path Coefficient Analysis

4.1 ANALYSIS OF VARIANCE

The numerical data collected on quantitative characters were statistically analyzed and the Analysis of Variance (Table 4.1) showed highly significant differences among the genotypes under study for all the eleven traits *viz.*, days to 50 % flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, capsule length (cm), capsule width (cm), number of seeds per capsule, 1000- seed weight (g), oil content (%) and seed yield per plant (g), indicating the presence of considerable genetic variability among the experimental material under study.

4.2 MEAN PERFORMANCE OF GENOTYPES

Presence of adequate genetic variability and critical analysis of genetic variability are needed for initiating any crop improvement programme and for adopting appropriate selection techniques. Greater variability in the initial breeding material ensures better chances of producing a desired genotype.

Table 4.1: Analysis of variance for eleven characters in 65 genotypes of sesame.

S. No.	Character	Mean sum of squares		
		Replications (df=1)	Treatments (df=64)	Error (df=64)
1	Days to 50% flowering	0.0076	26.59**	1.91
2	Days to maturity	3.392	51.42**	1.31
3	Capsule length (cm)	0.018	0.069**	0.0027
4	Capsule width (cm)	0.0015	0.0056**	0.00099
5	Plant height (cm)	13.33	242.24**	20.61
6	No. of branches per plant	0.135	0.974**	0.046
7	No. of capsules per plant	29.38	330.97**	20.86
8	No. of seeds per capsule	86.75**	210.75**	11.61
9	Seed yield (g)/ plant	0.603	27.26**	0.91
10	1000 seed weight (g)	0.0028	0.215**	0.0062
11	Oil content (%)	9.81	15.09**	0.572

4.2.1 Mean Performance

The mean performance of sixty five genotypes for seed yield and its components is presented in Table 4.2.The details of the results obtained in this regard are furnished below.

4.2.1.1 Days to 50 per cent flowering

For days to 50% flowering, a lower mean value is desirable. This character exhibited a range from 32 to 48 days with a general mean of 37.5 days. Among all the genotypes, SI-3168 was earliest (32 days), while Sweta (48 days) was late. Earliness was recorded in many genotypes when compared to the checks. Some of them are *Viz.*, SI-205-61SI-199-2-84, NIC-16220, EC-231-2-84, SI-983, DS-21, GM-NIC- 7913, GM-NIC- 8934, GM-NIC- 16146, GM-NIC-16332, SI-1003, GM-NIC- 8254, TKG-22, NIC-16324, TKG-306, EC-310439 and UKNM-2386 ranging from 33 to 37 days.

4.2.1.2 Days to maturity

Lower mean value is desirable for days to maturity. The average number of days taken for maturity varies from 73 days (SI-205-61) to 94 days (Swetha) with a general mean of 83 days. Early maturity was recorded in almost all genotypes when compared to the check Sweta. The genotypes SI-3168, SI-103, EC-310439, IS-424, EC-89111 and GM-NIC-8934 recorded quite early maturity (74 to 76 days).

4.2.1.3 Plant height (cm)

Plant height exhibited wide variability ranging from 62 cm to 126 cm with a general mean of 95.6 cm. GT-3 was the shortest; While Sweta was the tallest among the genotypes under study. All the genotypes recorded less plant height than the checks Swetha (126 cm). Genotypes EC-310439, DS-21, PKDS-8, TKG-306, EC-370840, NIC-16220, SI -

5354, and NIC-16104 exhibited higher plant height ranging 117 cm to 101 cm.

4.2.1.4 Number of branches per plant

The mean value of genotypes for this trait were ranged from 1.60 to 4.90 with a general mean of 3.57. G-1(1.60) had lower number of branches per plant, many genotypes shown higher number branches of plant when compared to checks JLT-408 (2.90), Maduri (2.20) and Sweta (3.70). Whil e EC-S-05233A (4.90) recorded the maximum number of branches per plant, the genotypes *viz.*, GM-NIC-16330 (4.73), GM-NIC-8254 (4.73), SI-5354 (4.70), JLT-07 (4.65) and PKDS-8 (4.60) recorded higher branches th an checks

4.2.1.5 Number of capsules per plant

The trait number of capsules per plant was found to be lowest in GT-3 (26) and the highest in check variety JLT-408 (85) with a general mean of 48.4 capsules per plant. The other check varieties recorded as follows Maduri (75), G-1 (44) and Sweta (63). The genotypes *viz.*, SI-199-2-84 (70), EC-370936 (71), JLT-07 (67), EC-209 (67), recorded more number of capsules per plant when compared the checks Swetha (63) and G-1(44).

4.2.1.6 Capsule length (cm)

The trait capsule length was found to be lowest in GM-NIC-8202 (2.03 cm) and the highest in check variety SI-983 (2.77 cm) with a general mean of 2.44 cm. The check varieties recorded as follows JLT-408 (2.67 cm), Maduri (2.66 cm), G-1 (2.53 cm) and Sweta (2.57 cm). The genotypes *viz.*, EC-101396 (2.75 cm), GT-3 (2.71 cm), EC-310439 (2.70 cm) and UKNM-1067 (2.67 cm) recorded more capsule length when compared the checks JLT-408 (2.67 cm) and Maduri (2.66 cm).

Table 4. 2 : Mean performance of 65 genotypes of sesame for yield and yield contributing characters.

S. No	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/ plant	No. of capsules/ plant	Capsule length (cm)	Capsule width (cm)	No. of Seeds/ capsule	1000 seed weight (g)	Oil content (%)	Seed yield/ plant (g)
1.	SI-413-A	35	85	107	3.8	41	2.37	0.63	74	2.68	44.3	8.3
2.	SI-205-61	34	**73**	91	3.9	43	2.26	0.54	60	2.75	44.3	7.1
3.	SI-199-2-84	33	80	104	3.9	70	2.30	0.62	65	2.61	43.6	11.8
4.	SI-1147	39	83	92	3.7	46	2.43	0.65	67	2.90	42.3	9.1
5.	IS-299A	41	88	105	4.2	51	2.60	0.67	73	2.96	43.7	10.9
6.	ES-44	35	77	101	4.4	61	2.48	0.67	65	2.91	43.5	11.5
7.	ES-146-1-84	39	83	102	4.5	53	2.49	0.63	72	3.18	45.2	12.0
8.	ES-113-18-84	40	83	91	3.9	45	2.46	0.69	84	2.81	43.3	10.7
9.	EC-370936	34	77	81	4.3	71	2.34	0.59	62	2.56	40.7	11.1
10.	IC-204001	43	85	89	2.4	37	2.38	0.71	72	2.49	46.8	6.7
11.	GM-NIC- 7909	40	82	91	2.4	44	2.48	0.59	64	2.43	41.2	6.9
12.	GM-NIC- 7913	34	79	87	3.6	46	2.29	0.64	61	2.70	42.2	7.4
13.	GM-NIC- 8202	38	80	92	3.6	42	**2.03**	0.64	58	2.8	43.1	6.6
14.	GM-NIC- 8631	39	90	86	2.6	46	2.61	0.68	94	3	44.2	12
15.	GM-NIC- 8934	35	76	74	3	44	2.27	0.57	58	2.30	42.5	5.9
16.	GM-NIC- 16146	35	83	95	3.9	38	2.59	0.63	66	2.65	43.1	6.5
17.	GM-NIC- 16226	38	83	98	3.9	59	2.09	0.57	62	2.63	40.7	9.5
18.	GM-NIC- 16330	41	87	99	4.7	49	2.19	0.60	60	2.82	43.7	8.3
19.	GM-NIC- 16332	34	77	98	3.5	39	2.51	**0.46**	70	2.62	43.4	7.1
20.	GM-NIC- 8254	37	84	99	4.7	69	2.30	0.62	69	2.61	41.3	12.5
21.	NIC-7855	39	76	86	3.2	30	2.62	0.66	**102**	2.85	42.8	8.7
22.	NIC-7903	35	82	92	3.8	41	2.26	0.65	63	2.93	43.2	7.5
23.	NIC-10621	37	84	107	4.1	60	2.35	0.63	65	2.46	43.3	9.6
24.	NIC-16114	40	84	105	2.7	52	2.48	0.57	68	2.46	39.7	8.6
25.	NIC-16324	36	77	86	3.1	59	2.58	0.62	76	2.60	43.7	11.6
26.	NIC-16104	38	88	102	3.4	52	2.09	0.77	68	2.40	44.3	8.5

27.	NIC-8263	40	88	91	3.5	48	2.30	0.62	67	2.48	41.4	7.9
28.	EC-310439	36	76	117	3.1	56	2.70	0.73	87	2.89	39.9	14.1
29.	ES-42-2-84	38	86	90	3.3	49	2.53	0.70	75	2.33	41.7	8.6
30.	K-5170	35	82	101	4	48	2.48	0.65	71	2.77	41.4	9.3
31.	UKNM-1067	35	87	83	3.5	52	2.67	0.68	72	3.64	42.9	13.7
32.	UKNM-2386	34	79	95	3	59	2.38	0.69	81	3.07	40.4	14.8
33.	IC-41962	45	90	92	3.8	33	2.58	0.70	68	2.74	43.2	6.1
34.	IC-42200	40	79	95	2.7	58	2.08	0.68	66	2.75	43.1	10.5
35.	IC-23233	39	88	98	3.6	35	2.49	0.65	88	2.68	43.1	8.2
36.	NIC-16220	36	84	110	3.8	48	2.60	0.63	76	2.31	41.6	8.3
37.	EC-231-2-84	34	82	95	2.8	41	2.13	0.57	77	2.68	42.1	8.5
38.	EC-370840	42	88	107	3.7	35	2.62	0.69	82	2.10	42.3	6
39.	EC-209	44	87	110	4.1	67	2.51	0.65	73	2.60	41.8	12.6
40.	EC-89111	36	77	96	3.5	55	2.40	0.68	67	2.65	42.1	9.8
41.	EC-377015	36	92	99	4.0	34	2.49	0.72	85	2.79	44.5	8.1
42.	SI-983	34	83	96	3.7	49	2.77	0.69	70	2.28	42.4	7.9
43.	OSC-3209	37	89	100	3.3	30	2.65	0.68	71	2.40	41.9	5.1
44.	DS-21	34	80	115	4.4	57	2.49	0.63	61	2.19	38.3	7.5
45.	EC-101396	44	89	93	3.7	58	2.75	0.63	81	2.34	40.8	11.1
46.	SI-5354	40	91	107	4.7	28	2.60	0.66	86	2.47	42.6	6.1
47.	IS-424	35	75	89	4.2	32	2.28	0.67	64	2.32	**36.4**	4.7
48.	SI-3168	32	75	86	3.4	47	2.07	0.69	69	2.47	37.9	8
49.	KMR-69	37	86	77	2.2	30	2.48	0.67	57	2.38	40.6	**4.04**
50.	KMR-114	37	84	83	2.5	26	2.53	0.60	67	2.52	39.7	4.3
51.	GT-3	36	80	**62**	2.6	**26**	2.71	**0.78**	100	2.85	41.4	7.3
52.	SI-1003	34	76	81	3.9	37	2.56	0.74	72	2.25	38.0	6
53.	YLM-17	33	86	92	3.4	39	2.15	0.62	61	3.00	41.8	7.1
54.	EC-303423	46	95	104	3.2	36	2.70	0.62	74	2.77	38.0	7.4
55.	PKDS-8	36	78	112	4.6	51	2.34	0.67	58	2.40	42.2	7.1
56.	JLT-07	34	81	99	4.7	67	2.53	0.65	65	2.70	47.4	11.8
57.	TKG-22	34	84	100	3.8	51	2.54	0.67	77	2.71	42.9	10.7

58.	EC-S-0523A	41	87	105	**4.9**	71	2.32	0.63	69	2.67	44.9	12.9
59.	EC-S-0223	38	82	97	3.7	51	2.19	0.65	73	2.66	46.7	9.9
60.	TKG-306	33	86	107	3.8	41	2.51	0.61	71	3.53	48.1	10
61.	IS-207	44	89	86	3.6	49	2.26	0.56	59	2.12	37.2	5.9
62.	JLT-408	39	79	89	2.9	**85**	2.67	0.63	81	**3.78**	**49.3**	**26**
63.	MADURI	33	74	94	2.2	75	2.66	0.67	93	3.03	48.1	21.2
64.	G-1	44	82	76	**1.6**	44	2.53	0.63	73	2.90	49.1	9.2
65.	SWETA	**48**	**94**	**126**	3.7	63	2.57	0.69	84	3.25	48.8	17.0
	Mean	**37.5**	**83**	**95.6**	**3.57**	**48.45**	**2.44**	**0.65**	**72**	**2.69**	**42.7**	**9.4**
	SEm ±	**0.97**	**0.81**	**3.21**	**0.15**	**3.23**	**0.10**	**0.063**	**2.41**	**0.05**	**0.53**	**0.67**
	CD at 5%	**2.76**	**2.99**	**9.06**	**0.43**	**9.12**	**0.13**	**0.083**	**6.80**	**0.15**	**1.51**	**1.91**
	CV%	**3.71**	**1.38**	**4.74**	**6.04**	**9.44**	**2.15**	**4.87**	**4.75**	**2.95**	**1.77**	**10.19**

4.2.1.7 Capsule width (cm)

The trait number of capsule width did not show much variation. It is found lowest inGM-NIC-16332 (0.46 cm) and highest in GT-3 (0.78 cm) with a general mean of 0.65 cm. The check varieties recorded as follows JLT-408 (0.635 cm), Maduri (0.67 cm), G-1 (0.63 cm) and Sweta (0.69 cm). The genotypes *viz.*, NIC-16104 (0.77 cm), SI-103 (0.74 cm), EC-310439 (0.73 cm), EC-377015 (0.71 cm), IC-204001 (0.70 cm), and IC-41962 (0.70 cm) recorded more number of capsules per plant when compared the check Swetha (0.69 cm) and Maduri (0.67 cm).

4.2.1.8 Number of seeds per capsule

The trait number of seeds per capsule was found to be lowest in KMR-69 (57) and highest in NIC-7855 (102) with a general mean of 72 seeds per capsule. The other check varieties recorded as follows JLT-408 (81), Maduri (93), G-1 (73) and Sweta (84). The genotype GT-3 (100), recorded more number of seeds per capsule when compared the check variety Maduri (93).

4.2.1.9 1000- Seed weight (g)

The mean values for this trait ranged from (2.09 g) to (3.78 g) with a general mean of 2.69 g. The genotype JLT-408 recorded the highest and was superior to all the other genotypes, whereas EC-370840 recorded the lowest. All genotypes recorded less compared to the check JLT-408 (3.78g). However UKNM-1067 (3.64 g), TKG-306 (3.52 g), exhibited more seed weight when compared to the Sweta (3.25 g).

4.2.1.10 Seed yield per plant (g)

Seed yield per plant ranged from 4.04 g (KMR-69) to 25.97 g (JLT-408) with a general mean of 9.40 g. No genotype outnumbered checks JLT-408 (25.9 g) and Maduri (21.16 g) and Sweta (17 g).

4.2.1.11 Oil content (%)

The mean values for this trait were ranged from 36.37 (IS-424) to 49.31 (JLT-408) with a general mean of 42.7%. No genotype recorded with more percentage of oil content when compared to checks JLT-408 (49.31%), Maduri (48.10%), G-1 (49.06%) and Sweta (48.75%).

4.2.1.12 Phyllody incidence

The Phyllody disease incidence in present sesame genotypes was not up to the level, only viz., GM-NIC-7913, NIC-16220 and JLT-07 recorded disease incidence only in first replication. Henceforth this character was not included further in present study.

Table 4. 3: Mean, range, variability, heritability (broad sense), genetic advance and genetic advance as per cent mean for eleven characters in 65 sesame genotypes.

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			
Days to 50% flowering	37.2	32	48	9.43	10.14	0.86	6.73	18.08
Days to maturity	82.7	73	94	6.04	6.2	0.95	10.05	12.14
Plant height (cm)	95.8	74	126	11.01	11.9	0.84	19.91	20.83
Number of branches/ plant	3.56	1.6	4.9	19.09	20.02	0.90	1.338	37.49
Number of capsules/ plant	48.3	25.5	85.25	25.75	27.43	0.88	24.08	27.11
Capsule length (cm)	2.44	2.02	2.76	7.49	7.80	0.92	0.36	14.84
Capsule width (cm)	0.64	0.46	0.78	7.45	8.90	0.70	0.08	12.85
Number of seeds/capsule	71.7	58	101.8	13.9	14.69	0.89	24.08	49.81
1000 seed weight (g)	9.4	2.09	3.78	12.06	12.42	0.94	0.64	24.14
Oil content (%)	42.7	36.3	49.3	6.31	6.55	0.92	5.34	12.51
Seed yield/plant (g)	2.68	4.04	26	38.60	39.92	0.93	7.22	76.88

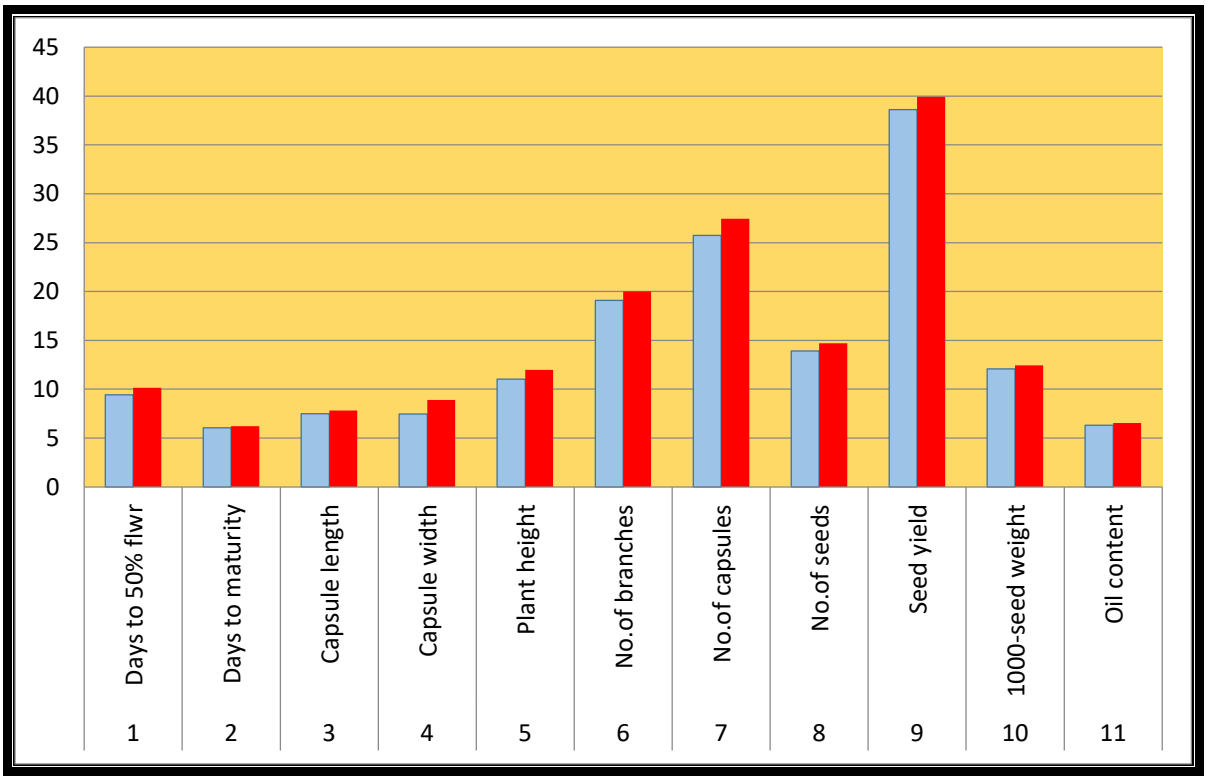

Figure: 4. 1 Graphic representation of phenotypic and genotypic coefficients of variation for various characters in 65 sesame genotypes.

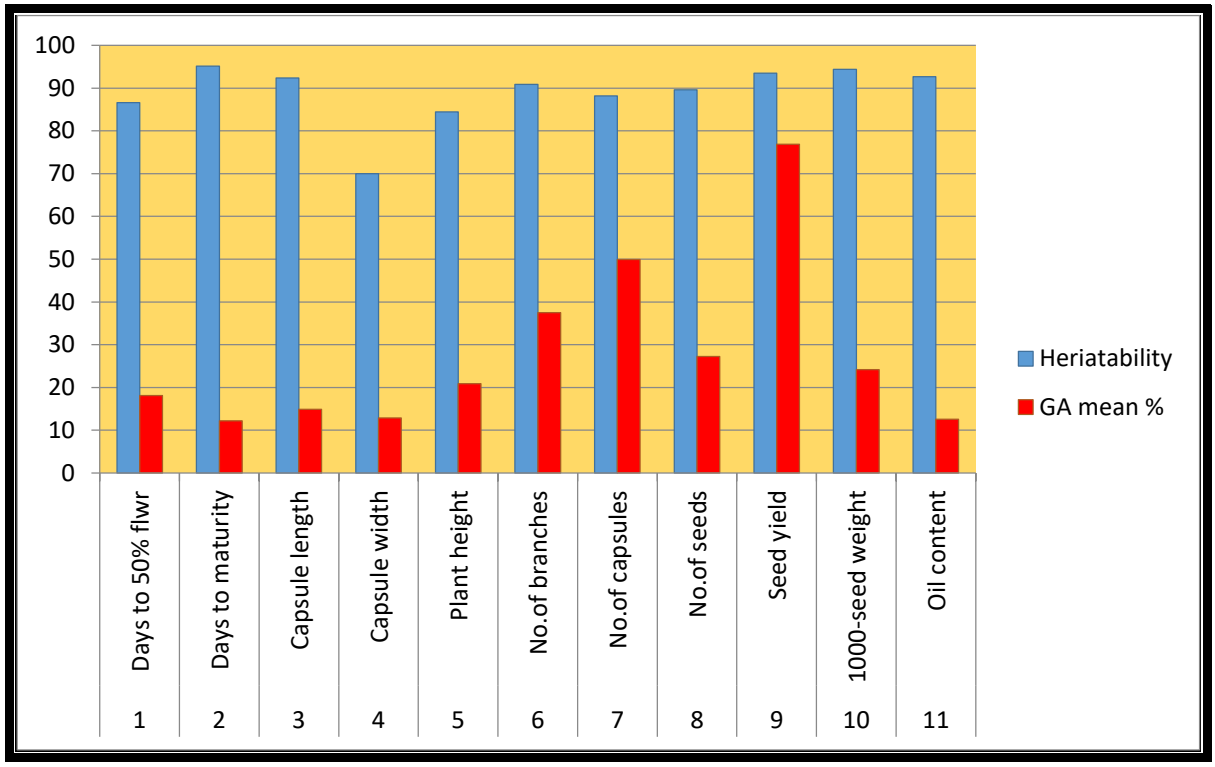

Figure 4.2 Graphic representation of heritability and Genetic advance as mean% of various characters of 65 sesame genotypes.

4.3 Genetic variability, heritability and genetic advance

The genotypic and phenotypic coefficients of variation, heritability and genetic advance and genetic advance as per cent of mean were estimated for sixty five genotypes and results are furnished in Table 4.3 and Fig 4.1and Fig 4.2.

4.3.1 Days to 50 per cent flowering

Low genotypic and phenotypic coefficients of variation were recorded for days to 50 per cent flowering i.e., 9.43 % and 10.14 %, respectively, indicating that there is narrow range of variability and high influence of environment in the expression of this character with little scope for selection.

The heritability observed for the trait was high (86.6%) with low genetic advance as per cent of mean (18.08 %) which is indicating that simple selection would be effective for this trait improvement.

4.3.2 Days to maturity

The trait, days to maturity exhibited low values for genotypic and phenotypic coefficients of variation i.e., 6.04 % and 6.20 %, respectively.

High heritability (95%) and low genetic advance as percent of mean (12.14 %) was observed for this trait. This indicates the presence of non additive gene action and hence selection would be ineffective.

4.3.2 Plant height (cm)

The genotypic and phenotypic coefficients of variation estimates observed for the trait were moderate i.e., 11.01% and 11.99 %, respectively, indicating that there is a scope for improvement this trait.

High heritability (84.3 %) and genetic advance as per cent of mean (20.83 %) were recorded for plant height which is indicating that, there is preponderance of additive gene action in controlling this trait. Hence, direct selection of the characters would be effective in improving the seed yield.

4.3.4 Number of branches per plant

Moderate genotypic and phenotypic coefficients of variation were observed for this trait i.e., 19.09 % and 20.02 %, respectively, suggesting wide spectrum of genotypic variation for this trait. The heritability estimates for this character was high (90.9%) with moderate genetic advance as per cent of mean (20.80%) indicating the presence of moderate genetic variability and preponderance of non-additive gene action. Hence for this trait selection is inefficient.

4.3.5 Number of capsules per plant

The trait, number of capsules per plant exhibited high values for genotypic and phenotypic coefficients of variation i.e., 25.75 % and 27.43 %, respectively. High heritability (88.1%) and high genetic advance as per cent of mean (49.81 %) indicating the predominance of additive gene effect, easily fixable and can be taken as unit character for effective selection.

4.3.6 Capsule length (cm)

The genotypic and phenotypic coefficients of variation estimates observed for this trait were low i.e., 7.49 % and 7.80 %, respectively. The heritability observed for this character was high (92.3 %) with moderate genetic advance as per cent of mean (14.84 %). Hence, there is a good scope of improvement for this trait through simple selection.

4.3.7 Capsule width

Low genotypic and phenotypic coefficients of variation were recorded for number of capsule width i.e., 6.04 % and 6.20 %, respectively.

High heritability (95.0%) and high genetic advance as per cent of mean (12.85%) observed for this trait. indicating the presence of non-additive gene action hence selection for this trait is ineffective.

4.3.8 Number of seeds per capsule

Moderate genotypic and phenotypic coefficients of variation were recorded for number of seeds per capsule i.e., 13.90 % and 14.69 %, respectively. High heritability (93.50%) and high genetic advance as per

cent of mean (76.88%) indicating that simple selection would be effective for this trait improvement.

4.3.9 1000- Seed weight (g)

The trait, 1000 seedweight exhibited moderate genotypic and phenoty pic coefficients of variation i.e., 12.06 % and 12.42 %, respectively. The heritability estimates for this character was high (94.4%) with high genetic advance as per cent of mean (24.14%) indicating the preponderance of additive gene action in controlling of the trait. Hence, direct selection would also be effective for the improvement of high yield.

4.3.10 Seed yield per plant (g)

The genotypic and phenotypic coefficients of variation estimates observed for the trait are high i.e., 38.6 % and 39.92 %, respectively. The heritability estimates for this character was high (93.5%) with high genetic advance as per cent of mean (76.88%) suggesting additive gene action control for this character. Therefore, simple selection would be rewarding f or improvin-g this trait.

4.3.11 Oil content (%)

Low genotypic and phenotypic coefficients of variation were obse rved for this trait i.e., 6.31 % and 6.55 %, respectively. High heritability estimates (92.70 %) and moderate genetic advance as per cent of mean (12.51%) suggested that selection for this character would be ineffective.

The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Information on coefficient of variation is useful in measuring the range of variability present in the characters. Heritability and genetic advance are important selection parameters. Genotypic coefficient of variation (GCV) along with heritabilit y estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). It is suggested that genetic gain should be considered in conjunction with heritability estimates (Johnson *et al.*, 1955). Heritability estimates along with genetic advance

are normally more helpful in predicting the gain under selection than heritability estimates alone. Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all traits indicating less influence of environment on the traits.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. High heritability for quantitati ve characters indicates the scope of genetic improvement of these character s through selection.

The genetic advance as per cent of mean is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. The traits with high heritability and high genetic advance indicate the control of additive gene action and selection may be effective for these characters.

4.4 GENETIC DIVERGENCE

Genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population. In order to generate variability, hybridization between genotypes of diverse origin is suggested to unlock new recombinations.

Genetic divergence has been used as an indirect parameter of moderate effectiveness in selecting parents to produce high yielding progenies.

Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology and plant breeding. Information on genetic diversity within and among closely related crop germplasm is essential for rational use of genetic resources. Parents selected on the basis of such study would help in obtaining higher amount of heterotic expression in F_1s and broad spectrum of variability in subsequent segregating generations for various quantitative characters and to study the genetic diversity among them so as to utilize them in the hybridization

programme for the development of new lines with improved grain yield, quality and tolerance to stress conditions.

The quantitative assessment of genetic divergence was made by adopting Mahalanobis D^2 statistic for yield and its contributing characters. Genetic divergence was estimated for sixty five sesame genotypes and the results obtained from the study are presented below.

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 704 degrees of freedom. The 'V' statistic value was highly significant indicatin g that the genotypes differed significantly when all the characters were considered simultaneously.

The significance of sixty five 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 assess the genetic diversity among sixty five genotypes, D^2 statistic was used following the procedure given by Rao (1952), since the entire 11 yield component characters were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method.

4.4.3 Grouping of genotypes into various clusters

Sixty five genotypes were grouped into four clusters based on D^2 values using Tocher's method (Rao, 1952) such that the genotypes belongin g to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters has been presented in Table 4.4 and Fig 4.3 out of four clusters, cluster I was the largest comprising of sixty genotypes followed by cluster II with three genotypes, clusters III and IV were mono-genotypic clusters, suggesting the existence of high degree of heterogeneity among the genotypes.

Table 4. 4. Clustering pattern among 65 sesame genotypes of sesame (Tocher's method)

Cluster no.	No. of genotypes included	Genotypes in cluster
I	**60**	GM-NIC- 16146,K-5170, TKG-22, SI-413-A, ES-113-18-84, NIC-10621, NIC-8263, SI-1147, SI-199-2-84, GM-NIC- 8254, ES-42-2-84, EC-209, EC-S-0223, EC-231-2-84, EC-89111, NIC-16114, NIC-16324, GM-NIC- 7909, GM-NIC- 16332, GM-NIC- 7913, GM-NIC- 16226, ES-44, NIC-7903, KMR-114, JLT-07, GM-NIC- 16330, EC-S-0523A, IS-299A, IC-41962, ES-146-1-84, UKNM-2386, EC-370936, PKDS-8, SI-983, NIC-16220, IC-23233, NIC-16104, OSC-3209, KMR-69, IC-204001, IC-42200, GM-NIC- 8202, DS-21, IS-207, GM-NIC- 8934, SI-205-61, YLM-17, EC-101396, EC-310439, EC-377015, GM-NIC- 8631, EC-303423, SI-5354, SI-3168, SI-1003, EC-370840, NIC-7855, IS-424, GT-3, G-1.
II	**3**	UKNM-1067, TKG-306and SWETA
III	**1**	MADURI
IV	**1**	JLT-408

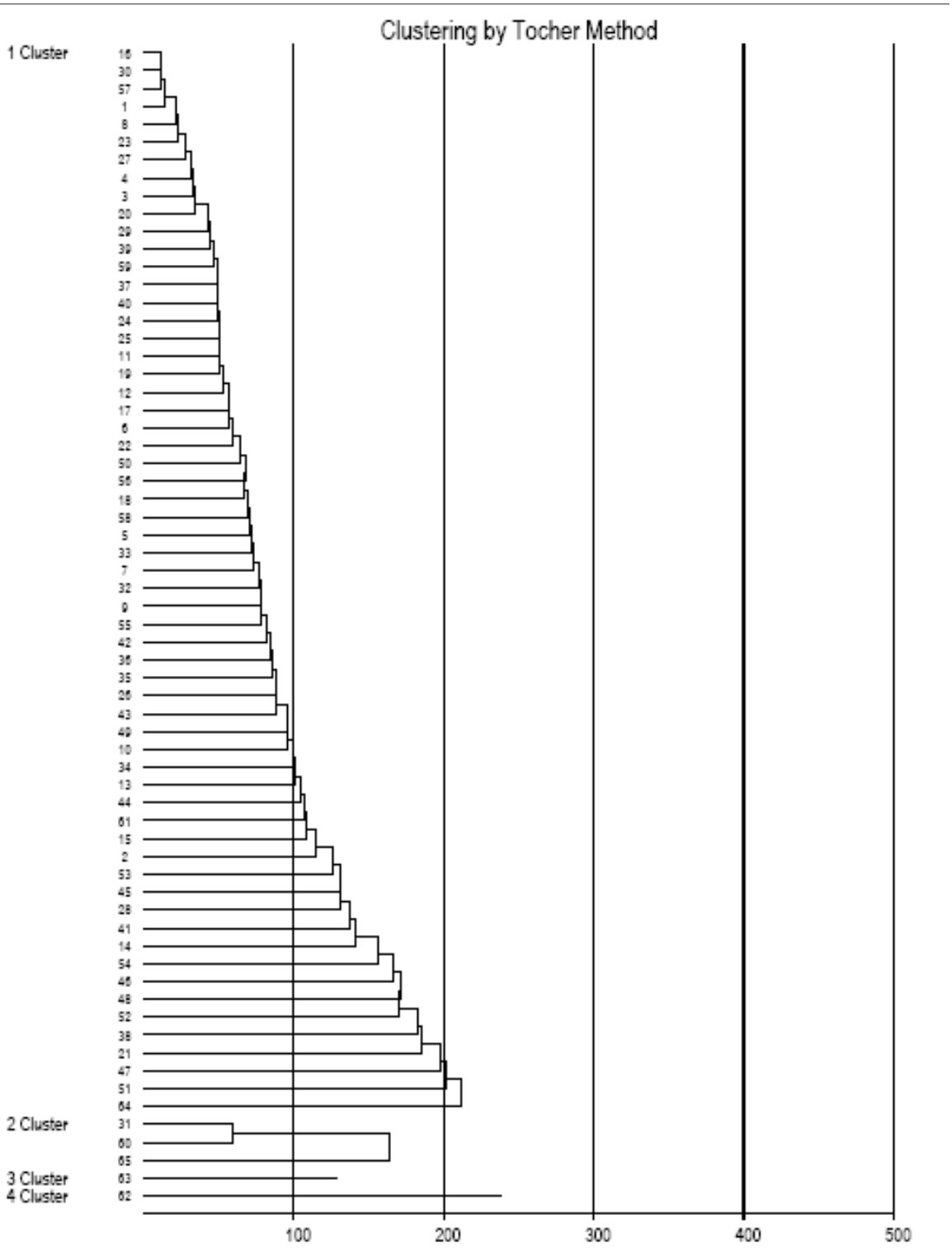

Fig: 4.3. Clustering pattern of 65 genotypes in sesame by (Tocher's method)

4.4.4 Average inter and intra cluster distances

D^2 analysis is considered as the most effective method to measure the forces of differentiation at two levels namely, intra cluster and inter cluster levels.

The inter cluster distance was higher than intra cluster distance (Table 4.5), indicating the presence of wide genetic diversity among the genotypes under study. The intra-cluster D^2 values varied from 0.00 to 13.55. The maximum intra-cluster distance was found in cluster II (13.55), followed by cluster I (10.87). The intra-cluster distance values were zero in the clusters, which had one genotype (III, IV) each.

The maximum average inter-cluster distance was found between cluster I and IV (24.75). While minimum inter-cluster distance was observed between clusters I and III (15.88). Among 4 clusters, cluster III (Maduri) and IV (JLT-408) were most divergent to other clusters.

i. Cluster I exhibited maximum divergence with cluster IV (24.75), followed by cluster II (17.90) and cluster III (15.88).
ii. Cluster II had maximum divergence with cluster I (17.90) followed by cluster IV (17.82) and cluster III (17.68).
iii. Cluster III displayed maximum divergence with cluster II (17.68) and followed by cluster I (15.88) and cluster IV (15.42).
iv. Maximum divergence of cluster IV expressed with cluster I (24.75) followed by cluster II (17.82) and cluster III (15.42).

Table 4.5: Intra (diagonal) andinter-cluster average of D and D^2 values of 65 Sesame genotypes.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	**10.87**	17.90	15.88	24.75
Cluster II		**13.55**	17.68	17.82
Cluster III			**0.00**	15.42
Cluster IV				**0.00**

4.4.5 Cluster means of the characters

The cluster means for each of eleven characters are presented in Table 4.6. It can be seen from the data that considerable differences existed for all the characters under study.

Cluster-I

Cluster-I showed low mean for capsule length (2.43 cm), number of capsules per plant (47.12), number of seeds per capsules (71.05), 1000 seed weight (2.62 g), seed yield per plant (8.72 g) and oil content (42.32 %).

The genotypes with low mean values for characters above mentioned are grouped in this cluster.

Cluster-II

Cluster II showed high mean values for days to maturity (88.50), plant height (105.40 cm) and number of branches per plant (3.65).

The genotypes with high plant height, more number days to maturity and number of branches per plant were grouped in this cluster.

Cluster-III

This cluster shown low mean values for days to 50% flowering (33.0), days to maturity (74.0) and number of branches per plant (2.20). The high mean values are observed for characters capsule width (0.68) and number of seeds per capsule (33.40).

The genotypes which shown low mean values for days to 50% flowering, days to maturity, number of branches per plant and high mean values for capsule width and number of seeds per capsule were grouped in this cluster.

Cluster-IV

Genotypes in this cluster had high mean values for days to 50% flowering (38.50), capsule length (2.67 cm), number capsules per plant (85.25), seed yield per plant (25.98 g), 1000 seed weight (3.78 g) and oil content (49.31%) and observed low mean values for capsule width (0.64) and plant height (89.15).

Cluster-IV was formed with genotypes having high days to 50% flowering, capsule length, number of capsules per plant, seed yield per plant, 1000 seed weight, and oil content.

4.4.6 Principal component analysis

In principal component analysis on correlation matrix the standardiza tion of columns (here characters) created 11 new variables for 65 genotypes without changing their relative positions. These 11 new variables are the principal components (PC_1, PC_2…..PC_{11}). Each principal component is a linear combination of the 11 attributes of data matrix. The loading values are scaled or standardized in such a manner that the sum of square of loadings within a principal component is equal to one. The loadings are viewed as weights defining the contribution of characters in respective principal components. Like regression coefficients, loadings sign (+/-) are indicative of direction of contribution. But unlike regression only the relative contribution are important, so all signs can be changed without affecting the analysis (Jackson, 1991).

The loadings for first principal component were chosen as to make its variance as large as possible. Loadings of second principal component were chosen such that the variance of PC_2 is as large as possible, subject to the constraint that PC_1 and PC_2 are uncorrelated. The process was continued to create 10 principal components, but PC's having eigene value less than one is not having any practical significance (Legendre and Legendre, 1984).

Principal components (eigene value greater than one), eigene values (Latent root), per cent variability, cumulative per cent variability componen t loading of different characters are presented in Table 4.5(a).

In the present studies, the first four principal components with eigene values more than one contributed 76.52 per cent towards the total variability. The principal component with eigene value less than one were considered as non-significant. It was therefore inferred that the essential features of data set had been represented in the first four principal components.

The first principal component contributed maximum towards variability (33.84%). Characters *viz.*, seed yield per plant (0.689), 1000-seed weight (0.503), oil content (0.390), capsules per plant (0.186), days to maturity (0.167), number of seeds (0.150), capsule length (0.129) days to 50% flowering (0.079), plant height (0.057), capsule width (-0.048) and number of branches (-0.074) defined the maximum variance in first principal component (PC_1) and signifying their importance in plant yield. Negative correlation was noticed with capsule width and number of branches while 1000 seed weight, seed yield per plant, oil content (%), capsules per plant, plant height, capsule length, seeds per capsule, days to maturity, and days to 50% flowering were positively correlated.

The second principal component (PC_2) which illustrated (22.94 per cent) of total variance and it reflected significant loadings of seeds per capsule (0.557), days to maturity (0.467), capsule length (0.445), oil content (0.216), days to maturity (0.210), plant height (0.168) which were positively correlated.

A total variance of 10.86% presented in third principal component (PC_3) was contributed by conspicuously high loading of seeds per capsule (0.267), capsule length (0.223), oil content (0.196), number of capsules (0.182) that were positively correlated. While days to maturity, plant

height, number of branches and 1000-seed weight were negatively correlated.

The fourth principal component (PC_4) was characterized by conspicuously high loadings of number of capsules (0.480), oil content (0.368), plant height (0.301), days to 50% flowering (0.270), number of branches (0.157), days to maturity (0.076) and seed yield (0.070) which were positively correlated while 1000-seed weight (-0.494), capsule length (-0.378), number of seeds (-0.190) and capsule width (-0.094) were negatively correlated. Contribution of this principal component towards variability was 8.86 per cent.

The PCA scores or genotypes mean scores for 65 genotypes in the first four principal components with eigene value more than one were computed and presented in Table 4.5(a). The genotypes were grouped based on the scores into 4 clusters. The first two principal components contributing more for the variance were taken to construct 3D plots. A three dimensional scattered diagram drawn by keeping the P.C.A I as X-axis, P.C.A-II as Y axis and P.C.A-III as Z axis (Fig.)

The clusters were obtained by individual PCA character score by each variety by plotting their values on PCA I, II and III vectors shown in table 4.5(b). There are 4 clusters obtained and cluster I is largest comprised of 60 genotypes out of 65 followed by cluster II comprising 3 genotypes and clusters III and IV are mono genotypic clusters. This PCA scores of three vectors helped to construct the 3D plot diagram (fig. 4.3(a)) by plotting PCA I, PCA II and PCA III on X, Y and Z axis respectively.

Table -4.5(a): Eigen values, proportion of the total variance represented by first four principal components, cumulative per cent variance and component loading of different characters in sesame (*Sesamum indicum* L.)

Character	PCA 1	PCA 2	PCA 3	PCA 4
Eigene value (Root)	1673.35	1134.71	537.25	438.08
% Var. Exp.	33.842	22.949	10.865	8.860
Cum. Var. Exp.	33.842	56.791	67.657	76.517
Days to 50% flowering	0.079	0.210	0.0127	0.270
Days to maturity	0.167	0.467	-0.673	0.076
Capsule length (cm)	0.129	0.445	0.223	-0.378
Capsule width (cm)	-0.048	-0.007	0.117	-0.094
Plant height (cm)	0.057	0.168	-0.203	0.30`1
Number of branches / plant	-0.074	-0.053	-0.430	0.157
Number of capsules / plant	0.186	-0.103	0.182	0.480
Number of seeds / capsule	0.150	0.557	0.267	-0.190
Seed yield / plant	0.689	-0.269	0.110	0.070
1000-seed weight (g)	0.503	-0.258	-0.315	-0.494
Oil content (%)	0.390	0.216	0.196	0.368

Table 4.5(b): Individual genotype PCA scores and clustering pattern.

S. No.	Genotype	PCA I	PCA II	PCA III	Cluster
		X Vector	Y Vector	Z Vector	
1	SI-413-A	59.580	72.756	-26.711	**I**
2	SI-205-61	57.374	62.917	-24.001	**I**
3	SI-199-2-84	59.457	68.501	-25.765	**I**
4	SI-1147	61.392	68.562	-26.025	**I**
5	IS-299A	64.214	73.627	-26.763	**I**
6	ES-44	60.620	67.035	-24.914	**I**
7	ES-146-1-84	65.256	69.491	-26.189	**I**
8	ES-113-18-84	58.766	73.048	-23.839	**I**
9	EC-370936	57.013	65.168	-25.263	**I**
10	IC-204001	59.268	73.046	-22.006	**I**
11	GM-NIC- 7909	57.887	69.814	-22.806	**I**
12	GM-NIC- 7913	58.513	65.685	-26.099	**I**
13	GM-NIC- 8202	58.632	63.500	-26.694	**I**
14	GM-NIC- 8631	62.477	78.516	-23.345	**I**
15	GM-NIC- 8934	54.712	64.808	-22.651	**I**
16	GM-NIC- 16146	59.490	71.152	-26.355	**I**
17	GM-NIC- 16226	58.485	66.386	-27.629	**I**
18	GM-NIC- 16330	61.748	68.175	-29.544	**I**
19	GM-NIC- 16332	57.649	69.247	-23.733	**I**
20	GM-NIC- 8254	58.486	69.937	-26.882	**I**
21	NIC-7855	53.119	74.485	-19.651	**I**
22	NIC-7903	61.191	66.431	-27.936	**I**
23	NIC-10621	58.357	71.331	-26.539	**I**
24	NIC-16114	57.864	71.496	-23.851	**I**
25	NIC-16324	58.170	70.337	-20.357	**I**
26	NIC-16104	57.608	72.396	-27.095	**I**
27	NIC-8263	58.917	71.624	-27.067	**I**
28	EC-310439	57.876	72.541	-20.072	**I**
29	ES-42-2-84	56.281	74.732	-24.243	**I**
30	K-5170	59.320	70.427	-26.674	**I**
31	UKNM-1067	72.736	68.665	-28.457	**II**
32	UKNM-2386	61.451	68.057	-23.033	**I**
33	IC-41962	61.781	74.031	-26.912	**I**
34	IC-42200	58.903	65.436	-22.999	**I**
35	IC-23233	57.932	77.201	-25.859	**I**
36	NIC-16220	55.412	75.959	-24.770	**I**
37	EC-231-2-84	57.704	69.343	-25.495	**I**
38	EC-370840	52.620	80.299	-23.800	**I**

39	EC-209	60.168	74.247	-24.757	**I**
40	EC-89111	56.951	67.324	-23.205	**I**
41	EC-377015	61.145	78.251	-29.028	**I**
42	SI-983	56.264	74.972	-24.225	**I**
43	OSC-3209	58.337	76.606	-27.026	**I**
44	DS-21	52.420	70.806	-26.604	**I**
45	EC-101396	57.748	78.287	-22.949	**I**
46	SI-5354	55.706	80.395	-28.087	**I**
47	IS-424	48.867	65.572	-24.917	**I**
48	SI-3168	50.950	64.333	-24.352	**I**
49	KMR-69	59.346	69.529	-25.380	**I**
50	KMR-114	57.824	70.648	-25.343	**I**
51	GT-3	54.643	75.445	-21.847	**I**
52	SI-1003	49.340	69.928	-22.854	**I**
53	YLM-17	63.491	66.364	-30.908	**I**
54	EC-303423	62.907	77.109	-28.222	**I**
55	PKDS-8	54.276	68.093	-25.950	**I**
56	JLT-07	62.050	70.401	-25.537	**I**
57	TKG-22	59.834	73.347	-25.545	**I**
58	EC-S-0523A	61.619	71.881	-26.941	**I**
59	EC-S-0223	58.866	70.239	-24.121	**I**
60	TKG-306	71.165	70.205	-29.833	**II**
61	IS-207	54.639	70.263	-26.756	**I**
62	JLT-408	78.940	66.212	-17.191	**IV**
63	MADURI	65.649	71.505	-14.363	**III**
64	G-1	65.267	70.429	-19.304	**I**
65	SWETA	71.988	78.198	-24.362	**II**

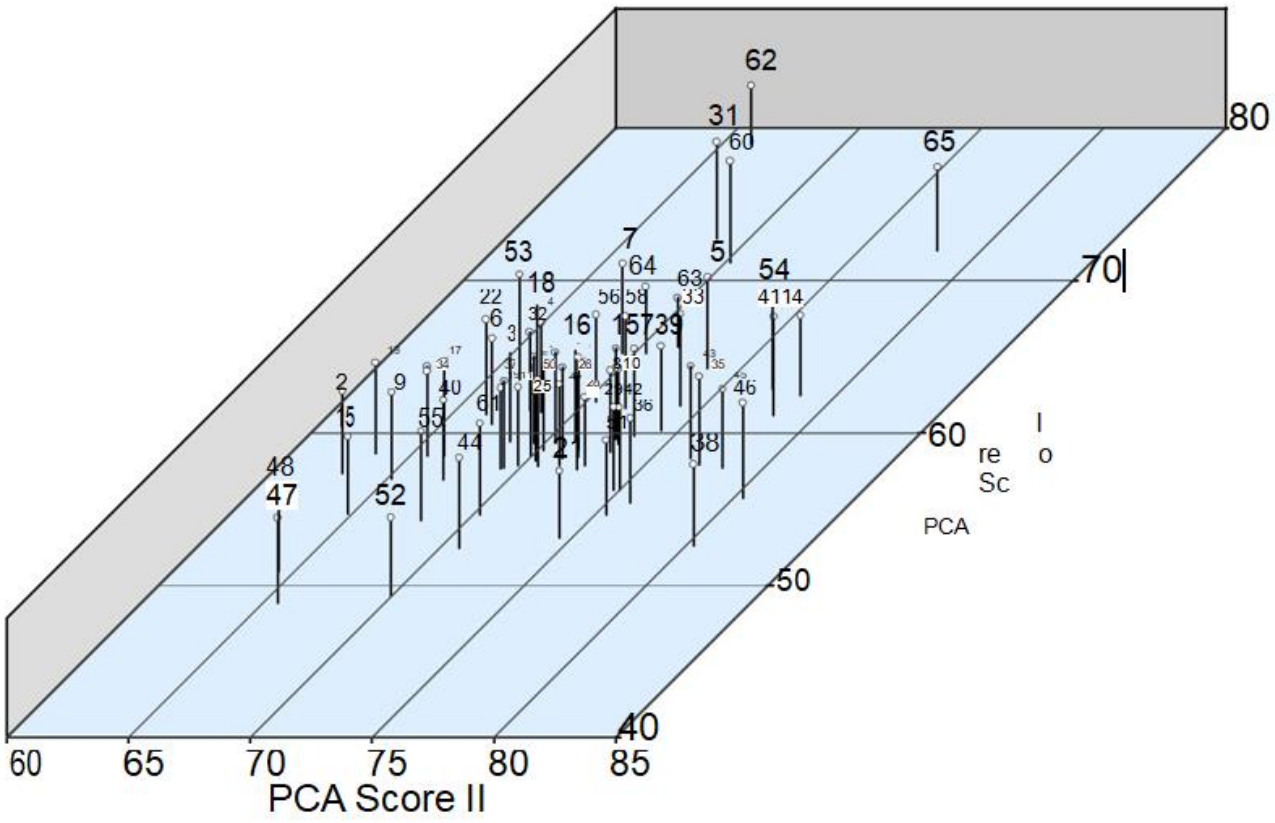

Fig 4.3(a): 3D plot diagram based on PCA scores

Table 4.6: Cluster means for 11 characters in 65 Sesame genotypes.

Cluster	Days to 50% flowering	Days to maturity	Capsule length	Capsule width	Plant height	Number of branches per plant	Number of capsules per plant	Number of seeds per capsule	Seed yield per plant	1000 seed weight	Oil content (%)
Cluster I	37.22	82.71	**2.43**	0.65	95.24	3.60	**47.12**	**71.05**	**8.72**	**2.62**	**42.32**
Cluster II	38.33	**88.50**	2.59	0.66	**105.40**	**3.65**	51.65	75.50	13.59	3.47	46.59
Cluster III	**33.00**	**74.00**	2.66	**0.68**	93.50	**2.20**	74.50	**93.40**	21.17	3.03	48.10
Cluster IV	**38.50**	78.50	**2.67**	**0.64**	**89.15**	2.90	**85.25**	80.60	**25.98**	**3.78**	**49.31**

4.4.6 Relative contribution of characters towards genetic divergence

The utility of D^2 statistics as a potential tool to quantify the extent of divergence in biological populations at genetic level is further enhanced by its applicability to estimate the relative contribution of the various plant characters to total genetic divergence. The number of times that each of ten characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 4.7.

The results showed that the contribution of 1000 seed weight was the highest towards genetic divergence (18.51 %) by taking 385 times ranking first, followed by days to maturity (16.30 %) by 339 times, oil content (13.13 %) by 279 times, number of seeds per capsule (11.88 %) by 247 times, capsule length (11.59%) by 241 times, seed yield per plant (10.05 %) by taking 209 times, number of branches per plant (9.28 %) by 193 times, days to maturity (2.89 %) by 55 times, days to 50% flowering (1.80 %) by 34 times and seed yield per plant (1.00 %) by 19 times to the genetic divergence in decreasing order.

Out of eleven characters studied, seven characters namely 1000 seed weight, days to maturity, oil content, number of seeds per capsule, capsule length, seed yield per plant and number of branches per plant together contributed 90.74 % towards total divergence. Therefore, these characters should be given importance during hybridization and selection of segregating populations.

Table 4.7: Relative contribution of different characters to genetic diversity in sesame genotypes.

S. No.	Character	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	56	2.69%
2	Days to maturity	339	16.30%
3	Capsule length	241	11.59%
4	Capsule width	18	0.87%
5	Plant height	41	1.97%
6	Number of branches per plant	193	9.28%
7	Number of capsules per plant	78	3.75%
8	Number of seeds per capsule	247	11.88%
9	Seed yield per plant	209	10.05%
10	1000 seed weight	385	18.51%
11	Oil content (%)	279	13.13%

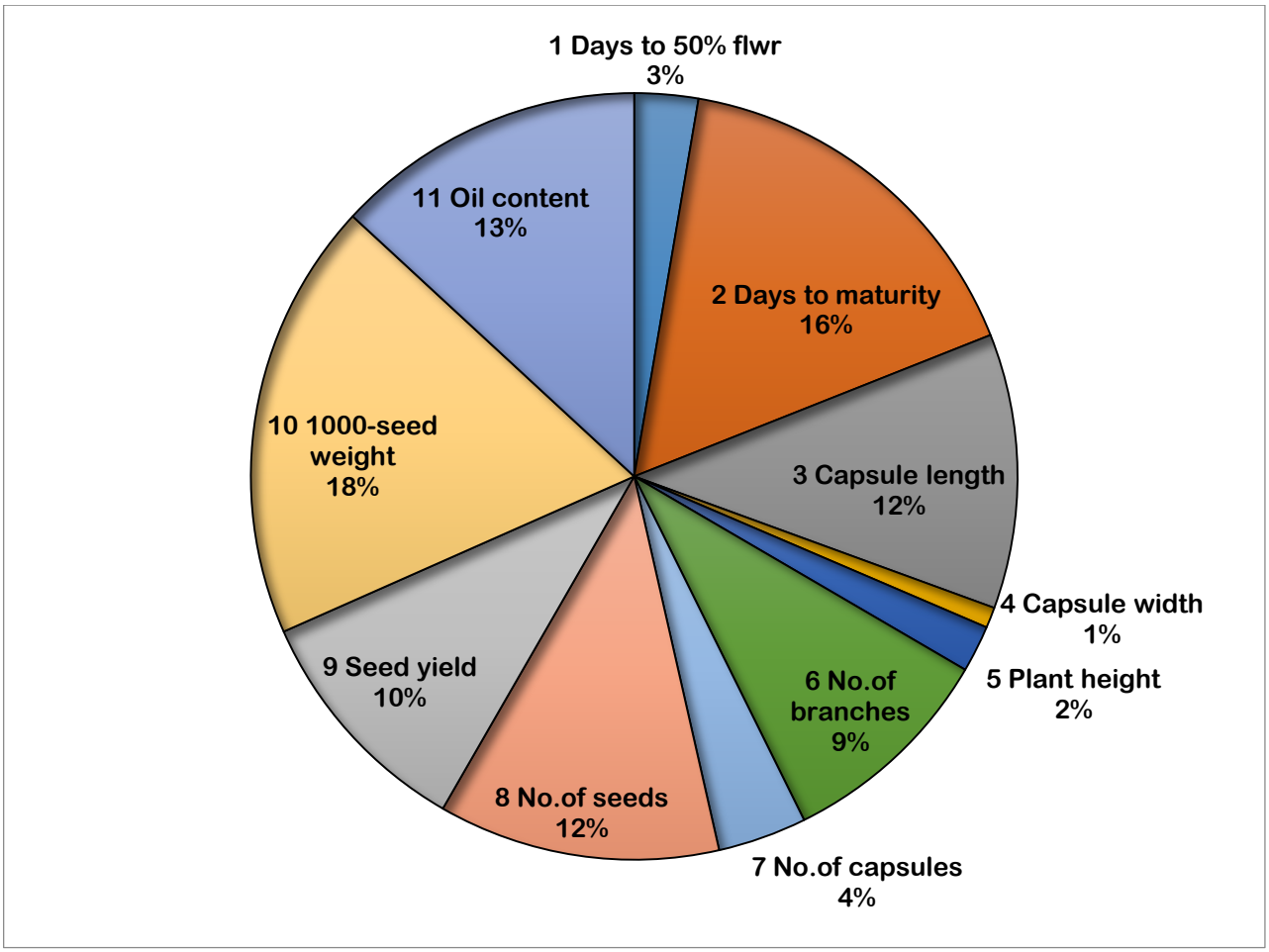

Figure 4.3(b): Relative contribution of each character towards the divergence.

4.5 CHARACTER ASSOCIATION

The primary importance of character association studies is to know the suitability of various characters for selection, because selection of a particular trait may induce desirable or undesirable changes in the associated characters. Generally, direct selection for yield was not aimed at, as it is a most complex trait which is the result of the interaction of a number of components and highly influenced by environment.

If the association of characters is due to manifold effects of a gene or genes, it is difficult to separate these characters by selecting a particular character so related. If the correlation is due to linkage it is possible to reverse the correlation, provided the linkage is not very close. Hence, it is important to establish genetic basis of correlations before launching any breeding programme. Further, the component characters of yield exhibit different associations among themselves and also with yield. Unfavorable associations between the desired attributes under selection may limit genetic advance. Therefore, knowledge on the magnitude of association between the yield and its attributing characters is essential for planning sound breeding programme.

Phenotypic and genotypic correlations between yield and its contributing traits for sixty five genotypes were estimated, are presented in Table 4.8. In general, for most of the characters under study, the phenotypic correlation coefficients were higher than genotypic correlation coefficients. High phenotypic correlations as compared to their genotypic counterparts indicated high influence of environment.

4.5.1 Days to 50 per cent flowering

It was evident from (table 4.8) that days to 50% flowering exhibited significant positive association with days to maturity (0.6305**/0.6479**) and capsule length (0.1769*/0.2029*) both at phenotypic and genotypic levels. The characters *viz*., capsule width (0.0434/0.0504), plant height (0.1 708/0.1373), number of seeds per capsule (0.1629/0.1538) and oil content

(0.1433/0.0979) exhibited positive but non-significant association, while number of branches per plant (-0.1128/-0.0870), number of capsules per plant (-0.0247/-0.0393) and 1000 seed weight (-0.0217/-0.0054) exhibited negative non-significant association. While seed yield per plant (0.0434/0.0350) exhibited positive non-significant association with this trait.

4.5.2 Days to maturity

Days to maturity registered positive significant association with days to 50% flowering (0.6479**/0.6305**), plant height (0.3166**/ 0.2751**), capsule length (0.2204/0.1995*) and negative significant association with number of capsules per plant (-0.2138*/-0.2076*) at both genotypic and phenotypic levels. While this trait exhibited positive but non-significant association with number of seeds per plant (0.1353/0.1160), capsule width (0.1203/0.1160), oil content (0.0838/0.0643) and number of branches (0.0815/0.0783) and negative non-significant association registered with the 1000 seed weight (-0.0039/-0.0120).

This character exhibited negative non-significant association with seed yield (-0.1226/-0.1308).

4.5.3 Capsule length (cm)

This trait had positive significant correlation with number of seeds p er capsule (0.6020**/0.5319**), capsule width (0.2720**/0.2277**), days to maturity (0.2204*/0.1995*) and days to 50% flowering (0.2029*/0.1769 *) at both genotypic and phenotypic levels and plant height (0.0597/0.0548), 1000 seed weight (0.1575/0.1322), and oil content (0.1127/0.1025) expressed positive non-significant association. While negative non-significant association is registered with number of branches (-0.1412/-0.1300), and number of capsules (-0.0835/-0.0640).

This character expressed positive significant correlation with seed yield (0.2378**/0.2189*) at both levels.

4.5.4 Capsule width (cm)

The character capsule width had significant positive correlation with number of seeds per capsule (0.4830**/0.3685**) and capsule length (0.2720**/0.2277**) at both genotypic and phenotypic levels and exhibited positive but non-significant correlation with days to maturity (0.1203/ 0.1160), days to 50% flowering (0.0434/0.0504), oil content (0.0372/0.034 0) and 1000 seed weight (0.0640/0.0508), While negative non-significant correlation registered with number of capsules per plant (-0.1538/-0.0961), number of branches per plant (-0.0646/-0.0612) and plant height (-0.0043/-0.0338).

This trait expressed positive non-significant correlation with seed yield (0.0864/0.0843).

4.5.5 Plant height (cm)

Positive significant correlation of this trait was observed with number of branches per plant (0.5133**/0.4726**), days to maturity (0.316 6**/0.2751**) and number of capsules per plant (0.3128**/ 0.2832**) at both genotypic and phenotypic levels and positive but non-significant correlation observed with days to 50% flowering (0.1708/0.1373), oil content (0.1320/0.1241), capsule length (0.0597/0.548) and 1000 seed weight (0.0273/0.0233).

Negative non-significant correlation was reported with capsule width (-0.0043/-0.0338) at both genotypic and phenotypic level and number of seeds per plant (0.0030/-0.0233) at phenotypic level. This trait exhibited positive significant correlation with seed yield (0.2225*/0.1986*)

Table 4.8: Phenotypic (P) and Genotypic (G) correlation coefficients among yield attributes in 65 sesame genotypes

Character		DF 50%	DM	CL (cm)	CW (cm)	PH (cm)	NBP	NCP	NSC	1000 SW (g)	OC (%)	SYP (g)
DF 50%	G	**1.0000**	0.6479**	0.2029*	0.0434	0.1708	-0.1128	-0.0247	0.1629	-0.0217	0.1433	0.0434
	P	**1.0000**	0.6305**	0.1769*	0.0504	0.1373	-0.0870	-0.0393	0.1538	-0.0054	0.0979	0.0350
DM	G		**1.0000**	0.2204*	0.1203	0.3166**	0.0815	-0.2138	0.1353	-0.0039	0.0838	-0.1226
	P		**1.0000**	0.1995*	0.1160	0.2751**	0.0783	-0.2076	0.1160	-0.0120	0.0643	-0.1308
CL (cm)	G			**1.0000**	0.2720**	0.0597	-0.1412	-0.0835	0.6020**	0.1575	0.1127	0.2378**
	P			**1.0000**	0.2277**	0.0548	-0.1300	-0.0640	0.5319**	0.1322	0.1025	0.2189*
CW (cm)	G				**1.0000**	-0.0043	-0.0646	-0.1538	0.4830**	0.0640	0.0372	0.0864
	P				**1.0000**	-0.0338	-0.0612	-0.0961	0.3685**	0.0508	0.0340	0.0843
PH (cm)	G					**1.0000**	0.5133**	0.3128**	0.0030	0.0273	0.1320	0.2225*
	P					**1.0000**	0.4726**	0.2832**	-0.0233	0.233	0.1241	0.1986*
NBP	G						**1.0000**	0.2232*	-0.2762**	-0.0861	-0.0914	-0.0411
	P						**1.0000**	0.2162*	-0.2501**	-0.0678	-0.0884	-0.0262
NCP	G							**1.0000**	-0.0875	0.2780**	0.3070**	0.8065**
	P							**1.0000**	-0.0975	0.2378**	0.2739**	0.7935**
NSC	G								**1.0000**	0.2548**	0.2412**	0.3726**
	P								**1.0000**	0.2864**	0.2164*	0.3812**
1000SW (g)	G									**1.0000**	0.5885**	0.6578**
	P									**1.0000**	0.5512**	0.6437**
OC (%)	G										**1.0000**	0.5325**
	P										**1.0000**	0.4941**
SYP (g)	G											**1.0000**
	P											**1.0000**

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

DF50%= Days to 50% flowering, **DM=** Days to maturity, **CL=** Capsule length, **CW=** Capsule width, **PH=** Plant height, **NBP=** Number of branches per plant, **NCP=** Number of capsules per plant, **NSC=** Number of seeds per capsule, **1000SW=** 1000 seed weight, **OC=** Oil content, **SYP=** Seed yield per plant.

4.5.6 Number of branches per plant

The number of branches per plant had positive significant correlation with plant height (0.5133**/0.4726**) and number of capsules per plant (0.2232*/0.2162*) at both levels and capsule length (-0.1412/-0.1300) days to 50% flowering (-0.1128/-0.0870), oil content (-0.0914/-0.0884), 1000-seed weight (-0.0861/-0.0678), capsule width (-0.0646/-0.0612) and seed yield (-0.0411/-0.0262) exhibited negative non-significant association at both phenotypic and genotypic levels. Negative significant correlation at both levels observed with number of seeds per capsule (-0.2762**/-0.2501**).

4.5.7 Number of capsules per plant

This trait registered positive significant genotypic and phenotypic correlation with plant height (0.0.3128**/0.2832**), 1000-seed weight (0.2780**/0.2378**), oil content (0.2412**/0.2739**) and number of branches (0.2232*/0.2162*). It showed negative significant correlation with days to maturity (-0.2138*/-0.2076*) at both levels and negative non-significant correlation with capsule width (-0.1538/-0.0961), number of seeds per capsule (-0.0875/-0.0975), capsule length (-0.0835/-0.0640) and days to 50% flowering (-0.0247/-0.0393).

This trait expressed positive significant correlation with seed yield per plant (0.8065**/0.7935**) at both levels.

4.5.8 Number of seeds per capsules

1000-seed weight exhibited significant positive genotypic and phenotypic correlation with capsule length (0.6020**/5319**), capsule width (0.4830**/0.3685**) 1000-seed weight (0.2548**/0.2864**) and oil content (0.2412**/0.2164*). This number of seeds per capsule will contrib ute directly towards the seed yield and this trait exhibited positive significa nt correlation with seed yield per plant (0.3726**/0.3812**) at both levels.

4.5.9 1000-seed weight (g)

The trait, 1000-seed weight shown positive significant correlation at both genotypic and phenotypic levels with oil content (0.5885/0.5512**),

number of capsules per plant (0.2780**/0.2378**) and number of seeds per capsule (0.2548**/0.2864**) and 1000-seed weight also directly contribute -s for seed yield and exhibited positive significant correlation with seed yield (0.6578**/0.6437**) at both levels.

4.5.10 Oil content (%)

This trait recorded positive significant genotypic and phenotypic correlation with 1000-seed weight (0.5885**/0.5512**), number of capsules per plant (0.3070**/0.2739**) and number of seeds per capsule (0.2412**/0.2164*). It showed positive non significant association with trai ts *viz.*, days to 50% flowering (0.1433/0.0979), capsule length (0.1127/0.10 25) plant height (0.1320/0.12410) and days to maturity (0.0838/0.0643) at genotypic and phenotypic levels. This trait exhibited positive significant co rrelation with seed yield (0.5325** /0.4941**) at both the levels.

4.5.11 Seed yield (g)

This trait exhibited positive significant correlation with number of capsules per plant (0.8065**/0.7935**), 1000-seed weight (0.6578**/ 0.6437**), oil content (0.5325**/0.4941**), number of seeds per capsule (0.3726**/0.3812**), capsule length (0.2378** /0.2189*) and plant height (0.0.2225*/0.1986*) and non-significant correlation with capsule width (0.0864/0.0843) and days to 50% flowering (0.0434/0.0350) at both the levels and negative non-significant correlation with days to maturity (-0.1226/-0.1308) and number of branches per plant (-0.0411/-0.0262) at both genotypic and phenotypic levels.

According to NeWall and Eberhart (1961) when two characters show negative phenotypic and genotypic correlation it would be difficult to exercise simultaneous selection for these characters in the development of a variety. Hence, under such situations, judicious selection programme might be formulated for simultaneous improvement of such important developmental and component characters

4.6 PATH COEFFICIENT ANALYSIS

The genetic architecture of seed yield is based on the balance or overall net effect produced by various yield components interacting with one another. The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and its component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. If relationship is due to multiple effects of gene(s) it is difficult to separate these effects by selecting a particular character. Hence, indirect selection by correlated response may not be some times fruitful.

When many characters are affecting a given character, splitting total correlation into direct and indirect effects of cause as devised by Wright (1921) would provide more meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield component characters. This kind of information will be helpful in formulating the selection criteria.

With this background, the direct and indirect effects of different yield contributing traits on yield were estimated using genotypic and phenotypic correlation coefficients and are presented in Table 4.9 .The cause-effect relationships at phenotypic and genotypic levels are diagrammatically represented in Figure 4.4 and Figure 4.5, respectively. As discussed in character association here also the results of both phenotypic and genotypic path coefficient analysis of yield and its contributing characters are discussed here under.

4.6.1 Days to 50 per cent flowering

The direct contribution of this character was positive on seed yield per plant (0.0082/0.0183) at genotypic and phenotypic level.

This trait exhibited positive indirect effects on seed yield per plant through number of seeds per capsule (0.0435/0.0456), capsule length

(0.0123/0.0081), number of branches per plant (0.0121/0.0080), plant heig ht (0.0060/0.0046), capsule width (0.0012/0.0008) and oil content (0.0011/ 0.0009) at both the levels.

This trait exhibited negative indirect effects *via* number of capsules per plant (-0.0185/-0.0292), days to maturity (-0.0148/-0.0201), and 1000-seed weight (-0.0077/-0.0020) at both the phenotypic and genotypic levels.

4.6.2 Days to maturity

Days to maturity exhibited negative direct effect (-0.0229/-0.0318) on seed yield per plant at both the levels.

This trait exhibited negative non-significant correlation (-0.1226/-0.1308) with seed yield per plant. It was mainly due to negative direct and indirect effects through number of capsules per plant (-0.1595/-0.1541), number of branches per plant (-0.0087/-0.0072) and 1000 seed weight (-0.0014/-0.0043) at both genotypic and phenotypic levels.

The positive indirect effects of this trait, was observed through number of seeds per capsule (0.0361/0.0344), capsule length (0.0134/0.009 1), plant height (0.0.0111/0.0092), capsule width (0.0034/0.0018), and oil content (0.0007/0.0006).

4.6.3 Capsule length (cm)

The direct contribution of this character towards seed yield per plant was positive (0.0608/ 0.0457) at both the levels.

The positive significant correlation of capsule length with seed yield per plant (0.2378**/0.2189*) was mainly due to indirect positive effects of this trait *via* number of seeds per capsule (0.1607/0.1575), 1000-seed weight (0.0561/0.0480), number of branches per plant (0.0151/0.0120), days to 50% flowering (0.0017/ 0.0032), capsule width (0.0077/0.0035), plant height (0.0021/0.0018) and oil content (0.0009/0.0003) at both the levels, while number of capsules per plant (-0.0623/-0.0475) and days to maturity (-0.0050/-0.0063) shown negative indirect effects at both levels.

4.6.4 Capsule width (cm)

The direct contribution of this character to seed yield per plant was positive (0.0283 / 0.0156) at both levels.

The positive non-significant correlation of number of branches per plant with seed yield per plant (0.0283 / 0.0156) was mainly due to indirect positive effects of this trait through number of seeds per capsule (0.1289/ 0.1091), 1000-seed weight (0.0228/0.0185), capsule length (0.0165/0.01 04), number of branches per plant (0.0069/0.0056) and days to 50% flowering (0.0004/ 0.0009) and negative indirect effects through number of capsules per plant (-0.1148 / -0.0714) and plant height (-0.0002/-0.0011) at both the levels.

4.6.5 Plant height (cm)

The direct contribution of this character on seed yield per plant is positive (0.0349/0.0334) at both levels.

The positive significant association of plant height with seed yield per plant (0.2225*/ 0.1986*) was mainly due to indirect positive effects of this trait *via* number of capsules per plant (0.2234/0.2103), 1000-seed weight (0.0097/0.0084), capsule length (0.0036/ 0.0025), days to 50% flowering (0.0014/0.0025), and oil content (0.0010/0.0012) at both the levels and number of seeds per capsule expressed indirect positive genotypic effect (0.0008/-0.0069),

This trait exhibited negative indirect effects on seed yield per plant through number of branches per plant (-0.0551/ -0.0435), days to maturity (-0.0072 / -0.0087), and capsule width (-0.0001/ -0.0005) at both the levels.

Table 4.9: Phenotypic (P) and Genotypic (G) Path coefficients among yield attributes in 65 sesame genotypes

Characters		DF 50%	DM	CL (cm)	CW (cm)	PH (cm)	NBP	NCP	NSC	1000 sw (g)	OC (%)	Correlation with SYP (g)
DF 50%	G	**0.0082**	0.0053	0.0017	0.0004	0.0014	-0.0009	-0.0002	0.0013	-0.0002	0.0012	0.0434
	P	**0.0183**	0.0115	0.0032	0.0009	0.0025	-0.0016	-0.0007	0.0028	-0.0001	0.0018	0.0350
DM	G	-0.0148	**-0.0229**	-0.0050	-0.0028	-0.0072	-0.0019	0.0049	-0.0031	0.0001	-0.0019	-0.1226
	P	-0.0201	**-0.0318**	-0.0063	-0.0037	-0.0087	-0.0025	0.0066	-0.0037	0.0004	-0.0020	-0.1308
CL	G	0.0123	0.0134	**0.0608**	0.0165	0.0036	-0.0086	-0.0051	0.0366	0.0096	0.0069	0.2378**
	P	0.0081	0.0091	**0.0457**	0.0104	0.0025	-0.0059	-0.0029	0.0243	0.0060	0.0047	0.2189*
CW	G	0.0012	0.0034	0.0077	**0.0283**	-0.0001	-0.0086	-0.0051	0.0366	0.0096	0.0069	0.0864
	P	0.0008	0.0018	0.0035	**0.0156**	-0.0005	-0.0010	-0.0015	0.0057	0.0008	0.0005	0.0843
PH	G	0.0060	0.0111	0.0021	-0.0002	**0.0349**	0.0179	0.0109	0.0001	0.0010	0.0046	0.2225*
	P	0.0046	0.0092	0.0018	-0.0011	**0.0334**	0.0158	0.0095	-0.0008	0.0008	0.0041	0.1986*
NBP	G	0.0121	-0.0087	0.0151	0.0069	-0.0551	**-0.1073**	-0.0240	0.0296	0.0092	0.0098	-0.0411
	P	0.0080	-0.0072	0.0120	0.0056	-0.0435	**-0.0921**	-0.0199	0.0230	0.0062	0.0081	-0.0262
NCP	G	-0.0185	-0.1595	-0.0623	-0.1148	0.2334	0.1666	**0.7462**	-0.0653	0.2075	0.2291	0.8065**
	P	-0.0292	-0.1541	-0.0475	-0.0714	0.2103	0.1605	**0.7424**	-0.0723	0.1765	0.2033	0.7935**
NSC	G	0.0435	0.0361	0.1607	0.1289	0.0008	-0.0737	-0.0234	**0.2670**	0.0680	0.0644	0.3726**
	P	0.0456	0.0344	0.1575	0.1091	-0.0069	-0.0741	-0.0289	**0.2961**	0.0848	0.0641	0.3812**
1000 SW (g)	G	-0.0077	-0.0014	0.0561	0.0228	0.0097	-0.0307	0.0990	0.0908	**0.3562**	0.2096	0.6578**
	P	-0.0020	-0.0043	0.0480	0.0185	0.0084	-0.0246	0.0863	0.1040	**0.3630**	0.2001	0.6437**
OC (%)	G	0.0011	0.0007	0.0009	0.0003	0.0010	-0.0007	0.0024	0.0019	0.0046	**0.0078**	0.5325**
	P	0.0009	0.0006	0.0010	0.0003	0.0012	-0.0008	0.0026	0.0020	0.0051	**0.0093**	0.4941**

Genotypic residual effect = 0.1671 Phenotypic residual effect = 0.1859

NCP= Number of capsules per plant, **CL**= Capsule length, **NSC=** Number of seeds per capsule**, 1000 SW**=1000 seed weight**,**
OC= Oil content**, SYP**= Seed yield/plant.

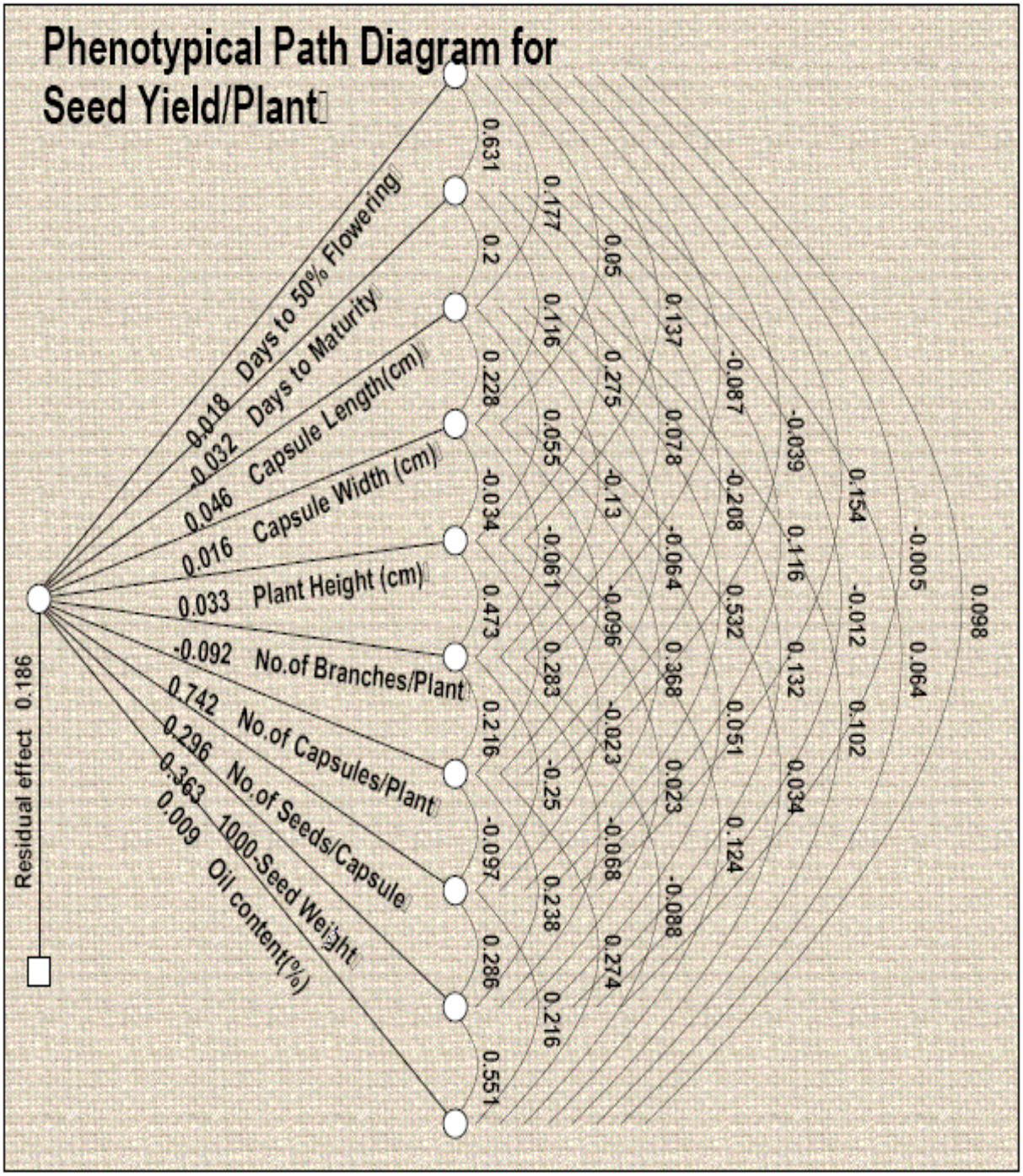

Fig 4.4: Phenotypic path diagram for seed yield/plant

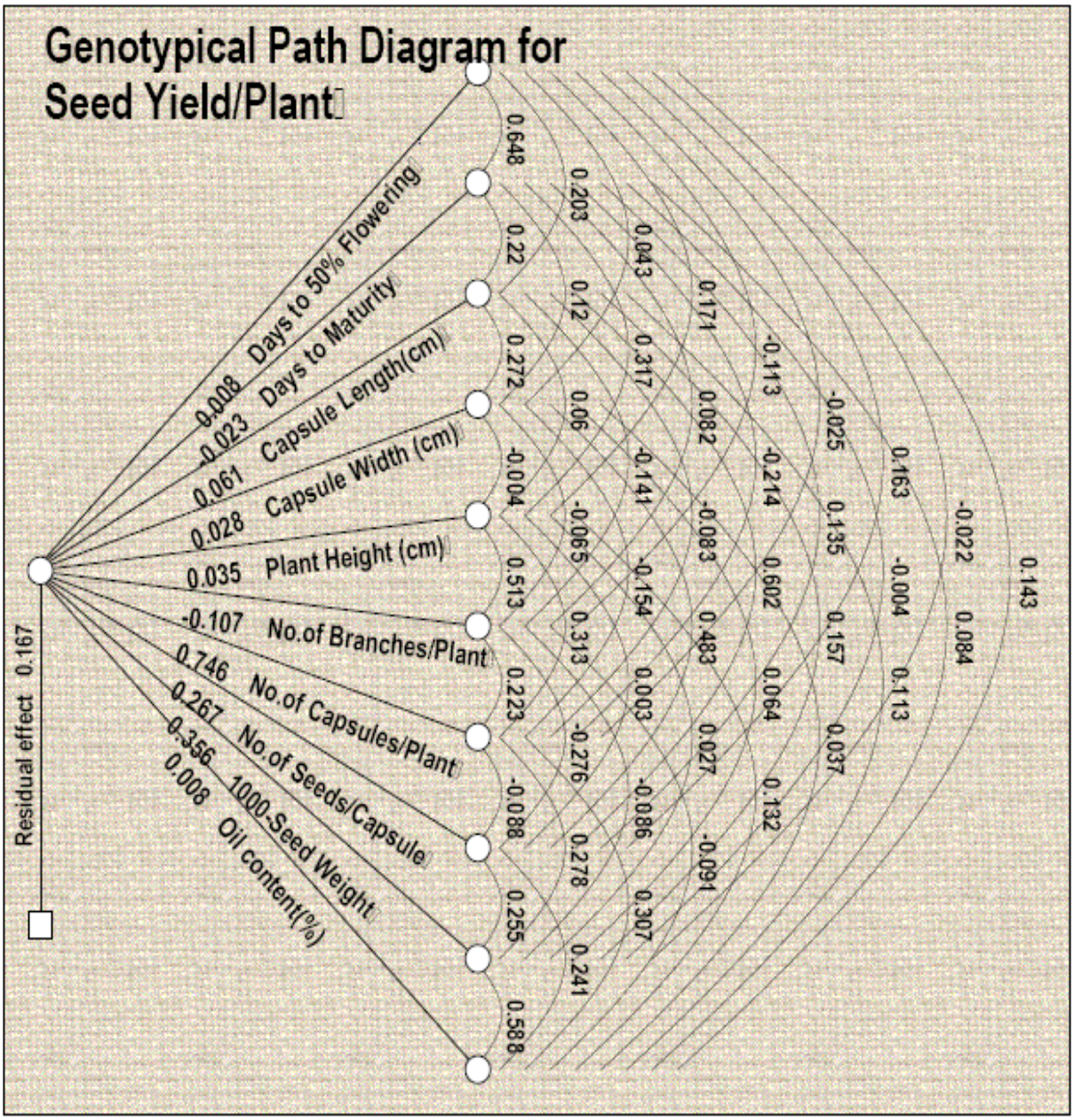

Fig 4.5: Genotypic path diagram for seed yield/plant.

4.6.6 Number of branches per plant

Number of branches had negative direct effect (-0.1073/-0.0921) on seed yield at both levels.

Positive indirect effects of this trait on seed yield per plant was recorded through number of capsules per plant (0.1666/0.1605) and plant height (0.0179/ 0.0158) at both the levels.

The negative non-significant correlation of capsule length with seed yield per plant (-0.0411/ -0.0262) was mainly due to indirect negative effects of this trait *via* number of seeds per capsule (-0.0737/-0.0741), 1000-seed weight (-0.0307/-0.0246), capsule length (-0.0086/-0.0059), days to maturity (-0.0019/-0.0025), capsule width (-0.0018/-0.0010), days to 50% flowering (-0.0009/-0.0016) and oil content (-0.0007/-0.0008) at both levels.

4.6.7 Number of capsules per plant

The positive significant correlation of number of capsules per plant with seed yield per plant (0.8605**/0.7935**) was mainly due to the direct contribution of this character towards seed yield per plant.

This trait showed negative indirect effects on seed yield per plant through, number of branches per plant (-0.0240/-0.0199), number of seeds per capsule (-0.0234/ -0.0289), capsule length (-0.0051/ -0.0029), capsule width (-0.0043/-0.0015), and days to 50% flowering (-0.0002/-0.0007) at phenotypic and genotypic levels.

However, number of seeds per capsule exhibited positive indirect effect *via* 1000-seed weight (0.0908/0.0863), plant height (0.0109/0.0095), and oil content (0.0024/0.0026) and days to maturity (0.0049/0.0066) at both genotypic and phenotypic levels.

4.6.8 Number of seeds per capsule

1000-seed weight had positive (0.2670/0.2961) direct effect at phenotypic and genotypic levels.

This trait showed positive significant association (0.3726**/0.3812**) with seed yield per plant at both levels. Indirect positive effects of this trait were exhibited *via* 1000-seed weight (0.0990/ 0.1040), capsule length (0.0366/0.0243), number of branches per plant (0.0296/ 0.0230), capsule width (0.0137/0.0057), and oil content (0.0024/0.0020) and days to 50% flowering (0.0013/0.0028). However, plant height recorded at positive indirect effect at genotypic level (0.0001) and negative indirect effect at phenotypic level (-0.0008).

This trait exhibited negative indirect effects on seed yield per plant through days to maturity (-0.0031/ -0.0037) and number of capsules per plant (-0.0653/-0.0723) at both the levels.

4.6.9 1000-seed weight (g)

The direct contribution of this character to seed yield per plant was positive (0.3562/0.3630) at both the levels and positive significant correlation of this trait with seed yield per plant (0.6578**/ 0.6437**) was mainly due to indirect positive effects on seed yield per plant manifested through number of capsules per plant (0.2075/0.1765), number of seeds per capsule (0.0680/0.0848), capsule length (0.0096/0.0060), number of branches per plant (0.0092/0.0062), oil content (0.0046/0.0051), capsule width (0.0018/0.0008), and plant height (0.0010/0.0008) at both the levels.

1000-seed weight recorded negative indirect effects on seed yield per plant *via* days to 50% flowering (-0.0002/-0.0001) at both the levels.

4.6.10 oil content (%)

Oil content reported positive direct effect on seed yield (0.0078/0.0093) at both levels. The positive significant correlation of oil content with seed yield (0.5325**/0.4941**) was mainl y due to indirect positive effects on seed yield manifested through number of capsules per plant (0.2291/0.2033), 1000-seed weight (0.2096/0.2001), number of seeds per capsule (0.0644/0.0641), number of branches per plant (0.0098/0.0081), capsule length (0.0069/0.0047), plant height (0.0046/0.0041), days to 50% flowering (0.0012/0.0018) and capsule width (0.0011/0.0005) at both levels.

The indirect negative effect was expressed *via,* days to maturity (-0.0019/-0.0020) at both levels.

The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. Hence, indirect selection by correlated response may not be some times fruitful. When many characters are affecting a given character, splitting the total correlation into direct and indirect effects of cause as devised by Wright (1921) would give more meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield components. This kind of information will be helpful in formulating the selection criteria, indicating the selection for these characters is likely to bring about an overall improvement in single plant yield directly.

Path coefficient analysis revealed that number of capsules per plant exerted the highest positive direct effect on seed yield followed by 1000-seed weight, capsule length, plant height, capsule width, days to 50% flowering and oil content at both levels of association. The traits *viz.*, number of branches and days to maturity exhibited negative direct effect at both the levels. Hence, the selection for these characters was likely to bring about an overall improvement in seed yield per plant directly. Therefore, it is suggested that preference should be given to these characters in the selection programme to isolate superior lines with genetic potentiality for high yield in sesame genotypes.

CHAPTER-V

DISCUSSION

Sesamum indicum L. known variously as gingelly, sesame, til, simsim *etc.*, is an important and very ancient oil-yielding species cultivated extensively in Indian sub-continent and also in the hotter and drier parts of Africa and the Mediterranean region. Sesame flourishes, in the tropical and sub-tropical regions, in the plains as well as up to an elevation of 4000 feet. It is an important crop as it is rich in oil (approx. 50 per cent) and protein (20-25 per cent)

For the improvement of any crop particularly of its yield, it is essential to have the knowledge of genetic variability for the characters that are associated with the yield. The extent of genetic variability available in the crop could be of immense value to the breeders to effectively design the breeding programmes for characters under improvement (Singh and Chaudhary, 1977). The genotypic coefficient of variation measures the range of variability available in crop species and also enables to compare the amount of variability present in different characters. However, the phenotypic expression of a character is the result of interaction between the genotype and environment. Hence, the total variance needs to be partitioned into heritable and non-heritable components so as to assess the true breeding nature of a particular trait (Falconer, 1964).

The present study comprised of investigation on extent of variability, genetic diversity, correlation and direct and indirect effects of different traits and of yield in sesame.

The results obtained for 11 characters in 65 genotypes of sesame are discussed character wise and are presented hereunder with the following headings to draw valid conclusions.

Analysis of variance and mean performance

Heritability and genetic advance.

Genetic divergence

Character association

Path coefficient analysis.

5.1 ANALYSIS OF VARIANCE AND MEAN PERFORMANCE

The analysis of variance and mean performance of sesame genotypes for various characters under study is presented in table 4.1 the results revealed that mean sum of squares due to genotypes were significant for all the characters under study, which indicated the existence of adequate amount of genetic variability among the genotypes.

An examination of mean performance for different characters revealed that none of the genotypes showed consistent high performance for all the characters. However the JLT-408 recorded highest mean values in desirable

direction for seed yield, number of capsules per plant, capsule length, number of seeds per capsule, 1000-seed weight and oil content (%). Maduri also found promising for early flowering and maturity, number of capsules per plant, capsule length, number of seeds per capsules, 1000-seed weight, oil content (%) and seed yield per plant, the check variety Sweta followed by UKNM-2386, EC 310439, UKNM-1067, EC-S-0523A and EC-209 also found promising for seed yield and its component traits.

The presence of a wide spectrum of variability in the existing population will enhance the chances of selecting a desirable genotype. Besides genetic variability, the knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted to its progeny, thereby helps the breeder to employ a suitable breeding strategy to achieve the objective quickly. Therefore, for successful improvement of any crop, it is necessary to have a thorough knowledge on the variability together with the heritability which would give a better idea on the amount of genetic advance expected out of selection.

5.2 HERITABILITY AND GENETIC ADVANCE

5.2.1 Days to 50% flowering

It was evident from the results that phenotypic coefficient of variability is moderate and genotypic coefficient of variability is low for this trait. Similar results were reported by Gidey *et al.* (2012), Tripathi *et al.* (2013). High heritability coupled with moderate genetic advance as per cent of mean

recorded for this trait and hence hybridization followed by selection could be best option for exploiting non-additive gene action for creating more variability in days to 50% flowering. These results are in conformity with Gangadhara *et al.* (2012), Gidey *et al.* (2012), Tripathi *et al.* (2013), and Abate and Mekbib (2015).

5.2.2 Days to maturity

The estimates PCV and GCV were low for this trait. Similar results were reported by Thirumala Rao *et al.* (2012) Tripathi *et al.*(2013), Vanishree *et al.* (2011), Bharathi *et al.* (2015) and Hika (2015) *et al.* High heritability with moderate genetic advance as per cent of mean were recorded for this trait indicating the operation of both additive and non-additive genes and offers be st possibility of improvement of this trait. This is in accordance with the result s reported by Velu and Shunmugavalli (2005), Sudhakar (2011) *et al.*, Parame shawarappa (2008) *et al.*, Gangadhara (2012) *et al.* and Vanishree (2013) *et al.*

5.2.3 Capsule length (cm)

This character exhibited low variation both at phenotypic and genotypic levels. Similar findings were reported by Sumati and Muaralidharan (2010), Nayak *et al.* (2011), Ukaan and Ogbonna (2012), Shekawat *et al.* (2013a) Tiru mala Rao *etal.* (2012) and Tripathi *et al.* (2013). High heritability associated with moderate genetic advance as per cent of mean revealed that there is

scope for improving this trait through simple selection. Our results are in harmony with that of Shekhawat *et al.* (2013a), Thirumala Rao *et al.* (2013), Tripathi *et al.* (2013) and Bharathi *et al.* (2014) for low GCV and PCV. Velu and Shunmugavalli (2005), Sudhakar *et al.* (2007), Parameshawarappa *et al.* (2009) and Ismaila and Usman (2014) for high heritability coupled with moderate genetic advance as percent mean.

5.2.4 Capsule width (cm)

This trait offered low PCV and low GCV. High heritability coupled with moderate genetic advance as percent of mean recorded for this trait revealed the predominance of both additive and non-additive gene action. This offers the best opportunity for improvement of this trait through mass selection and progeny selection. Similar results were obtained by Sumati and Muaralidharan (2010) and Bamrotiya *et al.* (2016). While high heritability and moderate genetic advance as percent mean is observed for this trait suggesting presence of both additive and non-additive gene action, however low heritability and genetic advance as percent mean was reported by Sumati and Muaralidharan (2010) and high heritability and moderate genetic advance as percent mean reported by Bamrotiya *et al.* (2016).

5.2.5 Plant height (cm)

The estimates of PCV and GCV were moderate for this trait. High heritability coupled with moderate genetic advance was recorded for this

character indicating that there is a scope for improvement in this trait. These results were in line with that of Bharathi *et al.* (2014), Chandra Mohan (2014), Abate and Mekbib (2015) and Mahmoud *et al.* (2015). High heritability and genetic advance as per cent of mean were recorded for plant height which is indicating that, there is preponderance of additive gene action in controlling this trait. Hence, direct selection of the characters would be effective in improving the seed yield. These results are in accordance with the findings of Gangadhara *et al.* (2012), Ukaan and Ogbonna (2012), Thirumala Rao *et al.* (2013) and Vanishree *et al.* (2013).

5.2.6 Number of branches per plant

This trait exhibited high PCV and moderate GCV. Similar results were reported by reported by Gangadhararao *et al.* (2012), Hika *et al.* (2015) and Mahmoud *et al.* (2015). High heritability and high genetic advance as per cent of mean revealed predominance of additive gene action and offers a better chance for improvement of this trait through simple selection. Similar track of results were observed by Vanishree *et al.* (2013), Bharathi *et al.* (2014), Ismaila and Usman (2014), Hika *et al.* (2015) and Mahmoud *et al.* (2015).

5.2.7 Number of seeds per capsule

The magnitudes of genotypic and phenotypic coefficient of variation were found to be moderate. These results are in agreement with Gangadhara *et al.* (2012), Vanishree *et al.* (2013) and Bharathi *et al.* (2014). High

heritability combined with high genetic advance as per cent of mean suggests the operation of additive gene action for this trait. Therefore, simple direct selection could be enough for improving seeds per capsule. These results are in agreement with the findings of Gangadhara *et al.* (2012), Narayanan and Murugan (2013) and Vanishree *et al.* (2013)

5.2.8 Number of capsules per plant

Both PCV and GCV estimates were high for number of capsules per plant. Gidey *et al.* (2012), Revathi *et al.* (2012), Thirumala Rao *et al.* (2013) and Vanishree *et al.* (2013) for this character. High heritability and high genetic advance as a per cent of mean were observed for this trait indicating the additive gene action and improvement could be done for this trait by simple direct selection. The results are in conformity with the findings of Vanishree *et al.* (2013), Bharathi *et al.* (2014), Chandra Mohan (2014) and Mahmoud *et al.* (2015).

5.2.9 Seed yield per plant (g)

This trait offered high PCV and GCV. The results are in accordance with Bharathi *et al.* (2014), Chandra Mohan (2014), Hika *et al.* (2015) and M ahmoud *et al.* (2015). High heritability associated with high genetic advance as per cent of mean was recorded for seed yield revealing the presence of additive genetic components and direct simple selection is enough for genetic

improvement. Similar findings were reported by Tripathi *et al.* (2013), Vanishree *et al.* (2013), Hika *et al.* (2015) and Mahmoud *et al.* (2015).

5.2.10 1000-seed weight (g) (g)

The magnitude of GCV and PCV were found to be moderate and high respectively. Whereas Narayanan and Murugan (2013) and Tripathi *et al.* (2013) noticed high PCV and GCV for this character, while Bharathi *et al.* (2014), Ismaila and Usman (2014) and Abate and Mekbib (2015) observed moderate GCV and PCV values. High heritability along with high genetic advance as a per cent mean recorded for this trait reveals the presence of additive gene action and improvement could be done for this trait through simple direct selection. Similar track of results were reported by Gangadhara Rao (2011), Gangadhara *et al.* (2012) and Vanishree *et al.* (2013).

5.2.11 Oil content (%)

This trait offered low GCV and PCV values. The results were in accordance with Velu and Shunmugavalli (2005), Abate (2015) and Saxena *et al.* (2016). High heritability coupled with moderate genetic advance as percent mean suggesting presence of both additive and non-additive gene action for this trait. The similar results were reported by Babu *et al.* (2004), Valarmathi *et al.* (2004), Velu and Shunmugavalli (2005) and Saxena *et al.* (2016).

In the present study, wide variability was observed for plant height (cm), capsules per plant, seeds per capsule, oil content (%) and seed yield per plant (g) in terms of mean values and range. When coefficients of variation (PCV and GCV) are considered, high mean was recorded for seed yield per plant and number of capsules per plant. Whereas other traits with wide range of variability, recorded moderate PCV and GCV values. The traits *viz.,* days to 50% flowering, days to maturity, capsule length and capsule width recorded narrow range of variability as well as low PCV and GCV values.

All of the traits recorded high heritability values. Plant height, number of branches, number of capsules per plant, number of seeds per capsule, seed yield and 1000-seed weight (g) registered high heritability coupled with high genetic advance as per cent of mean indicating the influence of additive gene action in the direction of desired improvement. High heritability with moderate genetic advance was recorded for days to 50% flowering, days to maturity, capsule length, capsule width and oil content suggesting the role of both additive and non-additive gene actions and direct selection for these traits may yield moderate genetic gains.

5.3 GENETIC DIVERGENCE

For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses made between the parents with maximum genetic divergence are more likely to yield desirable recombinants in the progenies. However, it is desirable to select suitable and genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm (Singh, 1998). Hence, the present study was undertaken to assess the nature and the magnitude of genetic diversity to identify suitable donors having wider genetic base in sesame.

5.3.1 D^2 analysis

The multivariate D^2 analysis using Mahalanobis' D^2 statistic provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). Further the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between the populations (Rao, 1952).

The data collected on eleven yield and yield contributing characters from 65 genotypes of sesame were subjected to multivariate analysis. Genetic divergence was estimated by using Mahalanobis' D^2 statistic. The magnitude

of D^2 values suggested that there was considerable variability in the material studied, which led to genetic diversity.

Based on D^2 analysis the pattern of distribution of 65 genotypes into 4 clusters was at random with maximum number of genotypes (60) in cluster I comprising genotypes *viz.*, GM-NIC- 16146,K-5170, TKG-22, SI-413-A, ES-113-18-84, NIC-10621, NIC-8263, SI-1147, SI-199-2-84, GM-NIC- 8254, ES-42-2-84, EC-209, EC-S-0223, EC-231-2-84, EC-89111, NIC-16114, NIC-16324, GM-NIC- 7909, GM-NIC- 16332, GM-NIC- 7913, GM-NIC- 16226, ES-44, NIC-7903, KMR-114, JLT-07, GM-NIC- 16330, EC-S-0523A, IS-299A, IC-41962, ES-146-1-84, UKNM-2386, EC-370936, PKDS-8, SI-983, NIC-16220, IC-23233, NIC-16104, OSC-3209, KMR-69, IC-204001, IC-42200, GM-NIC- 8202, DS-21, IS-207, GM-NIC- 8934, SI-205-61, YLM-17, EC-101396, EC-310439, EC-377015, GM-NIC- 8631, EC-303423, SI-5354, SI-3168, SI-1003, EC-370840, NIC-7855, IS-424, GT-3 andG-1. Cluster II possessed 3 genotypes *viz.*, UKNM-1067, TKG-306 and SWETA. Cluster III and Cluster IV consisted single genotypes each *viz.*, Maduri and JLT-408 respectively.

The pattern of distribution of genotypes from different eco-geographical regions into different clusters with different divergence values was at random supporting that geographical diversity is not related to genetic diversity. The

main forces other than geographical origin responsible for this genetic diversity may be natural and artificial selection, exchange of breeding material, genetic drift and environmental variation. Similar conclusions were drawn by Shekawat *et al.* (2013), Tripathi *et al.* (2013), Chandra Mohan *et al.* (2014) and Abate and Mekbib (2015).

The genotypes of common geographic origin or same location also were grouped into different clusters as evidenced by the distribution of genotypes from Jabalpur (M.P) into different clusters. K-5170, DCR-1794, SI-5354, VB-7901, SI-75, EC-357308 were grouped in cluster I, while PS-201 and DCB-1799 into cluster II and III, respectively. The results are in accordance with Ganesh and Thangavelu (1995) and Swain and Dikshit (1997) and Gangadhara Rao (2004).

The results on character wise contributed towards total genetic divergence shows that no single trait had a great contribution to total divergence. Relative contribution of 1000-seed weight (g) was maximum (18.51.%) towards diversity followed by days to maturity (16.30%), oil content (13.13%), number of seeds per capsule (11.88%), capsule length (11.59%), seed yield per plant (10.05%), number of branches (9.28) in that order. While the contribution of other four characters towards divergence was negligible. These results are in agreement with Sudhakar *et al.* (2006), Parameshawarappa *et al.* (2009), they reported higher contribution of 1000-

seed weight (g), seed yield per plant, number of branches per plant and plant height towards divergence. Similar track of findings was reported by Tripathy *et al.* (2013) for 1000-seed weight (g), Gangadhararao *et al.* (2012) for oil content and seeds per capsule. No report suggested contribution of days to maturity is maximum towards diversity. It was suggested that characters with maximum contribution towards diversity should also be given due consideration for sesame improvement.

The inter-cluster D^2 values were higher than the intra-cluster D^2 values. The maximum inter-cluster distance were observed between cluster I and IV (24.75) followed by cluster I and II (17.90) and least inter-cluster value was observed between I and III (15.88) followed by cluster II and III (17.68). Out of 4 clusters formed, two clusters III and IV are solitary and had no intra-cluster distances. Based on these studies crosses may be attempted between the genotypes of cluster III (Maduri) and cluster IV (JLT-408) to obtain new desirable recombinants in sesame. On the other hand, minimum distance occurred between cluster III and cluster IV (15.42) indicated almost parallel diversity among the genotypes included in this clusters. Maximum intra-cluster D^2 value was observed in cluster-IV (24.75) followed by cluster-II (17.90). The highest intra cluster distance in cluster-II indicates the presence of wide genetic diversity among the genotypes (UKNM-1067, TKG-306 and SWETA) within the cluster.

There was a wide range of cluster mean values among the characters studied, indicating the presence of variation among genotypes studied. Cluster-IV with single genotype *viz.,* JLT-408 had highest mean values for six characters *viz.*, days to 50% flowering, capsule length, number of seeds per capsule, seed yield per plant, 1000-seed weight (g), and oil content. While cluster III with single genotype (Maduri) had highest value for capsule width and number of seeds per capsule and cluster II (UKNM-1067, TKG-306 and SWETA) had highest values for days to maturity, plant height and number of branches per plant. So genotypes in these clusters can be used for creating variability for these yield component traits.

Based on multivariate analysis, the two clusters IV and III with single genotypes JLT-408 and Maduri respectively scored high mean values for 8 characters which are considered as important economic attributes. As the magnitude of heterosis depends largely on the degree of genetic diversity of parental lines, the genotypes JLT-408 belonging to cluster IV and Maduri from cluster III can be used to derive a broad spectrum of genetic variability in the segregating generations for seed yield per plant.

5.3.2 Principal component analysis

In the present investigation, the principal component analysis was performed on the correlation matrix of the traits, thereby removing the effects of scale. PCA will allow visualization of the differences among the individuals and identify possible groups. Principal component analysis was carried out to transform the interdependent traits into a set of independent

traits as well as to reduce the dimensionality data structure. Agglomerative hierarchical cluster analysis (canonical roots analysis) was followed to group the genotypes into various clusters. Results of PCA are discussed hereunder.

The first four principal components with eigene value more than one contributed 76.55 per cent of cumulative variability among 65 genotypes evaluated for 11 quantitative characters. Other principal component with eigene value less than one were considered as non-significant and were ignored as they were unlikely to have any practical significance.

Characters *viz.,* days to 50% flowering, days to maturity, capsule length, capsule width, plant height, number of branches, number of capsule, number of seeds, seed yield, 1000-seed weight (g) and oil content were loaded in first principal component and explained maximum variance in PCA. The characters *viz.,* seed yield per plant, 1000-seed weight (g), oil content (%), number of capsules per plant, days to maturity, number of seeds per capsule, plant height, capsule length, days to 50% flowering and plant height showed a greatest positive weight on first principal component (PC_1), whereas number of branches per plant and capsule width had a substantial negative weight. The performance of characters contribution suggests that the accessions that emphasize on more number of capsules per plant, high 1000-seed weight (g) and oil content (%) tend to have high seed yield per plant.

The second principal component (PC_2), accounted for 22.95 per cent of total variance, which reflected significant loadings of number of seeds per

capsule, days to maturity, capsule length, oil content, days to 50% flowering and plant height in a positive direction. However, the relative contributions are more important than the signs (indicative of direction) in principal component analysis. Thereby it suggests that the accessions with more seeds per capsule, capsules per plant and days to maturity tend to have high seed yield per plant.

The third principal component (PC_3), which described 10.86 per cent of total variance, which reflected significant loading of seeds per capsule, capsule length, oil content, number of capsules, capsule width and seed yield per plant had substantial positive weight.

In fourth principal component (PC_4), which accounted for about 8.86 per cent of total variance, reflected significant loading of number of capsules, plant height, days to 50% flowering, oil content, number of branches per plant, days to maturity and seed yield per plant with substantial positive weight.

The PCA scores for 65 genotypes in first four principal components with eigene value more than one were considered for plotting of genotypes in 3D scattered diagram. These three PCA scores for genotypes were plotted in graph to get the 3D PCA I as X-axis, PCA-II as Y-axis and PCA III as Z-axis scattered diagram. The genotypes of divergent clusters like 62 (JLT-408) and 46 (SI-5354) scattered far apart in the 3D plot. The genotypes falling in same cluster are placed close to each other in the center in the scattered diagram.

The genotypes JLT-408 (62), UKNM-1067(31), TKG-306 (60) and Sweta (65) showed maximum variance through PC I axis and these genotypes are considered to be highly divergent with required variability for further improvement in plant breeding programme. While, the genotypes IS-424 (47), SI-103(52), SI-3168(48) and DS-21(44) showed low variance on both sides of the axis so it may be considered that these genotypes are less efficient in breeding programme to improve yield unless they have special added advantage of high oil content in them.

In the present investigation 3D plot, indicated the grouping of genotypes of same cluster falling nearer to each other. For example, the genotypes UKNM-1067, TKG-306 and Sweta of cluster II fall nearer to each other on the positive axis of PC I. There are also indications of different genotypes of different clusters falling nearer to each other *i.e.*, JLT-408(62) (IV), UKNM-1067(31) (II), TKG-306(60) (II), Sweta(65) (II), GM-NIC-16330(18) (I), Maduri(63) (III) and ES-146-1-84(7) (I) fall nearer to each other even they belong to different clusters. While genotypes 48(SI-3168), 2(SI-205-61), 15(GM-NIC-8934), 1(SI-413-A) and 13(GM-NIC-8202) fall away from other genotypes indicating their specificity in clustering.

The principal component scores of genotypes were used as input for clustering procedures in order to group the genotypes into various clusters and confirm the results of principal component analysis.

5.3.3 Hierarchical cluster analysis

The varietal composition of the clusters indicated that the clustering of the varieties did not follow their geographic distribution as varieties from diverse sources were grouped in to the same clusters as similar to Mahalanobis' D^2 analysis.

In the present investigation, the genotype Sweta from Telangana and TKG-306 from Maharastra and UKNM-1067 from Jabalpur (M.P) are included in cluster II. Similarly JLT-408 and Madhuri are of Maharastra origin are included in clusters IV and III respectively. Cluster I is largest group consisting of 60 genotypes are selections from both Jabalpur and Maharastra. Therefore it is clearly indicating that Divergence not matched with geographical origin.

The relative importance of yield components contributing towards divergence can be judged by comparing group means of 11 characters. Cluster I had no high mean values for any of the 11 characters. Cluster IV recorded high mean value for most of important economic attributes like, days to 50% flowering, capsule length, number of seeds per capsule, seed yield per plant, 1000-seed weight (g), and oil content. Cluster III noticed high mean values for capsule width and number of seeds per capsule and Cluster II shown high mean values for days to maturity, plant height and number of branches per

plant. Inter crossing the genotypes from these clusters might result in wide array of variability for exercising effective selection for these traits.

The analysis showed that the genotypes in clusters IV, III and II had high cluster mean values for days to 50% flowering, capsule length, number of seeds per capsule, seed yield per plant, 1000-seed weight (g), and oil content, capsule width and number of seeds per capsule, days to maturity, plant height and number of branches per plant. The genotype JLT-408 from cluster IV, Maduri from cluster III and TKG-306, UKNM-1067 and Sweta can be effectively used for breeding programme.

Results of cluster analysis based on PCA scores were compared with results of the principal component analysis as a visual aid in discerning clusters in the 3D scattered diagram. The genotypes falling in same cluster represent closer to each other in scattered diagram.

Utilization of principal component analysis combined with clustering by Ward's method in genetic diversity in pulses studies was reported by Ghafoor *et al.* (2001), Subramanian and Muthaiah (2003), Saxena *et al.* (2005) and Sanjeev Gupta *et al.* (2005).

5.3.4Comparative study of D^2 analysis principal component analysis and cluster analysis

The grouping or clustering pattern using the D^2 analysis, principal component analysis and cluster analysis was compared and the implications are discussed here.

All the methods of grouping revealed a single concept of non-correspondence of genetic divergence and geographic diversity. In D^2 analysis, the intra- and inter-cluster distances are less while in the cluster analysis the distances are high as the standardization of the data by analysis made the attribute contribute equally to the divergence studies irrespective of the units taken. This is the same with the utilization of correlation matrix in principal component analysis derived from covariance matrix. This standardization made the principal component analysis to support the cluster analysis.

In the present investigation the genotypes JLT-408, Maduri, UKNM-1067, TKG-306 and Sweta (Showed maximum variance through PC1 axis and these genotypes are considered to be highly divergent) which were on the extreme positive side of PC1 axis in PCA 3D plot (Fig. 4.3a) indicating that these are better genotypes. The genotypes belonging to the common cluster have fallen nearer to each other and vice versa both in PC analysis and cluster analysis there by confirming the results of cluster analysis.

Comparative study of the intra-and inter-cluster distance based on D^2 analysis and cluster analysis showed the results as the intra-cluster distance ranged from zero to 13.55 in D^2 analysis. Similarly the inter-cluster distances ranged from 15.42 (III and IV) to 24.75 (VI and VII) in D^2 analysis and from 46.116 (VII and VIII) to 374.994 (I and IV) in cluster analysis.

The principal component analysis sorted out the total variables into four main principal components and the contribution of the main variables for variance is easily identified by the variables loaded on the PC1 and the cumulative variability studied up to the 4 PC will help to in-depth analysis for divergence. For example, D^2 analysis the variables 1000-seed weight (g) and days to maturity contributed more for the divergence but through PCA the important traits, seed yield (g), 1000-seed weight (g), oil content (%) and capsules per plant etc., were identified as the traits loaded on the first PC1. In a broad sense all the three methods of classifying genotypes into different groups were comparable but hierarchical cluster analysis gave an additional advantage of identifying sub-cluster of the major groups at different levels so that each small group can be critically analyzed.

Thus the present study has successfully classified different genotypes based on various morphological characters and reduced large number of variables into only four principal components and identified genotypes better for different combinations. The results of the present study can be used as a stepping stone for evolving well defined approach based on evaluation and

characterization of variation in sesame and can be utilized in various breeding programmes depending on their specific objectives.

5.4 Character association

Breeding for high yield is the major objective in any crop improvement programme. A study of the association of yield components with yield is useful for choosing the characters, which have a definite role in influencing the yield and may aid in selection from the breeding material. A better understanding of the contribution of such traits in building up the genetic makeup of the crop may be obtained through correlation. Genotypic correlations in general were higher than phenotypic correlations. This may be due to the relative stability of genotypes as majority of them were subjected to certain amount of selection (Johnson *et al.* 1955).

The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because selection on any particular trait may bring about undesirable changes in other associated characters.

In the present investigation, correlation estimates obtained for 11 yield component characters of sesame are discussed hereunder.

The correlation between seed yield per plant with different yield attributes and among the attributes themselves are presented in Table 4.8. Seed yield per plant recorded significant and positive association with capsule length (cm), plant height (cm), number of capsules, number of seeds, 1000-

seed weight (g) and oil content (%) at both phenotypic and genotypic levels. Based on the magnitude of correlation coefficient values capsules per plant, seeds per capsule and 1000-seed weight may be regarded as very closely related characters with seed yield per plant. Hence, higher yield could be obtained by exerting selection pressure over any of these traits. The results are in accordance with the earlier reports of Ismaila and Usman (2014) for capsule length and plant height, Bharathi *et al.* (2015), Fazal *et al.* (2015) and Mahmoud *et al.* (2015) for number of capsules, number of seeds per capsule and 1000-seed weight, Kumar *et al.* (2012) and Tripathy *et al.* (2016) reported positive correlation for oil content. Therefore, these characters can be used as selection criteria for improving seed yield per plant.

The characters days to maturity, capsule width exhibited positive non-significant association with seed yield.

5.4.1 Days to 50% flowering

The character days to 50% flowering had positive significant association with days to maturity and capsule length. These results were in agreement with Thirumala Rao *et al.* (2013), Vanishree *et al.* (2013) and Bharathi *et al.* (2015) for days to maturity and Shekhawat *et al.* (2013) and Abate and Mekbib (2015) for capsule length.

This trait shown positive non-significant association with seed yield and similar results are reported by Tirumalarao *et al.* (2013), Vanishree *et al.* (2013) and Mahmoud *et al.* (2015).

5.4.2 Days to maturity

The trait days to maturity had positive significant association with days to 50 flowering, capsule length and plant height and shown negative significant association with number of capsules per plant. These results are in agreement with Vanishree *et al.* (2013) and Bharathi *et al.* (2015) for days to 50% flowering and plant height, Gangadhara *et al.* (2012) for capsule length.

Seed yield shown negative non-significant association with this trait. Kumar *et al.* (2012), Tirumalarao *et al.* (2013) and Abate and Mekbib (2015) reported similar findings

5.4.3 Capsule length (cm)

This trait capsule length had positive significant association with days to 50% flowering, days to maturity, capsule width and number of seeds per capsule. These results are in harmony with Gangadhara *et al.* (2012) for days to maturity, Shekawat *et al.* (2013) and Abate and Mekbib (2015) for days to 50% flowering.

Seed yield had positive non-significant association with this trait. This trait is an important character contributes for the seed yield and similar

findings were reported by Gidey *et al.* (2012), Abate and Mekbib (2015) and Bharathi *et al.* (2015).

5.4.4 Capsule width (cm)

Capsule width has positive significant correlation with capsule length and number of seeds per capsule and shown positive non-significant association with seed yield. Tripathy *et al.* (2016) reported positive non-significant association of capsule width with seed yield.

5.4.5 Plant height (cm)

The trait Plant height is an important character which majorly contributes for yield, which provides space for more number of capsules and this is an additive character. This trait shown positive significant association with days to maturity, number of branches, number of capsules and seed yield. The positive significant association of plant height with days to maturity reported by Vanishree *et al.* (2013) and Bharathi *et al.* (2015) and Fazal *et al.* (2015) for number of branches, number of capsules per plant and seed yield.

5.4.6 Number of branches per plant

This trait shown positive association with plant height, number of capsules and number of seeds per capsules. Seed yield per plant had negative non-significant association with this trait.

These results are in harmony with Shekawat *et al.* (2013) for plant height and number of capsules per plant. Gnanashekaran *et al.* (2008) and Gangadhara *et al.* (2012) for number of seeds per capsule. Mukhekar *et al.* (2002) and Bharathi *et al.* (2015) reported negative non-significant association of this trait with seed yield.

5.4.7 Number of capsules per plant

The trait number of capsules per plant had positive significant association with plant height, number of branches, 1000-seed weight, oil content and seed yield.

Number of capsules directly contributes for seed yield. Similar track of results are reported by Vanishree *et al.* (2013) and Bharathi *et al.* (2015) for plant height. Gangadhara *et al.* (2012) and Shekawat *et al.* (2013) for number of branches, Bharathi *et al.* (2015) and Fazal *et al.* (2015) for 1000-seed weight and Tripathy *et al.* (2016) at phenotypic level for oil content. Bharathi *et al.* (2015), Fazal *et al.* (2015) and Mahmoud *et al.* (2015) for seed yield.

5.4.8 Number of seeds per capsules

This trait directly contributes towards the seed yield and this trait shown high positive significant association with capsule length, capsule width, seed yield, 1000-seed weight and oil content.

These results are in accordance with Vanishree *et al.* (2013) and Bharathi *et al.* (2015) for capsule length, 1000-seed weight and seed yield, Tripathy *et al.* (2016) for capsule width and oil content.

5.4.9 1000-seed weight (g)

The 1000-seed weight exhibited high positive significant association with seed yield, oil content, number of seeds per capsule and number of capsules per plant. The results obtained are in agreement with Vanishree *et al.* (2013), Bharathi *et al.* (2015) and Fazal *et al.* (2015).

5.4.10 Oil content (%)

The oil content an important economic character in sesame. This trait shown high positive significant association with 1000-seed weight, seed yield, number of capsules per plant and number of seeds per capsule.

The similar results are reported by Pawar *et al.* (2002) and Babu *et al.* (2004) for number of capsules, Rai *et al.* (1997) and Tripathy *et al.* (2016) at phenotypic level for number of seeds per capsule, Pawar *et al.* (2002) for seed yield.

5.4.11 Seed yield/plant (g)

The seed yield per plant had shown high positive significant association with number of capsules per plant, 1000-seed weight, oil content, number of seeds per capsule, capsule length and plant height.

These results on par with Thirumala Rao *et al.* (2013), Fazal *et al.* (2015) and Bharathi *et al.* (2015) for number of capsules, number of seeds and 1000-seed weight, Abate and Mekbib (2015) and Bharathi *et al.* (2015) for capsule length and plant height and Pawar *et al.* (2002) for oil content.

Character association between the characters show phenomenon of corre lated response. The genetic factors responsible for correlated response are linkage and pleiotropy. Magnitude of correlation due to pleiotropy depends upon the direction of their effects. In the present study, correlation observed between any two characters which were also correlated with yield and these led to influence that association among different characters was mostly due to pleiotropy. The present investigation shows that 1000-seed weight (g) and oil content are positively correlated with each other and also correlated with seed yield. This may be due to pleiotropy.

But for some correlations one character was correlated with yield and other was not correlated with yield. This led to the association among the different characters mostly due to linkage and not due to pleiotropy. These were supported by the fact that the genetic variability parameters for some of the characters correlated with yield were not of same magnitude as that of yield (Mallikarjun *et al.,* 2003). Capsule width is not significantly correlated with yield, but this trait recorded positive association with capsule length, number of seeds, days to maturity, days to 50% flowering, 1000-seed weight and oil content. Association of these characters may be due to linkage. If

genes controlling different traits are tightly linked, selection of one trait may automatically favour the other linked traits, and correlated response is inevitable. However, unfavourable negative correlations can be broken by repeated hybridization between random individuals or more preferably selected ones. Bi-parental mating in selected F_2 segregants tends to achieve this goal with remarkable rapidity.

5.5 Path coefficient analysis

The correlation coefficient between yield and a particular yield component was the net result of direct effect of that attribute and indirect effect through other yield contributing traits. The total correlation between yield and a component trait may sometimes be misleading as it might be an over-estimate or under-estimate. Hence direct selection by correlation response may not fruitful. Therefore, it is necessary to partition the total correlation coefficients into direct and indirect effect of cause as devised by Wright (1921).

If the correlation coefficient between causal factor and the effect is almost equal to its direct effect, this correlation explains the true relationship and direct selection through this trait will be useful. If the correlation coefficient is positive, but if the direct effect is negative or negligible, the indirect effect appears to be the cause of that positive correlation. In such situation, the other factors are to be considered simultaneously for selection. Sometimes, correlation coefficient may be negative, but the direct effect may be positive and high, under such circumstances, a restricted simultaneous

selection has to be followed *i.e.*, restriction has to be imposed to nullify the undesirable indirect effect in order to make use of the direct effect.

Based on the above, the characters subjected to correlations were also subjected to path coefficient analysis for estimating the direct and indirect effects, so as to formulate a sound basis for selection in sesame.

In the present study path coefficient analysis was performed for seed yield per plant taking it as a dependent variable and ten other characters *viz.*, days to 50% flowering, days to maturity, capsule length, capsule width, plant height, number of branches, number of capsules per plant, number of seeds per capsule, 1000-seed weight (g) and oil content (%) as independent variables. Both phenotypic and genotypic paths were worked out, since the phenotypic path will have a greater influence of environmental factors, the genotypic path was considered with a greater weightage.

It is observed that number of capsules per plant exhibited highest direct positive effect and indirect effect through other characters 1000-seed weight and plant height. Since this trait showing high correlation and high direct effect on seed yield per plant, one can improve the seed yield per plant by making selection for this character during yield improvement programme. These results are in agreement with Vanishree *et al.* (2013), Abate and Mekbib (2015), Bharathi *et al.* (2015) and Fazal *et al.* (2015).

Next to capsules per plant, 1000-seed weight (g) exhibited a considerable amount of direct effect on seed yield per plant at both genotypic

and phenotypic levels and its correlation with seed yield was also positively significant. It is indicated that 1000-seed weight should be considered as one of selection criteria for higher seed yield. Positive direct effect of this trait was also reported by Thirumala Rao *et al.* (2013), Vanishree *et al.* (2013), Abate and Mekbib (2015), Bharathi *et al.* (2015) and Fazal *et al.* (2015). This trait recorded indirect effects on seed yield per plant through days to 50% flowering at both levels.

Number of seeds per capsule exhibited good amount of direct effect on seed yield per plant and its correlation with this character was also positively significant. This character directly contributes to the seed yield. Hence it should be regarded as important criteria in selection programme. Similar findings were also reported by Shekawat *et al.* (2013), Vanishree *et al.* (2013), Bharathi *et al.* (2015) and Fazal *et al.* (2015). Capsule length also exhibited fair amount of direct effect and is correlated positively significant with seed yield per plant. This finding signifies the importance of this character during selection. This result is in harmony with the reports of Gidey *et al.* (2012) and Shekhawat *et al.* (2013).

Plant height influenced seed yield per plant by positive direct effect. These results are in agreement with Gangadhara *et al.* (2012), Shekawat *et al.* (2013), Vanishree *et al.* (2013) and Abate and Mekbib (2015).

Capsule width influenced seed yield per plant by positive direct effect. These results are in agreement with Bamrotiya *et al.* (2016). However

Sumathi and Muaralidharan (2010), Tripathy *et al.* (2016) reported negative association of this trait with seed yield.

Days to 50% flowering influenced seed yield per plant by low positive direct effect at both levels. These results are in agreement with Gangadhara *et al.* (2012), Kumar *et al.* (2012), Thirumala Rao *et al.* (2013), Vanishree *et al.* (2013) and Abate and Mekbib (2015).

Oil content influenced seed yield plant^{-1} by low positive direct effect at both levels. These results are in accordance with Abate and Mekbib (2015), Tripathy *et al.* (2016) and Saxena *et al.* (2016).

Days to maturity influenced seed yield per plant negatively direct effect at both levels. The similar reports were reported by Gidey *et al.* (2013), Kumar *et al.* (2012), Tirumalarao *et al.* (2013) and Abate and Mekbib (2015).

Number of branches also showed negative direct effect on seed yield at both levels. These results are in accordance with Vanishree *et al.* (2011), Bharathi *et al.* (2015) and Fazal *et al.* (2015).

In the present investigation direct effects are the main causes for the strong correlation exhibited by these characters with seed yield per plant. Indirect contribution of these characters towards yield is negligible.

The results indicated those characters with positive correlation have shown high direct effects. Hence, number of capsules, 1000-seed weight, oil

content (%), number of seeds per capsule, capsule length and plant height has high direct and correlation values.

The residual effect in the present study was found to be high at phenotypic level in path analysis indicating that there is a need to include other characters in order to drive a much clear picture of the causal relationship.

Chapter VI
SUMMERY AND CONCLUSIONS

The present investigation in sesame entitled “studies on genetic diversity, path analysis and correlation in sesame” was undertaken to generate the information on the extent of genetic variability, diversity, correlation and path analysis in sesame. The experimental material comprised of 65 germplasm lines and evaluated at oilseeds research station, Latur during the *kharif* 2016 in a randomized block design with two replications, observations recorded for eleven characters.

From the results and discussion on various aspects in the present investigation, the following conclusions could be drawn.

- Analysis of variance showed significant differences among the 65 genotypes for all the characters under study.

- Variability studies indicated that the material used in present investigation possessed variability, which provides sufficient basis for selection.

- The results on heritability (broad sense) revealed that all characters exhibited high heritability estimates.

- Presence of high heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of branches, number of capsules, seeds per capsule, 1000-seed weight (g) and seed

yield per plant indicating the operation of additive gene action and possibility of improving these characters through direct selection.

- The results of multivariate analysis indicated the presence of considerable genetic divergence among the 65 genotypes studied. The 65 genotypes were grouped into 4 clusters in D^2 analysis.

- The mode of distribution of genotypes from different ecological regions into different clusters was at random indicating that factors other than geographical isolation such as hybridization followed by natural selection exercised on the donor parents and free exchange of seed materials between different places may be responsible for observed divergence among the germplasm studied.

- 1000-seed weight (g) contributed maximum to genetic diversity followed by days to maturity, oil content (%), number of seeds per capsule, capsule length, and seed yield revealing the possibility of genetic improvement of these traits in the genotypes studied.

- The maximum inter cluster distance was observed between cluster I and cluster IV followed by cluster I and cluster II as per D^2 analysis. Hence crosses can be made between the genotypes of these clusters during hybridization programme for obtaining superior hybrids or segregants.

- Principal component analysis identified four principal components (PCs) with eigene values more than one contributed 76.52 per cent to cumulative variance. The population with high PC_1 values were characterized by seed yield per plant (g), 1000-seed weight (g), oil content (%), number of capsules per plant, days to maturity, number of seeds per capsule, capsule length and days to 50% flowering whereas population with high PC_2 values were characterized by number of seeds, day to maturity, capsule length, oil content (%), days to 50% flowering, plant height and capsules per plant.

- Genetic diversity studies by cluster analysis revealed that cluster II and cluster II had maximum inter cluster distances and cluster III and cluster IV shown zero distance. Hence, superior parents can selected from these divergent clusters for hybridization and crosses can be made for obtaining superior segregants.

- Correlation studies indicated that capsule length, plant height, number of capsules, number of seeds, 1000-seed weight and oil content (%) except days to 50% flowering and capsule width had significant positive association with seed yield.

- Path coefficient analysis revealed that high positive direct effect of number of capsules, number of seeds, 1000-seed weight and capsule length with seed yield. Therefore simultaneous selection for these traits is suggested for improvement of seed yield in sesame.

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- Path coefficient analysis revealed that high positive direct effect of number of capsules, number of seeds, 1000-seed weight and capsule length with seed yield. Therefore simultaneous selection for these traits is suggested for improvement of seed yield in sesame.

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*** Original not seen**

"STUDIES ON GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS IN SESAME (*Sesamum indicum* L.)

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ABSTRACT

In the present investigation, sixty five genotypes of sesame which are selected on the basis of duration, suitable for *kharif* season and yield were evaluated to study the genetic diversity present in the experimental material for selection of the diverse parents, to estimate the genetic variability parameters among the genotypes for yield, and the extent of association between yield and its component characters including direct and indirect effects. The experiment was laid out in a Randomized Block Design with two replications at Research farm, Oilseeds Research Station during *kharif*, 2016.

Analysis of variance indicated the existence of significant genotypic differences among the genotypes for yield and its components for all characters. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficient of variation indicating the effect of the environment. The high GCV and PCV values are observed for traits number of capsules plant^{-1} and seed yield^{-1}.

High heritability coupled with high genetic advance as per cent mean was observed for number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000-seed

weight and seed yield plant^{-1}indicating the influence of additive gene action, as such simple selection would likely to be effective for improvement of these traits.

Based on relative magnitude of D^2 values, the genotypes are grouped into four clusters. Clustering pattern of germplasm is not associated with the geographical distribution due to their morphological differences. Out of four clusters the cluster-I is the largest comprising of sixty genotypes followed by cluster-II comprising of three genotypes and remaining clusters III and IV were mono-genotypic clusters suggesting the ample amount of heterogeneity among the genotypes. Highest divergence occurred between the clusters I and IV followed by clusters I and II, II and IV, II and III and III and IV.

Based on the inter cluster distance, it is suggested that hybridization between the genotypes JLT-408 of cluster IV and Maduri of cluster III, JLT-408 of cluster IV and UKNM-1067, TKG 306 of cluster II, between Maduri of cluster III and UKNM-1067 of cluster II and between Maduri of cluster III and Sweta of cluster II are suggested to generate promising segregants for seed yield.

Seven characters 1000-seed weight, days to maturity, oil content, number of seeds capsule^{-1}, capsule length, seed yield plant^{-1} and number of branches plant^{-1} together contributed 90.74% towards the total divergence. The data means for four clusters indicated that the cluster IV is having highest mean value for days to 50% flowering, capsule length, number of capsules plant^{-1}, seed yield plant^{-1}, 1000 seed weight and oil content and cluster II for days to maturity, plant height and number of branches plant^{-1} and cluster III for capsule width and number of seeds capsule^{-1}.The promising genotypes from these clusters with high mean values for different traits may be directly used for adaptation as parents in future hybridization.

The results revealed that the estimates of phenotypic correlation coefficients were higher than the genotypic correlation coefficients.Capsule length, plant height, number of capsules, number of seeds, 1000-seed weight and oil content (%) had high significant positive association with seed yield.This indicated that simultaneous selection of all these characters was important for yield improvement.

A critical analysis of the results by path coefficient analysisrevealed that high positive direct effect of number of capsules, number of seeds, 1000-seed weight and capsule length with seed yield. Therefore simultaneous selection for these traits is suggested for improvement of seed yield in sesame.Hence, these traits were considered as important attributes in formulating selection criterion for achieving desired targets.