STUDIES ON GENETIC DIVERSITY IN ADVANCED MUTANT BREEDING LINES OF SESAME (*Sesamum indicum* L.)

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B.Sc. (Ag.)

MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)

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BY

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B.Sc. (Ag.)

THESIS SUBMITTED TO THE
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2018

DECLARATION

I, **Ms. K. DIVYA,** hereby declare that the thesis entitled **"STUDIES ON GENETIC DIVERSITY IN ADVANCED MUTANT BREEDING LINES OF SESAME (*Sesamum indicum* L.)"** submitted to the **Professor Jayashankar Telangana State Agricultural University,** for the degree of **Master of Science in Agriculture** is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place: Hyderabad **(K. DIVYA)**

Date: **I.D. No. RAM/16-54**

CERTIFICATE

Ms. K. DIVYA has satisfactorily prosecuted the course of research and that thesis entitled **"STUDIES ON GENETIC DIVERSITY IN ADVANCED MUTANT BREEDING LINES OF SESAME (*Sesamum indicum* L.)"** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by him/her for a degree of any University.

(T. SHOBHA RANI)

Date: **Chairperson**

CERTIFICATE

This is to certify that the thesis entitled **"STUDIES ON GENETIC DIVERSITY IN ADVANCED MUTANT BREEDING LINES OF SESAME (*Sesamum indicum* L.)"** submitted in partial fulfillment of the requirements for the degree of 'Master of Science in Agriculture' of the Professor Jayashankar Telangana State Agricultural University, Hyderabad is a record of the bonafide original research work carried out by **Ms. K. DIVYA** under our guidance and supervision.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance received during the course of the investigations have been duly acknowledged by the author of the thesis.

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(K. Divya)

Date:
Place:

LIST OF SYMBOLS AND ABBREVIATIONS

%	: Per cent
$\overline{X}$	: grand mean
χ^2	: Chi-square
$\sum$	: Summation
γ	: Gamma radiation
>	: greater than
ANOVA	: Analysis of variance
AICRP	: All India Coordinated Research Project
AVT	: Advanced Varietal Trial
bs	: broad sense
^{0}C	: Degree centigrade
CLS	: *Cercospora* leaf spot
cm	: Centimeter
cov.	: Covariance
d.f.	: degrees of freedom
et al.	: and others
etc.	: excetra
E	: East
F_1	: First filial generation
Fig	: Figure
g	: gram
G	: Genotypic
GA	: Genetic Advance
GAM	: Genetic Advance as percent of mean
GCV	: Genotypic Co-efficient of Variation
h^2	: Heritability in broad sense
i.e.	: that is
IVT	: Intial Varietal Trial
kg	: kilogram

$kgha^{-1}$	: kilogram per hectare
Kr	: kilo rad
m	: meter
m^2	: square meter
M_9	: 9^{th} mutation generation
min	: minimum
max	: maximum
MLT	: Multi-Location Trial
MSS	: Mean Sum of Squares
mm	: milli meter
N	: North
NBPGR	: National Bureau of Plant Genetic Resources
P	: Phenotypic
PCV	: Phenotypic Co-efficient of Variation
PDI	: Per cent Disease Index
PJTSAU	: Professor Jayashankar Telangana State Agricultural University
rp	: Phenotypic Correlation Co-efficient
rg	: Genotypic Correlation Co-efficient
r	: Correlation Co-efficient
RARS	: Regional Agricultural Research Station
RBD	: Randomized Block Design
RIL	: Recombinant inbred lines
S.Em	: Standard error difference from mean
S. No.	: Serial number
viz.	: Namely

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ABSTRACT

In the present investigation, a set of 133 genotypes comprised of mutant breeding lines (37), germplasm lines (31), local cultivar lines (15), promising germplasm lines (20), RILs (4), IVT's (12), AVT's (2), MLT's (4), popular varieties (4) and checks (3) were received from AICRP on sesame, RARS, Jagtial and UAS, Raichur. These genotypes were evaluated for genetic diversity for selection of diverse parents. Various genetic parameters for different yield and yield contributing traits and disease parameters along with the interrelationship of yield and yield traits with seed yield including direct and indirect effects were assessed. The experiment was laid out in a randomized block design with three replications at Regional Agricultural Research Station, Polasa, Jagtial, Karimnagar, during *kharif*, 2017.

Analysis of variance indicated the existence of significant genotypic differences among the genotypes for yield, its components and disease parameters except for test weight. Highest GCV, PCV, Heritability and genetic advance as per cent of mean were observed for the characters namely number of branches per plant, number of capsules per plant, seed yield per plant and phyllody (% incidence) indicating the influence of additive gene action, as such these traits can be improved through simple selection. The genotypes with highest means for these characters can be used in breeding programmes to develop into high yielding cultivars with disease resistance.

Based on the relative magnitude of D^2 values, the genotypes were distributed into 19 clusters. Out of them, cluster I being the largest with 54 genotypes and with one genotype each in 13 clusters forming the solitary clusters. The highest divergence occurred between cluster XIV and XV while the lowest was observed between clusters X and XI. The parents chosen from different clusters for hybridization generate promising segregants for seed yield.

Data on character means for these clusters indicated that the cluster III had highest mean, cluster XI for plant height and cluster XIV for days to maturity and plant height. Genotypes SDSN-15-98 and SGPS-17-15 were grouped into two clusters IV and XV respectively depicting more amount of diversity among them. Therefore, they can be confirmed for resistance and further can be used as donors in resistance breeding programme and they were found promising for disease resistance in field conditions. For seed yield, YLM-66 had highest mean which may be directly used as a parent in future hybridization with promising genotypes for development of high yielding resistant lines.

Correlation studies revealed that seed yield per plant showed positive significant association with number of capsules per plant, plant height, number of branches per plant and among characters between 50 per cent flowering and days to maturity. All the three diseases (phyllody (% incidence), *Alternaria* and *Cercospora* leaf spot) showed negative significance with seed yield, which indicated the severity of disease causing decrease in economic yield of the crop. While positive direct effect was highest with number of capsules per plant on seed yield followed by test weight and plant height. Biotic stress caused by diseases clearly revealed negative direct effect on seed yield.

The study resulted in identification of two resistant lines (SDSN-15-98 and SGP-17-15) and seven moderately resistant genotypes for phyllody. For *Alternaria* and *Cercospora* leaf spot none of the entries showed resistance reaction. The lines identified can be confirmed and used as donors in the resistance breeding programme. By imparting host plant resistance in the genotypes, the cost of cultivation decreases which is a very effective method.

Chapter I

INTRODUCTION

In the country oilseeds sector occupies an important position contributing to the Gross Domestic Product. India is still the world leader with maximum (25.8 %) production from the largest (29.8 %) area and highest export (40 %) of sesame in the world. In India, sesame is being grown over an area of 19.50 lakh hectares with production of 8.50 lakh tonnes and productivity of 436 $kgha^{-1}$ (www.indiastat.com, 2016). In Telangana, it is grown over an area of 0.14 lakh hectares with an annual production of 0.03 lakh tonnes and productivity of 214 $kgha^{-1}$ (www.indiasta.com, 2016). Major sesame growing states in India are West Bengal, Madhya Pradesh, Uttar Pradesh, Punjab and Gujarat. In Telangana state, it is grown as *summer* crop in Jagtial, Nizamabad, Nirmal, Adilabad, Karimnagar, Khammam, Asifabad and Mahaboobnagar *etc.* In recent years, its performance as a catch crop in *rabi* and after *Bt* cotton and turmeric in *summer* season and late *kharif* (under contingency) particularly in area under cultivation is encouraging.

Sesame (*Sesamum indicum* L.) is called the "**Queen of Oilseeds**". It is also known as 'benni seed', 'gingelly', 'simsim', 'til' *etc*., and the oldest and an ancient oil seed crop known to man. It is a short-day plant and cultivated extensively from tropical regions to the temperate zones in the world and its domestication lost in the mists of antiquity. The genus *Sesamum* belongs to the family Pedaliaceae and to order Tubiflore, which comprises 16 genera and 60 species, but only *Sesamum indicum* L. (2n = 26) has been recognized as cultivated species which has a wide distribution covering tropical Africa, Madagascar, Arabia, Srilanka, India, tropical Australia and a few of the Eastern Islands of the Malayan Archipelago. Other species like *S. laciniatumthis* (2n=28), *S. angolens, S. prostratum* are having 2n=32, *S. occidenale, S. radiatum* are having 2n=64. Along with the cultivated species of sesame others like *S. angustifolium, S. malabaricum, S. radiatum* are also harvested and eaten occasionally, particularly during famine or food shortage (Ashri, 2007).

Due to the presence of diverse wild species, Africa is considered the primary centre of origin, while, India and Japan are considered as the two secondary centers of origin of this crop. India, China, Sudan, Mexico, Turkey, Burma and Pakistan are the important sesame producing countries. The historic origin of sesame was favored by its ability to grow in areas that do not support the growth of other crops. It is also

a robust crop that needs little farming support it grows in drought conditions with residual moisture. Sesame has been called a survivor crop (Langham, 2007).

Sesame is considered to have both nutritional and medicinal values. The seeds are used either decorticated or whole in sweets such as sesame bars and halva, in baked products, or milled to get high-grade edible oil or tahini, an oily paste (Bedigian, 2004). Tahini is widely used in foods in the Middle East. Sesame seed contains 50-60 % oil and 19-25 % protein with two lignans *i.e.*, sesamin and sesamolin, which prevent rancidity and gives sesame oil long shelf life. The lignan contents have useful physiological effects in human and animal health (Ashakumary *et al*., 1999). The phenolic groups (benzodioxide) of molecules are generally responsible for the anti-oxidant activity and also possess anti- tumor, anti-cancer and many other biological activities. The principal unsaturated fatty acids (80%) are oleic and linoleic with about 40 % of each and about 14 % saturated acids.

The seeds are very rich in iron, magnesium, manganese, copper and calcium (90 mg per tablespoon for un-hulled seeds, 10 mg for hulled), and contain vitamin B1 (thiamine) and vitamin E (tocopherol). Sesame seeds also contain phytosterols associated with reduced levels of blood cholesterol (Bedigian, 2004).

It is noteworthy that in recent times sesame seeds have been found to contain immunoglobulin E (IgE) - mediated food allergens, with research reports from Israel (Dalal *et al*., 2002) and France (Agne *et al.,* 2003). Sesame, as a quality oilseed crop, can help tide over the problem of edible oil shortage in the country if production and productivity is enhanced.

Despite, sesame possessing high nutritional value and resistance to abiotic stress like drought it has low yielding capacity compared to other oilseed crops. The low ranking of sesame among the oilseed crops may be attributed to several factors including its susceptibility to pests and diseases, seed shattering, indeterminate growth habit and strong competition from other oil crops such as soybean, sunflower and groundnut. Further, sesame has been given less attention by the farmers because of poor yield due to non-availability of cultivars to suit the diverse agro-climatic conditions. Hence, development of improved high yielding cultivars adapted to local conditions has become top priority.

Creation of newer variation for morphological, yield and yield attributing traits is possible through germplasm augmentation, hybridization and mutation breeding. Yield being a complex character, is collectively influenced by various

component characters, which is polygenically inherited and subjected to environmental variation. Critical analysis of genetic variability present in the germplasm of a crop and its estimation is a pre-requisite for initiating any crop improvement programme as well as adopting appropriate selection techniques and helps breeding of high yielding and good quality cultivars that will increase production.

Heritability indicates the extent of transmissibility of a character into future generations. It is very difficult to judge whether observed variability is heritable or non-heritable. Hence, the knowledge of heritability is also essential for selection of component traits for yield improvement. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected.

A study of interrelationships among the contributing characters with seed yield will be of great significance in planning successful breeding strategies in any crop. Besides partitioning of the variance into genotypic and phenotypic, interrelationships existing among yield and its components and their contribution towards yield are of great value in planning and evaluating breeding programmes. Further, path coefficient analysis is helpful in the partitioning of correlation coefficient into direct and indirect effects, which reveals the relative contribution of each component to the yield among the genotypes.

Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different characters and ultimately for rational use of genetic resources. D^2 analysis is a useful statistical method for analyzing the various causative factors and their interrelationships operating on and within the plant populations, under natural and human selections.

The production and productivity was declined due to many biotic and abiotic stresses. Among the biotic stresses, diseases are causing substantial yield losses. Among the diseases, phyllody, powdery mildew, *Alternaria* and *Cercospora* leaf spot and *Macrophomina* root rot are of more concern to southern India. Phyllody is caused by phloem limiting Mycoplasma-like organism (phytoplasma) and transmitted by leafhopper *Orosius albicinctus.* The affected plants become stunted and the floral parts get modified into leafy structures bearing no fruits and seeds causing yield loss up to 100 %. This is because of hormonal imbalance in plants. Development of resistant varieties against phyllody is one of the thrust areas

identified in sesame crop improvement programme. *Alternaria* leaf spot of sesame caused by *Alternaria sesame* or *Alternaria sesamicola* is a major fungal disease distributed throughout the sesame growing areas of India. It is also reported to be seed borne disease. *Cercospora* leaf spot is caused by *Cercospora sesame* or *Cercospora sesamicola*. It occurs at 4-6 leaf stage and continues till maturity. Powdery mildew disease is another common disease, especially in southern India during *summer* season. It is known to be caused by many different pathogens of fungal origin *viz*., *Oidium erysiphoides, Leveillula taurica, Sphaerotheca fuliginea* and *Erysiphe cichoracearum etc*. The disease causes yield loss between 25 and 50% depending on the level and severity. The incidence or occurance of disease under field conditions at Jagtial center may vary from season to season. It is considered as one of the hot spots centers for evaluation of genotypes for resistance against key diseases (AICRP on sesame).

For creation of newer variability and multiple disease resistance, mutant lines were developed by irradiation through Gamma (γ) rays of different doses. These mutants were advanced to M_9 generations to make uniform at phenotypic levels. Hence, the present investigation was planned to see that the variability available in mutants and RILs which form advanced breeding lines along with advanced lines from AICRP on sesame, Project Co-ordinated Unit, Jabalpur, local cultivar lines, popular varieties, National, Zonal and Local checks for variability and disease resistance reactions for phyllody, powdery mildew, *Alternaria* and *Cercospora* leaf spot. Therefore, it is needed to screen under natural epiphytotic conditions. In the light of above facts, the study was planned with following objectives.

1. To study the genetic diversity in advanced mutant breeding lines for yield and yield attributing traits.
2. To study correlation and path coefficient analysis for yield and yield attributing traits.
3. Screening for major diseases (phyllody, powdery mildew, *Alternaria* and *Cercospora* leaf spot) under natural field conditions.

Chapter II

REVIEW OF LITERATURE

The review documented in the extensive literature pertaining to the present investigation is presented in the following sub headings.

2.1 Genetic variability, Heritability and Genetic advance as per cent of mean.

2.2 Genetic diversity through D^2 analysis

2.3 Character association studies of yield and yield contributing characters and disease parameters

2.4 Path co-efficient analysis of yield and yield contributing characters and disease parameters

2.5 Screening of Advanced Breeding Lines for diseases under natural field conditions.

2.1 Genetic variability, Heritability and Genetic advance as per cent of mean.

The development of an effective plant breeding programme is dependent upon the existence of magnitude of variability present in that plant population. Thus, the success of genetic improvement of any character depends on the nature of variability present in the gene pool for that character. This existence of variability is essential for resistance to biotic and abiotic factors as well as for wider adaptability. According to Allard (1960) yield is polygenically controlled quantitative character and is highly influenced by environment.

Partitioning of observed variability into heritable and non-heritable components is very much essential to get a true indication of the genetic coefficient of variability as a useful measure of the magnitude of genetic variance present in the population.

2.1 Review of literature on variability for yield and yield contributing characters.

Traits studied	Variability parameters				Study based on
	PCV (%)	**GCV (%)**	***h²* (%)**	**GAM**	
1. Days to 50 per cent flowering	Moderate	Moderate	Medium	Moderate	Jadhav and Mohrir (2012)
	High	High	Medium	High	Narayanan and Murugan (2013b)
	Low	Low	High	Moderate	Rajani Bisen *et al.* (2013)
	Moderate	Moderate	Medium	Moderate	Vanishree *et al.* (2013)
	Low	Low	High	Low	Thirumala Rao *et al.* (2013)
	Low	Low	High	High	Anitha and Manivannan (2014)
	Low	Low	High	Low	Bharathi *et al.* (2014)
	Low	Low	Medium	Low	Bindu *et al.* (2014)
	-	-	High	Moderate	Abate and Mekbib (2015a)
	Low	Low	High	Moderate	Hamouda *et al.* (2016)
	Low	Low	High	High	Tripathy *et al.* (2016)

Traits studied	PCV(%)	GCV(%)	h^2 (%)	GAM	Study based on
	Low	Low	High	Moderate	Saxena and Bisen (2017)
2. Days to maturity	Low	Low	High	Moderate	Sumathi and Muralidharan (2010)
	Low	Low	High	Moderate	Gayatree *et al.* (2011)
	Low	Low	High	Moderate	Ahadu Menzir (2012)
	Low	Moderate	Low	Low	Jadhav and Mohrir (2012)
	Low	Low	Medium	Low	Rajani Bisen *et al.* (2013)
	Low	Low	High	Low	Bindu *et al.* (2014)
	Low	Low	High	Low	Bharathi *et al.* (2014)
	Low	Low	Medium	Low	Abate *et al.* (2015)
	Low	Low	High	Low	Hamouda *et al.* (2016)
	Low	Low	High	Moderate	Monpara (2016)
	Low	Low	High	Moderate	Tripathy *et al.* (2016)
	Low	Low	Low	Low	Saxena and Bisen (2017)
3.Plant height (cm)	Moderate	Moderate	High	High	Sumathi and Muralidharan (2010)

Traits studied	PCV (%)	GCV (%)	h^2 (%)	GAM	Study based on
	High	High	High	High	Sandipan *et al.* (2010)
	Moderate	Moderate	High	Moderate	Gayatree *et al.* (2011)
	Moderate	Moderate	Medium	Moderate	Ahadu Menzir (2012)
	Moderate	High	High	High	Jadhav and Mohrir (2012)
	Low	Low	High	-	Khairnar and Monapara (2013)
	Low	Low	Medium	Moderate	Rajani Bisen *et al.* (2013)
	Moderate	Moderate	High	Moderate	Thirumala Rao *et al.* (2013)
	Moderate	Moderate	High	Moderate	Bindu *et al.* (2014)
	Moderate	Moderate	Low	Moderate	Bharathi *et al.* (2014)
	Moderate	low	Medium	Low	Abate *et al.* (2015)
	Moderate	Moderate	High	High	Hamouda *et al.* (2016)
	Low	Low	High	Moderate	Monpara (2016)
	Low	Low	Medium	Moderate	Tripathy *et al.* (2016)
	Low	Low	Medium	Low	Saxena and Bisen (2017)

Traits studied	PCV(%)	GCV(%)	h^2 (%)	GAM	Reference
4. Number of branches per plant	High	High	High	High	Sandipan *et al.* (2010)
	High	High	High	High	Gayatree *et al.* (2011)
	High	High	Medium	High	Ahadu Menzir (2012)
	High	High	High	High	Revathi *et al.* (2012)
	High	High	High	Low	Fadia *et al.* (2013)
	High	High	High	Low	Thirumala Rao *et al.* (2013)
	High	High	High	High	Bharathi *et al.* (2014)
5. Number of capsules per plant	Moderate	Moderate	High	High	Sandipan *et al.* (2010)
	High	High	High	High	Sumathi and Muralidharn (2010)
	High	High	High	High	Gayatree *et al.* (2011)
	High	Moderate	Medium	High	Ahadu Menzir (2012)
	High	High	High	High	Jadhav and Mohrir (2012)
	High	High	High	High	Khairnar and Monpara (2013)
	High	High	High	High	Thirumala Rao *et al.* (2013)

Traits studied	PCV (%)	GCV (%)	h^2 (%)	GAM	Study based on
	High	High	High	High	Bharathi *et al.* (2014)
	High	Moderate	Medium	Moderate	Abate *et al.* (2015)
	Moderate	Moderate	High	High	Monpara (2016)
	Moderate	High	Medium	Moderate	Tripathy *et al.* (2016)
6. Test weight (g)	High	High	High	High	Gayatree *et al.* (2011)
	Moderate	Moderate	High	High	Vanishree *et al.* (2013)
	Low	Low	High	Low	Ahadu Menzir (2012)
	High	High	High	High	Jadhav and Mohrir (2012)
	High	High	Medium	High	Rajani Bisen *et al.* (2013)
	High	Moderate	Medium	High	Bharathi *et al.* (2014)
	Low	Low	Moderate	Low	Bindu *et al.* (2014)
	Moderate	Low	Medium	Moderate	Abate *et al.* (2015)
	Low	Low	Low	Low	Saxena and Bisen (2017)
7. Seed yield per plant (g)	High	High	High	High	Sandipan *et al.* (2010)

Traits studied	PCV(%)	GCV(%)	h^2 (%)	GAM	Reference
	High	High	High	High	Sumathi and Muralidhran (2010)
	High	High	High	High	Gayatree *et al.* (2011)
	High	High	High	High	Jadhav and Mohrir (2012)
	High	High	High	High	Khairnar and Monpara (2013)
	High	High	High	High	Rajani Bisen *et al.* (2013)
	High	High	High	High	Bharathi *et al.* (2014)
	High	Moderate	Medium	Moderate	Abate *et al.* (2015)
	High	High	High	High	Hamouda *et al.* (2016)
	Moderate	Low	High	High	Monpara (2016)
	Moderate	Moderate	High	High	Tripathy *et al.* (2016)
	Moderate	Moderate	High	Moderate	Saxena and Bisen (2017)

Not only for the quantitative traits but also for the diseases the variability analysis can be done which shows the available variation in the genotypes for respective diseases. Some work was carried out which is presented below.

2.1.2 Review of literature on variability for disease parameters.

Parameter	PCV (%)	GCV (%)	h^2 (%)	GAM	Crop	Study based on
1. *Alternaria* leaf spot	High	High	---	---	Sunflower	Shobharani and Ravikumar (2002)
	---	----	Moderate	Moderate	Sunflower	Shobharani and Ravikumar (2003)
	---	---	Moderate	Moderate	Safflower	Harish Babu *et al.* (2005)
	High	High	Moderate	---	Sunflower	Maheshwari *et al.* (2011)
	High	High	Moderate	Low	Onion	Abubakar and Ado (2013)
	High	High	Moderate	Low	Sunflower	Sujatha and Nadaf (2013)
2. *Cercospora* leaf spot	Moderate	Moderate	High	High	Okra	Patro and Sankar (2004)
	High	Moderate	---	Moderate	Groundnut	Kumari (2008)
	---	---	High	Moderate	Groundnut	Khedikar (2008)
	High	High	High	High	Groundnut	Vishnuvardhan *et al.* (2012)
	High	Moderate	High	High	Groundnut	Adana and Abel (2017)

2.2. Genetic Diversity through D^2 analysis:

Diversity is the asset of nature but the magnitude of variability present in a crop species is of utmost importance as it forms the basis for any crop improvement programme. Genetic divergence and genetic variability have together played an important role in evolution of crop plants (Allard, 1961). D^2 analysis is a useful statistical method for analysing the various causative factors and their interrelationships operating on and within the plant populations, under natural and human selections. It has been successfully used to classify the biological populations and to identify factors influencing genetic divergence.

Selection of parents in hybridization programme based on Mahalanobis D^2 statistic is more reliable as the pre-requisite knowledge of parents in respect of many traits available to crossing. Nair and Mukherjee (1960) are the pioneers to use D^2 statistic as a measure of genetic divergence in the field of plant breeding for classification of teak. Bhatt (1973) conducted comparative study of D^2 technique, with other statistical methods with an objective of rationalizing the procedure for choosing parents for hybridization. He observed that the application of D^2 statistic in finding parents for hybridization to be more efficient than any other methods.

Assessment of the exact of genetic diversity within sesame advanced breeding lines is fundamental for sesame breeding and is potentially useful as guide in the choice of parents for developing hybrids.

Solanki and Gupta (2001) reported by assessing the D^2 values were significant among the 52 genotypes, which were grouped into nine clusters. Grouping of genotypes in different clusters was not related to their geographic origin. Capsules per plant, seed yield per plant, plant height and branches per plant contributed maximum to total genetic divergence. Based on mean performance and clustering pattern, hybridization involving ES-46-1-84, ES-81-1-84, EC-234278 and EC-362397 could be exploited for developing higher yielding varieties.

Seymus and Bulent (2010) studied the developmental characters such as days to emergence, flowering, capsule initiation and seed yield were the major determinants of the genetic diversity in the collection. Cluster analysis identified eight main clusters based on agro-morphological characters indicating the diversity could mainly be attributed to diverse agro-climatic conditions. Single plant selection was made from these populations based on different agronomic characteristics and yield potential. These results have an important implication for sesame germplasm characterization, improvement, agro-morphological evaluation and conservation.

Venkatesh *et al.* (2011) conducted an experiment on genetic divergence using D^2 analysis among 53 sesame genotypes for 13 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.

Ahadu Menzir (2012) estimated genetic diversity using D^2 values based on the pooled mean of genotypes resulted in classifying the 64 genotypes in to nine distinct clusters. This indicated that the presence of wide diversity or variability among the genotypes. Clusters III and IV were the largest clusters containing 34, (53.12%) of genotypes together. Cluster I and II (23.43%) had 7 and 8 genotypes respectively, Clusters VI and VII had 10 genotypes together (15.65%) 5 genotypes each and cluster V and VIII constituted 4 genotypes (6.25%) with 2 genotypes each, Cluster IX had 1 genotype (1.56%) and this cluster had outstanding performance than any other genotypes tested in this study.

Genetic divergence was assessed by Parameshwarappa *et al.* (2012) in 131 genotypes of sesame for six characters using Mahalanobis D^2 statistics. Seed yield and plant height 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 and Mohrir (2013) identified seven clusters based on D^2 values in which 31 germplasm lines of sesame collected from AICRP on Sesame & Niger, Jabalpur and NBPGR Regional Station, Akola were evaluated for genetic divergence using Mahalanobis D^2 analysis. Analysis of variances for dispersion indicates significant differences among the genotypes. Thirty-one genotypes were grouped into seven clusters and cluster I (10) was largest, followed by cluster II (8), cluster III (7) and cluster V (3) while clusters IV, VI and VII were solitary. Inter cluster distance ranged from 51.96 (between clusters V and VII) to 423.26 (between clusters II and VII), while maximum intra cluster distance observed within cluster V (48.03). Character oil content contributed maximum (91.83%) towards genetic divergence. On the basis of the inter cluster distance, cluster I, II, III and VII were identified as distant clusters and genotypes *viz.*, S-0434, IC-413209, GRT-8637, NIC-16328, TKG-22, IC-413204, IC-413231, Lalguda local, KMR-116, SI331517, IC-413208, KMS-5-343, ES-111-284, KMS-5-873, SI-3218 and SI-2973 from these clusters could be used for inter-crossing to obtain heterosis and also wider variability.

Narayanan and Murugan (2013a) through genetic diversity observed 16 sesame genotypes using Mahalanobis D^2 statistics. The study indicated wider genetic diversity. Considerable variability was observed for days to 50% flowering, days to maturity, plant height, number of capsules per plant and seed yield due to non-linear pooled deviation. The variability was low for number of primary branches per plant and test weight. Among the seven characters studied, seed yield contributed the most (89.49 %) towards the divergence of genotypes followed by number of capsules per plant, days to 50% flowering and plant height. The genotypes were grouped into eight clusters, maximum inter cluster distance being observed between the clusters III and VII (725.69). Hence selection and crossing of parental lines from these clusters would be desirable for combining earliness, short plant height and more primary branches per plant with more capsule number coupled with high seed yield. The genotypes JTS 8, TMV 3 and Guathama were identified as desirable and stable for days to maturity. Stability parameters along with performance across three *kharif* seasons revealed JTS 8, and Guathama were stable genotypes for seed yield and were found to be suitable for low input cultivation. While, TMV 3 was found to be suitable for input rich cultivation.

On the basis of D^2 values, Rajani Bisen *et al*. (2013) grouped the germplasm lines into eleven clusters using Mahalanobis D^2 statistics. Clustering was not associated with the geographical distribution instead accessions were mainly grouped due to their morphological differences. Maximum inter cluster distance was observed between cluster VI and cluster XI (134.72) followed by clusters V and XI (124.23) while, lowest divergence was noticed between cluster IV and V (9.37). Among the nine characters studied, days to 50% flowering contributed highest towards genetic divergence (21.05 %) followed by seed yield per plant (20.85 %). Cluster VI exhibited highest means for days to 50 % flowering (62.5), plant height (119.8), number of primary and secondary branches per plant (10.4, 19.3) and days to maturity (110.5). Cluster XI exhibited lowest means for days to 50 % flowering (46), plant height (81.4), number of primary branches per plant (6.7) and days to maturity (100.5). Greater genetic divergence was found between clusters VI and XI followed by clusters V and XI indicating superior and novel recombinants and explore the fullest range of variability for the characters and to realize good recombinant can be realized by mating between the lines of these clusters in a definite fashion.

Chandramohan (2014) observed genetic diversity in 280 sesame genotypes for seven characters using Mahalanobis's D^2 statistic and grouped them into 12 clusters. Among the traits studied capsules per plant and plant height contributed maximum for divergence while no contribution from capsule length.

Abate and Mekbib (2015b) said that based on D^2 values, the genotypes were grouped into seven clusters. The clustering pattern suggested that genotypes of the same origin were distributed into different clusters, indicating the absence of parallelism between clustering and geographic distributions. Maximum inter cluster distance was observed between clusters VI and VII while lowest distance was noticed between cluster I and III. Traits *viz*., harvest index, seed yield, bio-mass yield and plant height had highest contribution towards genetic divergence. There was high level of genetic variability in the studied germplasm with regard to seed yield and its component traits. The clustering pattern suggested the absence of relationship between geographic diversity and genetic diversity. Genotypes from distant clusters were suggested to be

used as parents for hybridization program to achieve novel recombinants. The use of the selected traits in sesame improvement program would increase yield.

An investigation about genetic diversity among genotypes resulted in seven different clusters by Abate *et al.* (2015) based on Mahalanobis statistics. Genotypes were not grouped in relation to their geographical distribution. Maximum inter cluster distance was observed between cluster V and VII; hence, genotypes from these two clusters were suggested as parental lines for hybridization program to achieve promising recombinants.

Iqbal *et al.* (2016) studied 33 genotypes for grouping. Three distinct clusters were found. Cluster I comprised of 23 genotypes where cluster II consisted of 6 genotypes and cluster III consisted of 4 genotypes. Four distinct sub-clusters were identified for cluster I. The sub- clusters IA, IB, IC and ID contained 8, 7, 2 and 6 genotypes respectively. Cluster IA has been further grouped into two distinct sub clusters IA-i and IA-ii comprising 4 genotypes and 2 genotypes each. The maximum Euclidean distance recorded between RT-346 and EC-303435 followed by EC-204704 and RT-346, IC-20477 and RT346. Desirable segregates are expected if crossing is done between genotypes with high dissimilarities coefficient.

Kindeya (2017) study gave information about the pattern of clustering for 17 white seeded sesame genotypes which were classified into different four distinct clusters. Cluster II, III and IV had high mean yield, oil content and oil yield than the other clusters. Genotypes grouped in those clusters had also greater genetic divergence important for yield improvement program breeding in northern Ethiopia. Sesame growing environments also clustered in to four groups. Environments grouped in Cluster I, II and IV had high seed yield, oil content and oil yield. Hence, environments grouped in those clusters are important for seed yield, oil content and oil yield production improvement program in the study areas.

Ramprasad *et al.* (2017) classified 41 sesame genotypes comprising advanced breeding lines and varieties into three clusters. Cluster I consist of 23 genotypes, cluster II consists of 15 genotypes and cluster III contained only 3 genotypes. All four lines (Hima, Rajeswari, Swetha, Madhavi) from Jagtial were placed in close proximity in

cluster I because of high morphological similarity. The dissimilarity index ranged from 0.00 to 0.94 (DSS-9/Prachi, G. Til-2/Prachi and Prachi/JLS-9707-2) with mean of 0.55. Six genotype pairs namely Nirmala/TKG-22, RT-125/LT-8, JLS-403-33/CST-2008-2, TKG-87/YLM-17, Swetha/DS-10 and IsAgi-95-10/Rajeswari showed no variability for all qualitative traits like plant height, number of branches per plant, days to maturity, 1000 seed weight and seed yield per plant.

2.3 Character association studies of yield and yield contributing characters and disease parameters:

Correlation coefficient, 'r' measures the degree (intensity) and nature (direction) of association between two characters by Pearson (1905). The covariance indicates that the two related characters (X being the 'cause' or independent variable, and Y being the 'effect' or dependent variable) tend to vary together, i.e. they are correlated with each other. The intensity of this correlation between the cause and effect can be measured by correlation coefficient symbolized as 'r'. Thus 'r' is a conventional statistic to determine the degree to which the two related variates can vary together.

To make the use of relationships in selection, understanding the relationship between yield and its components is more important. Character association is the base for selecting desirable plant and aiding in evaluation of relative influence of various component characters on seed yield.

The review of work on the association of characters in sesame is presented here:

2.3.1 Association of yield contributing characters and disease parameters with seed yield.

Character	**Nature of association**	**References**
1. Days to 50 per cent flowering	Positive significant	Thiyagu *et al.* (2007) Alake *et al.* (2010) Sumati and Muralidharan (2010) Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Thirumala Rao *et al*. (2013) Teklu *et al.* (2014) Mahmoud *et al.* (2015) Bamrotiya *et al.* (2016) Laghari *et al.* (2016)
	Positive non-significant	Parameshwarappa *et al.* (2009) Goudappagoudr *et al.* (2011) Sivaprasad and Yadavalli (2012) Yirgalem *et al.* (2013) Bharathi *et al.* (2015) Saxena and Bisen (2016) Abhijatha *et al.* (2017)
	Negative significant	Yol *et al.* (2010) Ismaila and Usman (2014) Sabiel *et al.* (2015) Kindeya (2017)

Character	Nature of association	References
	Negative non-significant	Sivaprasad *et al.* (2013) Abate *et al.* (2015) Iqbal *et al.* (2016) Monapara and Khairnar (2016) Agrawal *et al.* (2017) Teklu *et al.* (2017)
2. Days to maturity	Positive significant	Thiyagu *et al.* (2007) Sumati and Muralidharan (2010) Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Bamrotiya *et al.* (2016) Abhijatha *et al.* (2017) Agrawal *et al.* (2017)
	Positive non-significant	Parameshwarappa *et al.* (2009) Goudappagoudr *et al.* (2011) Sivaprasad and Yadavalli (2012) Yirgalem *et al.* (2012) Abate *et al.* (2015) Bharathi *et al.* (2015) Laghari *et al.* (2016) Saxena and Bisen (2016)
	Negative significant	Teklu *et al.* (2014) Monpara and Khairnar (2016) Kindeya (2017) Teklu *et al.* (2017)
	Negative non-significant	Thirumala Rao *et al.* (2013) Sivaprasad *et al.* (2013) Abate and Mekbib (2015a) Sabiel *et al.* (2015)

Character	Nature of association	References
3. Plant height (cm)	Positive significant	Thiyagu *et al.* (2007) Parameshwarappa *et al.* (2009) Alake *et al.* (2010) Yol *et al.* (2010) Goudappagoudr *et al.* (2011) Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Teklu *et al.* (2014) Abate *et al.* (2015) Bharathi *et al.* (2015) Mahmoud *et al.* (2015) Sabiel *et al.* (2015) Bamrotiya *et al.* (2016) Iqbal *et al.* (2016) Abhijatha *et al.* (2017) Kindeya (2017)
	Positive non-significant	Anitha *et al.* (2010) Sandipan *et al.* (2010) Yirgalem *et al.* (2012) Baraki *et al.* (2015) Monpara and Khairnar (2016) Bilmez and Sogut (2017) Agrawal *et al.* (2017)
	Negative significant	Teklu *et al.* (2017)
	Negative non-significant	Sivaprasad and Yadavalli (2012) Sivaprasad *et al.* (2013) Laghari *et al.* (2016) Saxena and Bisen (2016)

Character	Nature of association	References
4.Number of branches per plant	Positive significant	Anitha *et al.* (2010) Yol *et al.* (2010) Goudappagoudr (2011) Vanishree *et al.* (2011) Sivaprasad and Yadavalli (2012) Bulent *et al.* (2013) Teklu *et al.* (2014) Abate *et al.* (2015) Mahmoud *et al.* (2015) Iqbal *et al.* (2016) Laghari *et al.* (2016) Abijatha *et al.* (2017) Agrawal *et al.* (2017)
	Positive non-significant	Sandipan *et al.* (2010) Sivaprasad *et al.* (2013) Yirgalem *et al.* (2013) Bharathi *et al.* (2015) Bamrotiya *et al.* (2016) Mansouri (2016)
	Negative non-significant	Bilmez and Sogut (2017)
5. Number of capsules per plant	Positive significant	Thiyagu *et al.* (2007) Parameshwarappa *et al.* (2009) Sandipan *et al.* (2010) Sumati and Muralidharan (2010) Yol *et al.* (2010) Goudappagoudr *et al.* (2011) Vanishree *et al.* (2011)

Character	Nature of association	References
		Ibrahim and Khidir (2012) Sivaprasad and Yadavalli (2012) Bulent *et al.* (2013) Sivaprasad *et al.* (2013) Teklu *et al.* (2014) Abate *et al.* (2015) Bharathi *et al.* (2015) Mahmoud *et al.* (2015) Iqbal *et al.* (2016) Laghari *et al.* (2016) Monpara and Khairnar (2016) Abhijatha *et al.* (2017) Agrawal *et al.* (2017)
	Positive non-significant	Gidey *et al.* (2013) Bamrotiya *et al.* (2016) Saxena and Bisen (2016) Bilmez and Sogut (2017)
	Negative non-significant	Mukhekar *et al.* (2003)
8. Test weight (g)	Positive significant	Yol *et al.* (2010) Goudappagoudr *et al.* (2011) Abate *et al.* (2015) Bharathi *et al.* (2015) Sabiel *et al.* (2015) Abhijatha *et al.* (2017) Bilmez and Sogut (2017) Agrawal *et al.* (2017)

Character	Nature of association	References
	Positive non-significant	Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Yirgalem *et al.* (2013) Ismaila and Usman (2014) Teklu *et al.* (2014) Saxena and Bisen (2016) Teklu *et al.* (2017) Kindeya (2017)
	Negative non-significant	Alake *et al.* (2010) Chandramohan (2011) Bamrotiya *et al.* (2016) Iqbal *et al.* (2016) Laghari *et al.* (2016)
7. *Alternaria* leaf spot	Negative significant	Sujatha and Nadaf (2013) Shobharani and Ravikumar (2003)
8. *Cercospora* leaf spot	Negative significant	Patro and Sankar (2004)

2.3.2 Association among the yield component traits with Days to 50 per cent flowering

Character	Nature of association	References
1. Days to maturity	Positive significant	Thiyagu *et al.* (2007) Parameshwarappa *et al.* (2009) Sumathi and Muralidharan (2010) Goudappagoudr *et al.* (2011) Vanishree *et al.* (2011)

Character	Nature of association	References
		Gidey *et al.* (2013) Teklu *et al.* (2014) Abate *et al.* (2015) Bharathi *et al.* (2015) Bamrotiya *et al.* (2016) Monpara (2016) Saxena and Bisen (2016) Teklu *et al.* (2017)
	Positive non-significant	Ibrahim and Khidir (2012) Sivaprasad and Yadavalli (2012) Sivaprasad *et al.* (2013) Sabiel *et al.* (2015) Iqbal *et al.* (2016) Agrawal *et al.* (2017)
	Negative significant	Abate and Mekbib (2015a)
	Negative non-significant	Abhijatha *et al.* (2017)
2. Plant height (cm)	Positive significant	Thiyagu *et al.* (2007) Goudappagoudr *et al.* (2011) Teklu *et al.* (2014) Bharathi *et al.* (2015) Mahmoud *et al.* (2015) Iqbal *et al.* (2016) Teklu *et al.* (2017)
	Positive non-significant	Parameshwarappa *et al.* (2009) Vanishree *et al.* (2011) Ismaila and Usman (2014) Abate *et al.* (2015)

Character	Nature of association	References
		Sabiel *et al.* (2015) Bamrotiya *et al.* (2016) Monpara (2016) Saxena and Bisen (2016) Agrawal *et al.* (2017)
	Negative significant	Kindeya (2017)
	Negative non-significant	Yol *et al.* (2010) Sivaprasad and Yadavalli (2012) Sivaprasad *et al.* (2013) Abate and Mekbib (2015a) Abhijatha *et al.* (2017)
3. Number of branches per plant	Positive significant	Thiyagu *et al.* (2007) Vanishree *et al.* (2011) Thirumala Rao *et al.* (2013) Teklu *et al.* (2014) Bharathi *et al.* (2015) Mahmoud *et al.* (2015) Teklu *et al.* (2017)
	Positive non-significant	Goudappagoudr *et al.* (2011) Sivaprasad and Yadavalli (2012) Bamrotiya *et al.* (2016) Iqbal *et al.* (2016) Agrawal *et al.* (2017)
	Negative significant	Shekhawat *et al.* (2013) Ismaila and Usman (2014)
	Negative non-significant	Yol *et al.* (2010) Sivaprasad *et al.* (2013) Kindeya (2017)

Character	Nature of association	References
4. Number of capsules per plant	Positive significant	Thiyagu *et al.* (2007) Chandramohan (2011) Goudappagoudr *et al.* (2011) Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Mahmoud *et al.* (2015) Saxena and Bisen (2016)
	Positive non-significant	Parameshwarapa *et al.* (2009) Sivaprasad and Yadavalli (2012) Teklu *et al.* (2014) Bharathi *et al.* (2015) Bamrotiya *et al.* (2016) Iqbal *et al.* (2016)
	Negative significant	Yol *et al.* (2010) Ismaila and Usaman (2014)
	Negative non-significant	Sivaprasad *et al.* (2013) Abate *et al.* (2015) Monpara (2016) Abhijatha *et al.* (2017) Teklu *et al.* (2017)
5.Test weight (g)	Positive significant	Thiyagu *et al.* (2007)
	Positive non-significant	Sumati and Muralidharan (2010) Ibrahim and Khidir (2012) Thirumala Rao *et al.* (2013) Abate *et al.* (2015) Bamrotiya *et al.* (2016)
	Negative significant	Yol *et al.* (2010) Vanishree *et al.* (2011) Kumar *et al.* (2012)

Character	Nature of association	References
		Isamaila and Usman (2014) Teklu *et al.* (2014) Teklu *et al.* (2017)
	Negative non-significant	Goudappagoudr *et al.* (2011) Ibrahim and Khidir (2012) Bharathi *et al.* (2015) Sabiel *et al.* (2015) Iqbal *et al.* (2016) Saxena and Bisen (2016) Agrawal *et al.* (2017)

2.3.3 Association among the yield component traits with Days to maturity

Character	Nature of association	References
1. Plant height (cm)	Positive significant	Thiyagu *et al.* (2007) Goudappagoudr *et al.* (2011) Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Teklu *et al.* (2014) Bharathi *et al.* (2015) Monpara (2016) Agrawal *et al.* (2017)
	Positive non-significant	Parameshwarappa *et al.* (2009) Sivaprasad *et al.* (2013) Abate *et al.* (2015) Iqbal *et al.* (2016) Saxena and Bisen (2016)

Character	Nature of association	References
	Negative significant	Sabiel *et al.* (2015)
	Negative non-significant	Sivaprasad and Yadavalli (2012) Thirumala Rao *et al.* (2013) Bamrotiya *et al.* (2016) Abhijatha *et al.* (2017) Kindeya (2017)
2. Number of branches per plant	Positive significant	Thiyagu *et al.* (2007) Vanishree *et al.* (2011) Gangadhara *et al.* (2012) Gidey *et al.* (2013) Abate and Mekbib (2015a) Agrawal *et al.* (2017)
	Positive non-significant	Ibrahim and Khidir (2012) Sivaprasad and Yadavalli (2012) Thirumala Rao *et al.* (2013) Teklu *et al.* (2014) Bharathi *et al.* (2015) Bamrotiya *et al.* (2016) Ahijatha *et al.* (2017)
	Negative non-significant	Parameshwarappa *et al.* (2009) Goudappagoudr *et al.* (2011) Iqbal *et al*. (2016) Kindeya (2017)
3. Number of capsules per plant	Positive significant	Thiyagu *et al.* (2007) Chandramohan (2011) Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Saxena and Bisen (2016)

Character	Nature of association	References
		Ahijatha *et al.* (2017)
	Positive non-significant	Parameshwarappa *et al.* (2009) Goudappagoudr *et al.* (2011) Sivaprasad and Yadavalli (2012) Sivaprasad *et al.* (2013) Teklu *et al*. (2014) Abate *et al.* (2015) Bharathi *et al.* (2015) Iqbal *et al.* (2016)
	Negative significant	Monpara (2016)
	Negative non-significant	Abate and Mekbib (2015a) Bamrotiya *et al.* (2016) Kindeya (2017) Teklu *et al.* (2017)
4. Test weight (g)	Positive significant	Thiyagu *et al.* (2007) Gidey *et al.* (2013)
	Positive non-significant	Goudappagoudr *et al.* (2011) Ibrahim and Khidir (2012) Abate *et al.* (2015) Bharathi *et al.* (2015) Iqbal *et al*. (2016)
	Negative significant	Chandramohan (2011) Vanishree *et al.* (2011) Teklu *et al.* (2014) Sabiel *et al.* (2015) Ahijatha *et al.* (2017)
	Negative non-significant	Thirumala Rao *et al.* (2013) Abate and Mekbib (2015a) Bamrotiya *et al.* (2016)

Character	Nature of association	References
		Saxena and Bisen (2016) Agrawal *et al.* (2017) Kindeya (2017) Teklu *et al.* (2017)

2.3.4 Association among the yield component traits with Plant height

Character	Nature of association	References
1. Number of branches per plant	Positive significant	Thiyagu *et al.* (2007) Sandipan *et al.* (2010) Sumati and Muralidharan (2010) Yol *et al.* (2010) Goudappagoudr *et al.* (2011) Sivaprasad and Yadavalli (2012) Gidey *et al.* (2013) Teklu *et al.* (2014) Mahmoud *et al.* (2015) Agrawal *et al.* (2017) Kindeya (2017)
	Positive non-significant	Anitha *et al.* (2010) Vanishree *et al.* (2011) Sivaprasad *et al.* (2013) Bharathi *et al.* (2015) Iqbal *et al.* (2016) Monsouri (2016) Teklu *et al.* (2017)
	Negative significant	Ibrahim and Khidir (2012) Ismaila and Usman (2014)

Character	Nature of association	References
	Negative non-significant	Bulent *et al.* (2013) Bamrotiya *et al.* (2016) Abhijatha *et al.* (2017)
2.Number of capsules per plant	Positive significant	Thiyagu *et al.* (2007) Sandipan *et al.* (2010) Suamti and Muralidharan (2010) Yol *et al.* (2010) Goudappagoudr *et al.* (2011) Vanishree *et al.* (2011) Gidey *et al.* (2013) Teklu *et al*. (2014) Abate *et al.* (2015) Bharathi *et al.* (2015) Bamrotiya *et al.* (2016) Agrawal *et al.* (2017)
	Positive non-significant	Ibrahim and Khidir (2012) Sivaprasad *et al.* (2013) Iqbal *et al.* (2016) Monpara (2016) Saxena and Bisen (2016) Abhijatha *et al.* (2017)
	Negative non-significant	Sivaprasad and Yadavalli (2012) Bulent *et al.* (2013) Ismaila and Usaman (2014) Mahmoud *et al.* (2015) Bilmez and Sogut (2017)
3.Test weight (g)	Positive significant	Yol *et al.* (2010) Gidey *et al.* (2013) Ismaila and Usman (2014)

Character	Nature of association	References
		Sabiel *et al.* (2015)
	Positive non-significant	Alake *et al.* (2010) Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Gidey *et al.* (2013) Abate *et al.* (2015) Bilmez and Sogut (2017)
	Negative significant	Chandramohan (2011) Agrawal *et al.* (2017) Teklu *et al.* (2017)
	Negative non-significant	Goudappagoudr *et al.* (2011) Bulent *et al.* (2013) Teklu *et al.* (2014) Bharathi *et al.* (2015) Bamrotiya *et al.* (2016) Saxena and Bisen (2016) Kindeya (2017)

2.3.5 Association among the yield component traits with Number of branches per plant

Character	Nature of association	References
1.Number of capsules per plant	Positive significant	Anitha *et al.* (2010) Sandipan *et al.* (2010) Yol *et al.* (2010) Goudappagoudr *et al.* (2011) Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Sivaprasad *et al.* (2013)

Character	Nature of association	References
		Ismaila and Usman (2014) Teklu *et al.* (2014) Abhijatha *et al.* (2017) Kindeya (2017)
	Positive non-significant	Bulent *et al.* (2013) Thirumala Rao *et al.* (2013) Bharathi *et al.* (2015) Bamrotiya *et al.* (2016) Mansouri (2016)
	Negative non-significant	Mahmoud *et al*. (2015) Bilmez and Sogut (2017)
2.Test weight (g)	Positive significant	Yol *et al.* (2010) Shekhawat *et al*. (2013)
	Positive non-significant	Bulent *et al.* (2013) Gidey *et al.* (2013) Bamrotiya *et al.* (2016) Abhijatha *et al.* (2017)
	Negative significant	Ibrahim and Khidir (2012) Isamaila and Usaman (2014) Bharathi *et al.* (2015)
	Negative non-significant	Goudappagoudr *et al.* (2011) Vanishree *et al.* (2011) Teklu *et al.* (2014) Bilmez and Sogut (2017) Kindeya (2017) Teklu *et al.* (2017)

2.3.6 Association among yield component traits with Number of capsules per plant

Character	Nature of association	References
1.Test weight (g)	Positive significant	Yol *et al.* (2010) Gidey *et al.* (2013) Bulent *et al.* (2013) Bharathi *et al.* (2015) Bamrotiya *et al.* (2016) Abhijatha *et al.* (2017)
	Positive non-significant	Alake *et al.* (2010) Gidey *et al.* (2013) Abate *et al.* (2015) Saxena and Bisen (2016) Bilmez and Sogut (2017)
	Negative significant	Vanishree *et al.* (2011) Ibrahim and Khidir (2012) Isamaila and Usaman (2014) Abate and Mekbib (2015a)
	Negative non-significant	Goudappagoudr *et al.* (2011) Teklu *et al.* (2014) Agrawal *et al.* (2017)

2.3.7 Association among yield component traits with disease parameters

Disease	Nature of association	With yield components	Study based on
***Alternaria* leaf spot**	Negative significant	Plant height, test weight, number of branches per plant and number of capsules per plant	Shabana (2000) Shobharani and Ravikumar (2003) Laxmi (2004)

Disease	Nature of association	With yield components	Study based on
	Negative non-significant	days to 50 per cent flowering	Shabana (2000)
***Cercospora* leaf spot**	Negative significant	Plant height, number of capsules per plant, test weight and number of branches per plant	Rangaswami and Mahadevan (2001)

2.4 Path co-efficient analysis of yield and yield contributing characters and disease parameters:

The concept of path analysis was originally developed by Wright in 1921 but technique was first used for plant selection by Dewy & Lu in 1959. It is simply a standardized partial regression coefficient which splits the correlation coefficients into the measures of direct and indirect effects. Grain yield being a complex character is associated with number of characters which are interrelated. This interrelation among characters affects their relationship with yield, making correlation ineffective. But this method proved useful in analysing correlation coefficients in this system of related variables.

In sesame, selection of factors which influence the seed production both directly and indirectly will be more appropriate as it is not possible through phenotypic selection because of polygenic nature and low heritability.

A review of work done utilizing path coefficient analysis is given in the table 2.4.1

2.4.1 Direct and indirect effects of yield contributing characters on seed yield

Character	Direct effect	Indirect effect via other characters on yield		References
		Positive via	Negative via	
1.Days to 50 per cent flowering	Positive	Days to maturity and number of branches per plant	Plant height and number of capsules per plant	Thiyagu *et al.* (2007)
	Positive	Days to maturity, plant height and number of capsules per plant	--	Parameshwarappa *et al.* (2009)
	Positive	Days to maturity, plant height, number of branches per plant and number of capsules per plant	Test weight	Goudappagoudr *et al*. (2011)
	Positive	Plant height and test weight	Days to maturity and number of capsules per plant	Gidey *et al.* (2013)
	Negative	Days to maturity, plant height, number of branches per plant and number of capsules per plant	--	Sivaprasad and Yadavalli (2012)
	Positive	Plant height and number of branches per plant	Days to maturity and number of capsules per plant	Teklu *et al.* (2014)

Character	Direct effect	Indirect effect (positive via)	Indirect effect (negative via)	References
	Negative	Test weight	Days to maturity, plant height and number of capsules per plant	Bharathi *et al.* (2015)
	Negative	Number of branches per plant, number of capsules of plant and test weight	Days to maturity and plant height	Bamrotiya *et al*. (2016)
	Positive	Days to maturity, plant height and number of capsules per plant	Test weight	Saxena and Bisen (2016)
	Negative	Days to maturity, number of branches per plant and number of capsules per plant	Plant height and test weight	Agrawal *et al.* (2017)
	Negative	Days to maturity and number of branches per plant	Plant height, number of capsules per plant and test weight	Teklu *et al.* (2017)
2.Days to maturity	Positive	Days to 50 per cent flowering and number of branches per plant	Plant height and number of capsules per plant	Thiyagu *et al.* (2007)
	Positive	Days to 50 per cent flowering, number		Parameshwarappa *et al.* (2009)

Character	Direct effect	Indirect effect (positive via)	Indirect effect (negative via)	References
		of capsules per plant and plant height	--	
	Negative	Number of branches per plant	Days to 50 per cent flowering, plant height number of capsules per plant and test weight	Goudappagoudr *et al.* (2011)
	Negative	Days to 50 per cent flowering, plant height and test weight	Number of capsules per plant	Gidey *et al.* (2013)
	Negative	Days to 50 per cent flowering, plant height and number of branches per plant	Number of capsules per plant and test weight	Teklu *et al.* (2014)
	Negative	Days to 50 per cent flowering, plant height, number of branches per plant, number of capsules per plant and test weight	--	Bharathi *et al.* (2015)
	Negative	Days to 50 per cent flowering and number of capsules per plant	Plant height, number of branches per plant and test weight	Bamrotiya *et al.* (2016)

Character	Direct effect	Indirect effect (positive effect)	Indirect effect (negative via)	References
	Negative	Test weight	Days to 50 per cent flowering, plant height and number of capsules per plant	Saxena and Bisen (2016)
	Positive	Number of branches per plant, number of capsules per plant and test weight	Days to 50 per cent flowering and plant height	Agrawal *et al*. (2017)
	Positive	Number of branches per plant	Days to 50 per cent flowering, plant height, number of capsules per plant and test weight	Teklu *et al.* (2017)
3.Plant height (cm)	Negative	Days to 50 per cent flowering, days to maturity and number of branches per plant	Number of capsules per plant	Thiyagu *et al.* (2007)
	Positive	Days to 50 per cent flowering and number of capsules per plant	--	Parameshwarappa *et al.* (2009)
	Positive	Number of capsules per plant	Number of branches per plant	Sandipan *et al.* (2010)
	Negative	Days to 50 per cent flowering and test weight	Days to maturity and number of capsules per plant	Gidey *et al*. (2013)

Character	Direct effect	Indirect effect (positive via)	Indirect effect (negative via)	References
	Positive	Days to 50 per cent flowering and number of branches per plant	Number of capsules per plant and days to maturity	Sivaprasad and Yadavalli (2013)
	Positive	Days to 50 per cent flowering and number of branches per plant	Days to maturity, number of capsules per plant and test weight	Teklu *et al.* (2014)
	Negative	Test weight	Days to 50 per cent flowering, days to maturity, number of branches per plant and number of capsules per plant	Bharathi *et al.* (2015)
	Negative	Days to maturity, number of branches per plant, number of capsules per plant and test weight	Days to 50 per cent flowering	Bamrotiya *et al.* (2016)
	Positive	Days to 50 per cent flowering and days to maturity	Number of capsules per plant and test weight	Saxena and Bisen (2016)
	Negative	Plant height, number of branches per plant, number of capsules per plant and test weight	Days to 50 per cent flowering	Agrawal *et al.* (2017)

Character	Direct effect	Indirect effect (positive via)	Indirect effects (negative via)	References
	Negative	Days to maturity, number of branches per plant and number of capsules per plant	Days to 50 per cent flowering and test weight	Teklu *et al.* (2017)
4.Number of branches per plant	Positive	Days to 50 per cent flowering and days to maturity	Plant height and number of capsules per plant	Thiyagu *et al*. (2007)
	Negative	Plant height and number of capsules per plant	--	Sandipan *et al.* (2010)
	Positive	Days to 50 per cent flowering, plant height and number of capsules per plant	Days to maturity and test weight	Goudappagoudr *et al.* (2011)
	Positive	Days to 50 per cent flowering and plant height	Days to maturity and number of capsules per plant	Sivaprasad and Yadavalli (2012)
	Positive	Days to 50 per cent flowering, plant height and number of capsules per plant	Days to maturity	Teklu *et al.* (2014)
	Positive	Days to 50 per cent flowering, days to maturity, plant height and number of	Test weight	Bharathi *et al.* (2015)

Character	Direct effect	Indirect effect (positive via)	Indirect effects (negative via)	References
		capsules per plant		
	Positive	Number of capsules per plant	Days to 50% flowering, days to maturity, plant height and test weight	Bamrotiya *et al*. (2016)
	Positive	Days to maturity and number of capsules per plant	Days to 50 per cent flowering, plant height and test weight	Agrawal *et al.* (2017)
	Positive	days to maturity, number of capsules per plant and test weight	days to 50 per cent flowering and plant height	Teklu *et al.* (2017)
5.Number of capsules per plant	Negative	Days to 50 per cent flowering, days to maturity and number of branches per plant	Plant height	Thiyagu *et al.* (2007)
	Positive	Days to 50 per cent flowering	--	Parameshwarappa *et al.* (2009)
	Positive	Plant height	Number of branches per plant	Sandipan *et al*. (2010)
	Positive	Days to 50 per cent flowering, days to maturity, plant height and number of branches per plant	Test weight	Goudappagoudr *et al.* (2011)

Character	Direct effect	Indirect effect (positive via)	Indirect effect (negative via)	References
	Positive	Days to 50% flowering, plant height and test weight	Days to maturity	Gidey *et al.* (2013)
	Negative	Days to 50% flowering and plant height	Days to maturity and number of branches per plant	Teklu *et al.* (2014)
	Positive	Days to 50% flowering, days to maturity, plant height and number of branches per plant	Test weight	Bharathi *et al.* (2015)
	Positive	Days to maturity and number of branches per plant	Days to 50% flowering, plant height and test weight	Bamrotiya *et al.* (2016)
	Positive	Days to 50% flowering, days to maturity and test Weight	Plant height	Saxena and Bisen (2016)
	Positive	Days to 50% flowering, days to maturity and number of branches per plant	Plant height and test weight	Agrawal *et al.* (2017)

Character	Direct effect	Indirect effect (positive via)	Indirect effect (negative via)	References
	Positive	Days to 50% flowering and number of branches per plant	Days to maturity, plant height and test weight	Teklu *et al.* (2017)
6.Test weight (g)	Positive	Days to maturity	Days to 50% flowering, plant height, number of branches per plant and number of capsules per plant	Goudappagoudr *et al*. (2011)
	Positive	Days to 50% flowering and plant height	Days to maturity and number of capsules per plant	Gidey *et al.* (2013)
	Positive	Days to maturity and number of capsules per plant	Days to 50% flowering, plant height and number of branches per plant	Teklu *et al.* (2014)
	Positive	Days to maturity and number of capsules per plant	Days to 50% flowering, plant height and number of branches per plant	Bharathi *et al.* (2015)
	Negative	Days to 50% flowering, days to maturity, plant height number of branches per plant and number of	-	Bamrotiya *et al.* (2016)

Character	Direct effect	Indirect effect (Positive via)	Indirect effect (Negative via)	References
		capsules per plant		
	Positive	Number of capsules per plant	Days to 50% flowering, days to maturity and plant height	Saxena and Bisen (2016)
	Positive	Days to 50% flowering and plant height	Days to maturity, number of branches per plant and number of capsules per plant	Agrawal *et al.* (2017)
	Positive	Days to 50% flowering, plant height and number of branches plant	Days to maturity and number of capsules per plant	Teklu *et al*. (2017)

2.5 Screening of Advanced Breeding Lines for diseases under natural field conditions.

The main reason for the lower productivity of this crop is due to the attack of various fungal, bacterial, viral and phytoplasma diseases. Among the diseases, phyllody, *Alternaria* leaf spot, *Cercospora* leaf spot and powdery mildew are of more concern to southern India.

2.5.1 Sesame phyllody

Phyllody is an important disease of sesame caused by pleomorphic mycoplasma-like organism (MLO) which is now called as Phytoplasma and is transmitted by leafhopper *Orosius albicinctus.* It was noticed that as much as 80 to 90 per cent of the plants may be affected, the symptoms manifesting themselves only in the flowering stage when the floral organs are changed in to green leaf-like structure, accompanied by abnormally abundant branching.

Kashiram (1930) was first to report sesame phyllody in India. He reported that transformation of vegetative parts as the sepaloid condition and considered it as physiological disease induced by early sowing and heavy rainfall.

Pal and Pushkarnath (1935) were first to prove the systemic, infectious and transmissible nature of the sesame phyllody disease by their grafting experiment. They suggested the disease may be caused by a virus and the humidity did not influence the disease incidence.

Rhind *et al.* (1937) reported that sesame phyllody may be due to "a failure of the normal progress of the reproductive phase induced by a combination of environmental conditions acting on complex genetic groupings and that it is a case of return in varying degrees of the reproductive tissues to the vegetative condition. The probability of a virus being the agent is not excluded wholly".

Phyllody disease can be managed indirectly by managing vector using insecticides against leafhopper (*Orosius albicinctus* L.). But use of insecticide to control this disease certainly increase the cost of production as crop is being grown on marginal and sub marginal land by many small and marginal farmers besides polluting environment. Use of crop varieties with substantial resistance to the phyllody could amply mitigate the ecological problem. Using host resistance would be more economical, appropriate and cheapest method to manage sesame phyllody. In case of phyllody of sesame, the affected plants become stunted and the floral parts get modified into leafy structures bearing no fruits and seeds causing yield loss up to 100 per cent because of hormone imbalance. So, there is a need to screen under natural condition for identification of resistant lines.

Mirza and Aslam (1996) screened 35 sesame accessions for their resistance to phyllody under natural field condition. Only 6 accessions, K-5, K-206, Pechequet-50, Reg-Canasto, P-35-40 and V-49/205 were found resistant (0.66 to 1.98 %).

Selvanarayanan and Selvamuthukumaran (2000) evaluated four promising cultivars for their field resistance against phyllody. The lowest incidence of phyllody was observed in *cv*. TMV 4 while, the highest incidence was detected in *cv*. TMV 3 followed by *cv*. SVPR 1 during the various periods of observation. The insect vector, leaf hopper (*Orosius albicinctus*) population was minimal and could not be significantly correlated to the disease incidence in the cultivars.

In field screening experiment of 42 advanced sesame genotypes for their resistance to phyllody disease under natural epiphytotic condition during rainy season of 1996 and 1998 by Gopal *et al.* (2005). None of the genotypes were free from phyllody disease. The results revealed that the genotypes, TMV 3, BT-892 and BAUT 1 exhibited partial resistance to phyllody. There was significant positive correlation between days to maturity and phyllody.

Saravanan and Nadarajan (2005) conducted a field experiment with eight cultivated sesame genotypes and its three wild relatives. The result revealed that cultivar SVPR 1 and three wild relatives were resistant to phyllody. Hence the sesame cultivar SVPR 1 and its wild relatives can be very well utilized as the donor parents in resistant breeding programme against phyllody disease.

Sarwar and Haq (2006) screened 106 genotypes of sesame for their reaction to phyllody disease under natural epiphytotic condition. Among 106 genotypes, phyllody disease was noted on nine genotypes.

Gayatree *et al.* (2011) studied 149 lines of cross E8 X TNL under natural conditions. Of these, two lines were immune with 0 grade (0 % PDI), 13 lines were resistant with 1 grade (1-10 % PDI), 79 lines were moderately resistant, with 2-grade (10.1-25 % PDI), 46 lines were moderately susceptible with 3-grade (25.1-50 % PDI) and nine plants were highly susceptible with 4-grade (>50).

Akhtar *et al.* (2013) gave a report from 133 sesame genotypes for phyllody belong to different regions in the field under high inoculum pressure for two consecutive years. During the first year (2007), three genotypes *viz*., NS98002-04, NS98003-04 and NS99005-01 were ranked as highly resistant as they remained symptomless till the harvest of crop while, 11 others *viz*., NS97001-04, NS01004-04, Sumboonkkae, NS940051-04, NS20005-04, NS11704, NS96019-04, Ahnsankkac, NS11504, Hansumkkae and NS99006-04 were scored as resistant with phyllody incidence of 3.12, 3.33, 3.40, 3.45, 5.0, 5.30, 5.88, 7.14, 8.69, 8.70 and 10 per cent, respectively. Other genotypes ranked between moderately resistant to highly susceptible with per cent incidence values ranging from 10.71 to 65.12 per cent. During second year, all the tested genotypes were found to be infected with phyllody disease. However, four genotypes *viz*., NS98002-04, NS98003-04, NS99005-01 and NS01004-04 were resistant with incidence of 3.25, 3.25, 3.75 and 10.0 % respectively. Combined analysis of data also showed that these genotypes could be considered as promising for breeding programmes.

Shobharani *et al*. (2016) assessed 130 sesame hybrids and three checks *viz*., TKG 22 (national check), Pragathi (zonal check) and Swetha til (local check). During first year three hybrids namely Swetha til x KMR-14, Hima x KMR-14 and Rajeswari x KMR-14 were ranked as highly resistant. Other hybrids ranked between moderately resistant to highly susceptible with PDI values ranging from 10.71% to 65.12%. During second year (*kharif*, 2015) all the tested hybrids were found to be infected with phyllody disease. However, four hybrids *viz.*, Swetha til x KMR-14(3.25), Hima x KMR-14(3.25), Rajeswari x KMR-14(3.75) and Rajeswari x VS- 07-023(9.0) were resistant.

2.5.2. Powdery mildew disease in sesame

This disease is of common occurance especially in South India. The disease is prevalent in all sesame growing areas. The powdery mildew causes considerable losses in yield depending upon the time of appearance of disease as well as intensity of the disease. The diseases appear normally at 45-60 days after sowing. The initial symptoms appear as dirty whitish fungal patches on the upper surface of the leaves. Later these

specks coalesce to cover the entire leaf and results into premature defoliation. Generally, it affects the leaves but in severe cases the disease may spread to petioles and other plant parts. In severe infection capsules are shriveled and produce small seeds. This is a devastating disease in sesame during *rabi* season causing considerable yield loss depending on locality, stage of crop, variety, the time of its appearance and intensity of the disease.

Rao and Padmavathi (1999) screened forty genotypes for their reaction to powdery mildew. Among them, two entries *viz*., 22 AN-8 (4.05 %) and Phule Til-1 (8.54 %) recorded the lowest disease incidence (< 10 %) and were categorized as highly resistant, while, seven entries *viz*., TRG-21, DS-1, GT-2, TMV-4, PbTil no-1, Krishna and B-14 (brown seeded) were found moderately resistant (< 20 % disease incidence).

Shamarao *et al.* (2003) evaluated nine entries sesame against powdery mildew resistance under field condition and reported four genotypes *viz*., MT-15, DORS-102, DS-14 and DS-10 were found to be resistant and remaining five genotypes showed susceptible reaction.

Gopal *et al.* (2005) assessed 42 advanced genotypes of sesame for their reaction to powdery mildew under natural infection for two consecutive years. Seven genotypes were found resistant and nine genotypes were moderately resistant.

Sharmila and Ganesh (2008) reported two resistant lines (VS 9701 and VS 9510), four testers (TMV 3, Co-1, SVPR 1 and VRI 1) and eight hybrids of sesame for powdery mildew resistance and reported lines VS 950 and Co1 were good general combiners for yield and powdery mildew resistance and the hybrid VS 9510 × Co-1 is highly heterotic and moderately resistant.

In the natural field conditions Ramana Rao *et al.* (2011) assessed 37 sesame genotypes along with a susceptible check Swetha til against powdery mildew during *rabi,* 2010-11. Twenty-four genotypes showed susceptible (PDI 53.08-89.62 %), and 11

showed tolerant reaction (PDI 29.56-47.32 %). Only three genotypes (TKG-22, NSKMS-260 and G-55) showed resistant reaction with a PDI range of 27.35-28.43 per cent and the susceptible check swetha til recorded PDI of 89.62 per cent. None of the genotypes recorded immune response.

Sravani *et al.* (2012) screened 104 F_2 plants obtained from cross between Swetha til and BB3-8 of *Sesamum mulayanum.* From these 61 showed susceptible reaction and 43 showed resistance reaction.

Mallaiah *et al.* (2016) in their investigation evaluated 37 genotypes along with susceptible local checks were screened under natural field conditions following infector row technique. Nineteen genotypes showed susceptible and ten showed moderately resistant reaction. Only eight genotypes showed resistant reaction (SSD-4, SSD-7, SSD-19, SSD-20, VRI-1, Co-1, T-12 and N-32) showed resistant reaction. None of the genotypes recorded immune reaction.

2.5.3 *Alternaria* leaf spot disease in sesame

Alternaria leaf spot of sesame caused by *Alternaria sesame* or *Alternaria sesamicola* is a major fungal disease distributed throughout the sesame growing areas of India which causes seed rot, pre and post-emergence death of seedlings and infect all the above ground parts resulting in considerable yield loss both qualitatively and quantitatively (Naik *et al.,* 2003b). It is considered as seed borne. So, there is a need to screening under natural condition for identification of resistant lines.

Alternaria leaf spot of sesame is one of the most common and economically important foliar diseases of sesame which appears mainly on leaf blade as small, brown and round to irregular spots varying from 1-8 mm in diameter. In the beginning minute brown spot appears on the upper surface of the blade that later become darker in color with concentric zonations demarcated with brown lines inside the spots. On the under surface the spots were grayish brown in colour. In severe infection several spots

coalesce involving major portions of leaf blade and the affected leaves dry and later drop off from the plants (Mohanty and Behera, 1958).

Alternaria leaf spot takes heavy toll resulting in sufficient losses (Naik *et al.*, 2003) affecting seed quantitatively and qualitatively (Ellis and Holiday, 1970). Complete loss of crop was reported in Maryland of the United States of America by many workers and recorded 15-20 per cent reduction yield loss due to *Alternaria alternata* to the extent of 55.2 per cent (Barbara *et al.*, 1996).

Jayaramaiah *et al.* (1981) reported that 4 genotypes *viz.*, No.1, JT-7, No. 2 and E8 were highly resistant against *Alternaria sesami* under natural field conditions.

Shekarappa (1999) screened 172 sesame genotypes including three wild species of sesame for reaction to *Alternaria sesami* and found that all the tested genotypes showed moderate to high susceptibility.

Naik *et al.* (2002) in their investigation evaluated 279 genotypes of sesame against *Alternaria sesami* to identify resistant sources under field condition. The results showed that 25 genotypes had resistance.

Naik *et al.* (2003a) observed that out of 280 genotypes of sesame which included wild species, genotypes from initial and Advanced variety trial and Multilocation trial against *Alternaria* leaf spot, only RT- 273 (an AICRP entry from Mandor, Rajasthan) from cultivated species and wild species, *Sesamum radiatum, Sesamum prostratum and Sesamum mulayanum* showed resistance under field condition.

Basavaraj *et al.* (2007) in their experiment exercised on 73 genotypes in 2002-03 and 2003-04 of sesame genotypes for resistance to leaf spot caused by *Alternaria sesami*. None of the genotypes have shown immune and highly resistant reaction. Some of the genotypes (Navile 1, 351888, 899, 908, TC-28, Madhavi, Co-1-12, Co-1-16, TC-25 and Tarikere local) were found moderately resistant. Further the genotypes 351887,

E-8, 357013, 357028, DS-11, Co-1-12, Co-1-14, Co-16, E-8-17, E-8-18, E-8-19, E-8-2 and Krishna showed moderate susceptibility to the disease. Susceptibility to the disease was observed in 18 genotypes *viz*., 351882, 351894, 351895, 357012, 357014, 357018, 357019, 357022, 357024, 357025, 357031, and 357032, DS-1-6, DS-1-7, DS-1-8, DS-1-9, Co-1-15 and DS-1-20. Remaining genotypes were found to be highly susceptible to the disease.

According to Marri *et al.* (2012) out of four sesame varieties (S-122, S-117, S-131 and Latifi) on 0-5 scale against *A. sesami* in pots and under field conditions for disease reaction none of the sesame variety was completely immune. The sesame variety S-122 appeared to be highly resistant and placed in "1" reaction category. Latifi and S-131, placed under category "3", they appeared as moderately susceptible. Variety S-117, placed in "5" reaction category, appeared as highly susceptible sesame variety against sesame leaf spot pathogen.

Pawar *et al.* (2013) conducted an experiment using 13 elite IVT entries under natural condition. None of the entry has shown immune reaction to *Alternaria* blight. IVT entries *viz*., IVT-14-10 and IVT-14-11 have shown disease reaction >1 % which comes in the resistant grade. Moderate resistance disease reaction (1-10 %) expressed by entries IVT-14-6 and IVT-14-9 whereas moderate susceptible disease reaction recorded by entries *viz*., IVT-14-7 and IVT-14-8. Susceptible disease reaction shown by entries *viz*., IVT-14-10 and IVT-14-11 remaining entries *viz*., IVT-14-1, IVT-14-2 and IVT-14-3 expressed highly susceptible which should be used with due care in the breeding programme. The resistant and moderately resistant entries may be used in the *Alternaria* leaf spot resistance breeding programme.

Goudappagoudr *et al.* (2013) evaluated straight and reciprocal crosses between RT-273 and Gulbarga Local Black in natural field conditions. From straight cross (RT-273 X GLB), 37 plants were resistant (pooling of plants with 0, 1 and 2 scores) and 13 plants were susceptible (pooling of plants with 3, 4 and 5 scores). From reciprocal cross

(GLB X RT-273), 26 plants were resistant (pooling of plants with 0, 1 and 2 scores) and 9 plants were susceptible (pooling of plants with 3, 4 and 5 scores).

2.5.4 *Cercospora* leaf spot:

Causal organism of the disease is *Cercospora sesame* or *Cercospora sesamicola*. Symptoms are disease appears as small, angular brown leaf spots of 3mm diameter with grey center and dark margin delimited by veins. Stage of crop at which disease appears is 4-6 leaf stage of crop and continues till maturity. Transmission of causal organism is through conidia by wind.

Rangaswami and Mahadevan (2001) reported that nothing is known about the resistance of sesame varieties to the serious *Cercospora* leaf spot caused by *Cercospora* sesame. However, the experimental findings on screening for disease resistance showed that all the cultivars were susceptible to *Cercospora* leaf spot disease and none showed disease resistance reaction. The disease incidence (80%) was recorded to be the lowest.

Nahunnaro and Tunwari (2012) to investigate the reactions of four adaptable sesame cultivars (Yandev 55, NCRIBEN 01M, E8 and NCRIBEN-03L) to *Cercospora* leaf spot (CLS) caused by *Cercospora sesami*. The field trials showed that E8 and NCRIBEN-01M reduced the amount (15.35% and 16.16%) of *Cercospoara* leaf spot disease compared with Yandev 55. The severity ratings revealed that E8 with severities between 43% were resistant under the ratings of 3.00, while NCRIBEN-01M, NCRIBEN-03L and Yandev 55 with severities of 46% to 56.58% are moderately resistant with ratings of 3.56 to 4.0.

Udo *et al.* (2017) studied 20 accessions of *Sesamum indicum*. The sesame accessions were obtained from various localities and raised in a greenhouse. The results obtained indicate that accessions from Adagum and Ndok were immuned or highly resistant to *Cercospora* leaf spot (CLS) disease with disease severity of 0 (zero). Also, collections from Ogoja, Akim Market and Watt Market were resistant to CLS diseases with disease severity of 1.621, 1.820 and 1.545 respectively. Nwang, Mbube East, Bansara, Obudu Market, Obanliku Market, Gboko Market, Ukpa Market, Yahe Market

and Ekpugrinya Market and Okpoma Market were either moderately susceptible or susceptible to CLS disease according to their mean disease severities.

From the above reviews it was found that screening for phyllody, powdery mildew, *Alternaria* and *Cercospora* leaf spot under field (natural) condition is necessary to identify and develop the crop variety with disease resistance coupled with high yield potential.

Chapter III

MATERIAL AND METHODS

The present investigation entitled "Studies on genetic diversity in advanced mutant breeding lines of sesame (*Sesamum indicum* L.)" was carried out with 133 genotypes including National check (TKG-22), Zonal check (Pragathi) and Local check (Swetha til) during *kharif,* 2017 at Regional Agricultural Research Station, Polasa, Jagtial. The details of the material used and methodologies adopted during the course of the present investigation are elucidated under appropriate heads.

3.1 EXPERIMENTAL SITE

The experiment was laid out at Regional Agricultural Research Station, Polasa, Jagtial, during *kharif,* 2017. The research station is situated in Northern Zone of Telangana, India at 18º 48' N latitude, 78º 56' E longitude and 281m altitude of mean sea level.

3.2 CLIMATE

Regional Agricultural Research Station is characterized with annual rainfall of 901 mm per year and average temperature 27.6º C. The climate is tropical in Polasa, Jagtial. The details of the weather prevailed during the experimental period is furnished in the table 3.1.

3.3 EXPERIMENTAL MATERIAL

The experimental material used in the present investigation comprised of 133 genotypes of sesame. Details of the genotypesevaluated are mentioned in the table 3.2.

Out of 133 entries, 37 advanced mutant breeding lines, 30 germplasm lines, 15 local cultivar lines and 4 RILs were obtained from University of Agriculture Sciences, Raichur. 20 germplasm lines, 10 genotypes from IVT *kharif*-2016, 2 genotypes from AVT *kharif*-2016, 2 genotypes from IVT *summer*-2017, 4 genotypes from MLT *summer*-2017, 5 popular varieties, 1 local cultivar line 1 National check, 1 Zonal check and 1 Local check were received from AICRP on sesame, RARS, Polasa, Jagtial.

Table 3.1. Weather data recorded at Regional Agricultural Research Station, Polasa, Jagtial during *kharif*, 2017.

S. No	Standard week	Temperature (^{0}C)		Relative Humidity (%)		Bright sunshine hours (hrs/day)	Evaporation mm/day	Rain (mm)	Rainy days
		Max	Min	7.14 AM	2.14 PM				
24	11 -17 June	33.2	24.1	87.4	68.7	1.6	2.2	5.2	1.0
25	18 - 24 June	36.3	25.0	80.3	53.0	6.4	4.6	42.0	1.0
26	25 June - 1 July	34.2	24.7	82.7	63.3	3.5	2.4	17.3	2.0
27	2 -8 July	33.8	24.2	85.4	61.4	4.7	3.8	21.6	2.0
28	9 - 15 July	32.8	23.8	86.4	64.6	1.3	2.3	21.0	3.0
29	16 - 22 July	30.6	23.5	87.1	70.1	2.3	2.3	25.0	3.0
30	23 - 29 July	33.2	24.7	80.9	57.9	6.6	5.3	0	0
31	30 July - 5 August	33.4	24.9	83.0	63.0	3.1	3.8	19.6	2.0
32	6 - 12 August	31.4	23.9	88.0	74.4	1.8	1.9	50.5	2.0
33	13 - 19 August	30.1	23.3	90.4	78.1	1.0	0.4	60.0	6.0
34	20 - 26 August	29.0	23.2	91.3	79.1	4.1	0.7	28.6	4.0
35	27 Aug - 2 September	31.6	23.8	89.6	64.1	5.6	2.7	6.6	1.0
36	3 - 9 September	33.3	25.0	91.9	64.7	6.2	4.4	0	0
37	10 - 16 September	33.6	30.6	89.0	61.3	5.8	4.4	0	0
38	17 - 23 September	32.4	23.3	88.4	62.4	5.3	3.5	0	0
39	24 - 30 September	34.7	23.8	90.6	51.6	6.6	4.3	0	0
40	1 - 7 October	34.6	23.3	87.1	56.0	5.5	3.7	20.0	1.0
41	8 - 14 October	32.5	22.5	85.6	68.1	4.5	1.0	112.3	3.0
42	15 - 21 October	33.2	21.9	83.1	54.6	5.8	2.7	0	0
43	22 - 28 October	34.2	20.1	79.6	44.4	6.7	8.2	0	0

Source: Department of Meteorology, RARS, Polasa, Jagtial.

Table 3.2. List of genotypes evaluated at Regional Agricultural Research Station, Polasa, Jagtial during *kharif*-2017.

S.No	Pedigree	Source	Number	γ-radiation dose	List of genotypes
1	Advanced mutant breeding lines	UAS, Raichur	37	10 Kr	10KRE8-1, 10KRE8-2, 10KRE8-3
				50 Kr	50KRE8-1, 50KRE8-2, 50KRE8-3
				30 Kr	30KRDS-1, 30KRDS-1-1, 30KRDS-1-2, 30KRDS-1-3, 30KRDS-1-5, 30KRDS-1-6, 30KRDS-1-7, 30KRDS-1-8, 30KRDS-1-10, 30KRDS-1-11, 30KRDS-1-14, 30KRDS-1-16, 30KRDS-1-18, 30KRDS-1-20, 30KRDS-1-22, 30KRDS-1-23, 30KRDS-1-25, 30KRDS-1-26, 30KRDS-1-27, 30KRDS-1-28, 30KRDS-1-29, 30KRDS-1-31, 30KRDS-1-71
				60 Kr	60KRE8-1-2, 60KRE8-1-3, 60KRE8-1-4, 60KRE8-1-5, 60KRE8-1-7, 60KRE8-1-9
				40 Kr	E840KR-2, E840KR-3
2	Germplasm lines		30	--	V-72, IISL, IISL-2, IISL-3, IISL-4, SGPS-17-15, R6127-8, R6134, R6135-7, RS Black, RS I-Black, RS Black-108, 73 RK, 82 RK, 162 RK, 188 RK, 196 RK, 223 RK, N-8, Mall-1, Mall-2, OSE-560-1, SSD-7, SSD-22, OSC-79, SC-50, DS-1, DSS-9, RT-273, VRI-1
3	Local cultivar lines		15	--	II IBL Local (1), II IBL Local (4), II IBL Local (5), II IBL Local (6), II IBL Local (7), L-2, L-3-1, L-3-2, L-7, RCR-L, Mall White, Rajasthan Kishore, Kanakapur Local, Indi Taluk-1, Indi Taluk-2
4	RILs		4	--	RIL-32, RIL-38, RIL-82, RIL-198
5	Local Cultivar Line	AICRP,	1	--	CPD Local-2016
6	Promising Germplasm Lines		20	--	SDSN-15-03, SDSN-15-14, SDSN-15-16, SDSN-15-58, SDSN-15-61, SDSN-15-65, SDSN-15-70, SDSN-15-72, SDSN-15-76, SDSN-15-77, SDSN-15-79, SDSN-15-81, SDSN-15-83, SDSN-15-84, SDSN-15-97, SDSN-15-98, SDSN-15-99, SDSN-15-109, SDSN-15-114, SDSN-15-115
7	Genotypes from IVT *Kharif*-2016		10	--	RT-376, RT-378, JLS-710, AT-314, AT-332, DS-46, GT-10, MT-2014-14, TKG-11, JTS-8
8	Genotypes from AVT		2	--	TKG-506, PT-10

Table 3.2. (Contd..)

	kharif-2016	Jagtial.			
9	Genotypes from IVT *summer*-2017		2	--	IVTS-2017-02, IVTS-2017-11
10	Genotypes from MLT-2017		4	--	JCS-2454, JCS-2696, JCS-2698, JCS-3280
11	Popular Varieties		5	--	Hima, Rajeswari, JLT-408, YLM-11, YLM-66
12	National Check		1	--	TKG-22
13	Zonal Check		1	--	Pragathi
14	Local Check		1	--	Swetha til

The mutant lines have undergone irradiation with different doses of gamma (γ) radiation. The doses include 10Kr, 30Kr,40Kr, 50Kr and 60Kr.

3.4 METHODS

3.4.1 Experimental design and layout

The experiment was laid out in Randomized Block Design (RBD) with three replications during *kharif*, 2017. Each genotype was sown in two rows of two metres length with plot size 1.6 m^2, inter-row spacing of 30 cm and intra row spacing of 10 cm. Sowing was done by dibbling the seed at 2-3 cm depth. All the standard package of practices were followed during crop growth period.

3.4.2 Recording of observations

Data were recorded on five randomly selected plants from each genotype and in each replication for all the disease, yield and yield contributing characters. However, data on 50 per cent flowering and days to maturity was noted on plot basis. The details of observations recorded and the technique to record the observations are mentioned below.

3.4.2.1 Days to 50 per cent flowering

Number of days from the date of sowing to the day on which 50 per cent of the plants flowered in each genotype were recorded.

3.4.2.2 Days to maturity

Number of days taken to maturity in each genotype was calculated from date of sowing to physiological maturity which was ascertained by yellowing of capsules and leaves.

3.4.2.3 Plant height (cm)

Height of the plant was measured in ‘cm’ at maturity from base of the plant to tip of the main stem.

3.4.2.4 Number of branches per plant

Total number of branches arise from the main shoot in each tagged plant was recorded.

3.4.2.5 Number of capsules per plant

Total number of capsules per plant was counted from five randomly selected plants in each genotype.

3.4.2.6 Test weight (g)

In total one thousand seeds were counted from each randomly selected five plants and weights recorded with high precision balance.

3.4.2.7 Seed yield per plant (g)

Five randomly selected plants harvested and threshed separately. These are cleaned, weighed and mean seed yield per plant was recorded.

3.4.2.8 PDI to Phyllody (% incidence)

The incidence of phyllody was recorded under natural field conditions by counting the phyllody infected plants over total number of plants. Severity of diseases is assessed by observing the disease intensity of infected plants on plot basis. Accordingly, the percent disease incidence was calculated and grouped as given by AICRP system.

3.4.2.9 PDI to powdery mildew

In the natural field conditions according 0-5 scale (AICRP system) disease score was recorded and Percent Disease Index was calculated. Disease severity observations were recorded for five randomly selected plants from each genotype according to the formula given by Wheeler (1969).

3.4.2.10 PDI to *Alternaria* leaf Spot

Disease score was recorded under natural field conditions using 0-5 scale (AICRP system) and Percent Disease Index was calculated using the formula suggested by Wheeler (1969). Disease severity was recorded on five randomly selected plants by observing the disease intensity of infected plants.

3.4.2.11 PDI to *Cercospora* leaf spot

Cercospora leaf spot score was taken under natural field conditions following 0-5 scale (AICRP system) and Percent Disease Index was calculated. By observing the intensity of disease on randomly selected infected plants, the disease severity was known and calculated using the formula suggested by Wheeler (1969)

3.5 STATISTICAL ANALYSIS

The data collected for disease, yield and yield contributing traits was analysed through WINDOSTAT statistical package at university library PJTSAU, Rajendranagar, Hyderabad.

3.5.1 Estimation of Mean

Average value of each character was recorded for total 133 genotypes.

3.5.2 Estimation of Range

The lowest and the highest values from mean of each character were recorded as range.

3.5.2 Analysis of Variation (ANOVA)

Analysis of Variance was computed for replicated data (RBD) in each characteras per the standard statistical procedure (Panse and Sukhatme, 1985). The significance was tested by referring to the values of "F" table (Fisher and Yates, 1963).

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

Where,

Y_{ij}= phenotypic observation of i^{th} genotype and j^{th} replication

μ = general mean

g_i = effect of i^{th} genotype

r_j=effect of j^{th} replication

e_{ij} = random error associated with i^{th} genotype and j^{th} replication

Table 3.3. Analysis of Variance for Randomized Block Design

Source	Degrees of Freedom	Mean Sum of Squares	F-ratio
Replication	(r-1	Ms	Ms/Me
Genotype	(t-1)	Mg	Mg/Me
Error	(r-1) (t-1)	Me	
Total	(tr-1)	Mt	

where,

r and g = Number of replications and genotypes respectively.

Ms, Mg, Me and Mt = Mean sum of squares due to replications, genotypes, error and total respectively.

3.5.4 Estimation of components of variance

The genotypic and phenotypic variance was calculated as per the formulae given by Burton and De Vane (1953)

(i) Genotypic variance (σ^2_g) = $\frac{Mg - Me}{\text{Number of replications}}$

where,

Mg = Mean sum of squares due to genotypes

Me = Mean sum of squares due to environment

(ii) Environmental variance (σ^2_e)= Me

(iii) Phenotypic Variance(σ^2_p)= (σ^2_g) + (σ^2_e)

where, (σ^2_e) = Environmental variance

3.5.5 Estimation of genetic variability parameters

The genotypic and phenotypic coefficients of variation for all the characters were calculated according to the formulae given by Burton and De Vane (1953).

(i) **Genotypic Coefficient of Variation (GCV)**

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

where,

σ_g^2= Genotypic variance

$\bar{X}$ = General Mean of the characters

(ii) **Phenotypic Coefficient of Variation (PCV)**

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

where,

σ_p^2= Phenotypic variance

$\bar{X}$ = General Mean of the characters

Categorization of the coefficients of variation was done as proposed by Sivasubramanian and Madhavamenon (1973).

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

(iii) **Heritability**

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population.

$$h^2 (bs) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

where,

σ_g^2= Genotypic variance

σ_p^2= Phenotypic variance

Heritability was classified as per Johnson *et al*. (1955)

Low	:	0-30%
Moderate	:	30-60%
High	:	Above 60%

(iv) **Genetic Advance (GA)**

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated.

$$GA = h^2(bs) \cdot \sigma_p K$$

where,

h^2(bs) = Heritability in broad sense

K = Selection differential, constant value is 2.06 at 5 per cent selection intensity (Lush, 1949)

σ_p= Phenotypic Standard Deviation

(v) **Genetic Advance as per cent of Mean (GAM)**

In order to visualize the relative utility of genetic advance among the characters, genetic advance as per cent of mean was computed.

$$GAM = \frac{GA}{\overline{X}} \times 100$$

Where,

GA = Genetic Advance

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

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al*. (1955)

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

High : More than 20%

3.5.6 Estimation of Genetic divergence using Mahalanobis's Generalized Distance (D^2)

Prof.P.C.Mahalanobis (1936) developed this D^2 statistics model to determine divergence among populations in terms of 'generalized group distance'. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in Plant Breeding.

D^2 value between i^{th} and j^{th} genotypes for 'P' characters was calculated as:

$$D^2_{ij} = \sum_{t=1}^{p} (\bar{Y}_{it} - \bar{Y}_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of i^{th} genotype for 't' character

Y_{jt} = Uncorrelated mean values of j^{th} genotype for 't' character

D^2_{ij} = D^2 between i^{th} and j^{th} genotype

3.5.6.1 Data collection:

Data on quantitative traits *i.e.*, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, seed yield per plant and test weight were recorded in three replications. In each genotype replicated means were used for 'D^2' analysis.

3.5.6.2 Test of Significance

After testing the difference between the genotypes for each of the character, a simultaneous test of significance for differences in the mean values for a number of correlated variables with regard to pooled effect of characters was carried out using "V" statistic, which in turn utilizes Wilk's "V" Criterion. The sum of squares and sum of products of error and error + genotype were used for this purpose.

The estimation of "V" (Wilk's criterion) was done by using the following relationship.

$$\text{"V"} = \frac{W}{S}$$

where,

"V" = Wilk's criterion

W = Determinant of error matrix and

S = Determinant of error + variety matrix

The significance of "V" was tested by

$$\chi^2 pq = V(stat) = -m \log_e 'V' = -[n - p+q+1/2] \log_e 'V'$$

where,

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

p = number of characters (or) variables

q = number of genotypes-1 (or) degrees of freedom for population

n = degrees of freedom for error + varieties at base of natural log (2.7183)

Log_e "V" = 2.3026 log10 "V"

V (stat) can be approximately considered to be distributed as χ^2 pq and if the calculated "V" value from the formulae exceeds χ^2 pq "K", the hypothesis is rejected at "K" level of significance; otherwise not.

3.5.6.3 Transformation of Correlated Variables

Transformation was done by using pivotal condensation method. Transformation of correlated variables into standardized uncorrelated ones was done before working out the D^2values because computation of D^2 values were reduced to simple enumeration of differences in mean values of various characters of the two genotypes *i.e.,* $\sum di^2$.

3.5.6.4 Testing the Significance of D^2 Values

The D^2 value obtained for a pair of genotypes was taken as the calculated value of χ^2 and tested against tabulated χ^2 at 'p' degrees of freedom where, 'p' is the number of characters included in the study. If the calculated value of χ^2 is higher than table value of χ^2, it is considered significant and vice versa.

3.5.6.5 Grouping of genotypes into different clusters

Grouping of genotypes into different clusters was done by using Tocher's method. The criterion used in clustering by this method was that any two genotypes belonging to the same cluster should have a 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 values of all the combinations for each genotype were arranged in the increasing order of their magnitude (Singh and Chaudhary, 1985). To start with two genotypes having the smallest distance from each other was considered first to which third population having the smallest average D^2 value from the first two genotypes was considered and so on. At certain stage when it was felt that after adding a particular genotype, there was an abrupt increase in the average D^2 value, then that genotype was not considered for inclusion in that cluster. Similarly, a second cluster was formed. This process was continued till all the genotypes were included in one or the other clusters.

3.5.6.6 Intra and Inter Cluster Distance

3.5.6.6.1 Average Intra Cluster Distance

The intra-cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

$$\text{Square of intra-cluster distance} = \sum D_i^2/n$$

where,

$\sum D_i^2$ = sum of distance between all possible combinations

n = number of genotypes included in a cluster

3.5.6.6.2 Average Inter Cluster Distance

The inter-cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

$$\text{Square of inter-cluster distance} = \sum Di^2/n_i.n_j$$

where,

$\sum D_i^2$ = Sum of distances between all possible combination ($n_i.n_j$) of the entries included in the cluster study (i and j)

n_i= Number of entries in cluster i

n_j= Number of entries in cluster j

The distance between the two clusters is the sum of D^2 value between the number one cluster to each of the members of other cluster divided by the product of number of genotypes in both the clusters under consideration. The square root of the average D^2 value gave the genetic distance 'D' between the clusters. Based on D^2 values (inter cluster distance), the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

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

3.5.6.7 Cluster Diagram

The clusters and their mutual relationship were presented diagrammatically. The square root of average D^2, which was an approximate measure of divergence between groups was used to denote the distance.

3.5.6.8 Contribution of individual characters towards total divergence

In all the combinations, each character was ranked on the basis of their contribution towards divergence between two entries ($di = y_{it} - y_{jt}$). Rank I was given to the highest mean difference and rank 'p'to the lowest difference; where p is the total number of characters considered.

Percentage contribution of each character (X) towards genetic divergence was calculated using the following formula:

$$\text{Percent contribution of character (X)} = \frac{N \times 100}{M}$$

where,

N = Number of genotype combinations where the characters ranked first

M = All possible combinations of genotypes considered

3.5.7 Estimation of Character Association

Correlation coefficients were calculated to determine the degree of association of yield components with seed yield and also among themselves. Correlation coefficients were calculated at genotypic and phenotypic level using, the formulae suggested by Falconer (1981).

$$\text{Genotypic coefficient of correlation } (r_g) = r(x_i . x_j)g = \frac{\text{Cov.}(x_i . x_j)g}{\sqrt{v(xi)g . v(xj)g}}$$

where,

$r(x_i.x_j)$ - genotypic correlation between i^{th} and j^{th} characters

$Cov.(x_i.x_j)g$ - genotypic covariance between i^{th} and i^{th} characters

$v(x_i)g$ - genotypic variance of i^{th} character

$v(x_j)$ - genotypic variance of j^{th} character

$$\text{Phenotypic coefficient of correlation } (r_p) = r(x_i . x_j)p = \frac{Cov.(x_i . x_j)p}{\sqrt{v(x_i)p . v(x_j)p}}$$

Where,

$r(x_i.x_j)p$ - phenotypic correlation between i^{th} and j^{th} characters

$Cov.(x_i.x_j)$ - phenotypic covariace between i^{th} and j^{th} characters

$v(x_i)p$ - phenotypic variance of i^{th} character

$v(x_j)p$ - phenotypic variance of j^{th} character

To test the significance of correlation coefficients, the estimated values were compared with the tables of correlation coefficients (Fisher and Yates, 1963) at 5 per cent and 1 per cent level of significance with (n-2) degrees of freedom where ‘n’ is the number of genotypes used in the experiment.

3.5.8 Path Coefficient Analysis

Path coefficient analysis explains the cause and effect relationship among the variables. It is standardized partial regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficients into components of direct and indirect effects (Dewey and Lu, 1959). This method permits the breeder to identify relatively important components of a variable, on the basis of their direct and indirect influences. The direct and indirect effects both at genotypic and phenotypic levels were estimated by taking seed yield as dependant variable, using path coefficient analysis as suggested by Wright (1921) and Dewey and Lu (1959).

The following equations were formed and solved simultaneously for estimating the various direct and indirect effects.

$$r_{1y} = P_{1y}r_{11} + P_{2y}r_{12} + P_{3y}r_{13} \ldots\ldots\ldots\ldots\ldots + P_{ny}r_{1n}$$

$$r_{2y} = P_{1y}r_{21} + p_{2y}r_{22} + P_{3y}r_{23} \ldots\ldots\ldots\ldots\ldots + P_{ny}r_{2n}$$

$$r_{ny} = P_{1y}r_{n1} + P_{2y}r_{n2} + P_{3y}r_{n3} \ldots\ldots\ldots\ldots\ldots + P_{ny}r_{nn}$$

where,

1 , 2 ……n	= Independent variables
y	= Dependent variables
r_{1y} , r_{2y} …….r_{ny}	= Coefficient of correlation between casual factors ‘1’ to ‘n’ on dependent character 1
P_{1y} , P_{1y} ……P_{ny}	= Direct effect of character ‘1’ to ‘n’ on character Y

Direct effects were as follows:

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

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

$$P_{ny} = \sum_{i=1}^{k} C_{ni} r_{iy}$$

Residual effect, which measures the contribution of characters not considered, was obtained as:

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

where,

P_{ny}=Direct effect of x_n on Y

r_{ny}=Correlation coefficient of x_n on Y

3.5.9 Screening of genotypes against phyllody, powdery mildew, *Alternaria* leaf spot and *Cercospora* leaf spot.

The 133 genotypes were screened against phyllody, powdery mildew, *Alternaria* and *Cercospora* leaf spot under field conditions during *kharif,* 2017. Grouping of advanced breeding lines under was done using 0-5 scale. Disease severity observations were recorded on five randomly selected plants from each genotype for powdery mildew, *Alternaria* and *Cercospora* leaf spot by observing the disease intensity of infected plants whereas for phyllody it was on plot basis.

3.5.9.1 Percent disease index (PDI) for powdery mildew, *Alternaria* and *Cercospora* leaf spot calculated by using formula suggested by Wheeler (1969).

$$PDI = \frac{\text{Sum of numerical ratings}}{\text{No. of leaves/ plants observed x Maximum disease grade}} \times 100$$

Table 3.4. Classification of rating scale for powdery mildew, *Alternaria* and *Cercospora* leaf spot based on per cent infection (AICRP System).

Grade scale (0-5)	Per cent infection	Disease reaction
0	0	Immune
1	1-10	Resistant
2	11-25	Moderately resistant
3	26-50	Moderately susceptible
4	51-75	Susceptible
5	>75	Highly susceptible

3.5.9.2 Per cent disease incidence for phyllody is calculated by using the following formula

$$\text{Disease incidence (\%)} = \frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

Table 3.5. Classification of rating scale for phyllody based on per cent incidence (AICRP system).

Per cent infection	Disease reaction
0	Immune
1-10	Resistant
11-25	Moderately resistant
26-50	Moderately susceptible
51-75	Susceptible
>75	Highly susceptible

Chapter IV

RESULTS AND DISCUSSION

Sesame (*Sesamum indicum* L.) is one of the world's most important oilseed cropdue to presence of high quality oil, protein and other nutritional elements. Study of magnitude of genetic variability for a set of traits is needed for effective selection that forms the basis of sesame crop improvement programme. Quantification of genetic diversity within and between groups of advanced breeding lines, though routine, is important and particularly useful in proper choice of parents for realizing higher heterosis and/or obtaining useful recombinants. Information on the association of plant traits with seed yield is of great importance in selecting desirable genotypes in sesame advanced breeding lines. The main reason for the lower productivity of this crop is due to the attack of various fungal, bacterial, viral and phytoplasma diseases. Several diseases (nearly 18) limit productivity of sesame, as more often neither the farming community is aware of the disease incidence or use any control measures; largely crop is grown with a strategy of sow it, forget it and harvest it because farmers who grow sesame are often poor, resource less and not ready for huge investments.

In general, in a randomized block design, the numbers of replications of the treatments are flexible and are useful for situations in which a large number of treatments are to be tested. In the present investigation, there were 133 breeding lines; it can be fit in three replications. These lines were found promising and consist of combinations of advanced mutant breeding lines, germplasm lines, local cultivar lines, RILs, local cultivar lines, promising germplasm lines, genotypes from IVT (*kharif*, 2016), genotypes from AVT (*kharif*, 2016), genotypes from IVT (*summer*, 2017), genotypes from MLT (*summer*, 2017), popular varieties, National, Zonal and Local checks.

Resistance breeding for phyllody, *Alternaria* and *Cercospora* leaf spot started almost a decade back with identification of genotypes such as RT-273 and TNL (Tamilnadu local) that were found to be resistance to *Alternaria* blight and Phyllody respectively. The genetics of resistance nature of these two diseases are well established with 3:1 (a single dominant gene conferring resistance to

Alternaria) as described by Goudappagoudr *et al.* (2013) and 9:7 (complementary interaction with two dominant genes conferring resistance to *Cercospora* leaf spot and phyllody) as described by Gayatree *et al*. (2011) respectively.

In the present study, seven quantitative traits and three disease parameters were studied *viz*., days to 50 per cent flowering (days), days to maturity (days), plant height (cm), number of branches per plant, number of capsules per plant, test weight (g) and seed yield per plant (g), phyllody (% incidence), powdery mildew, *Alternaria* leaf spot (PDI), and *Cercospora* leaf spot(PDI). These traits were most studied by other research workers and found most contributing towards yield.

WINDOSTAT is an advanced level statistical software which is user friendly as well as paper friendly and reports results in most comprehensive formats. The statistical capabilities of Windostat take beyond simple sums and percentages. Investigation and visualisation of data using exploratory data analysis, means, correlations, path analysis, analysis of variance, regression and other multi variate techniques can be done with ease using this programme. All the analyses can be done with a level of precision at a single stretch.

The results and discussions of the experiment are presented under the following headings.

4.1 Analysis of variance (ANOVA) and mean performance.

4.2 Genetic variability, heritability, genetic advance as per cent of mean.

4.3 Genetic diversity through D^2 analysis.

4.4 Character association of yield and yield contributing characters and disease parameters.

4.5 Path coefficient analysis of yield and yield contributing characters and disease parameters.

4.6 Screening of Advanced Breeding Lines for diseases under natural field conditions.

4.1 Analysis of Variance (ANOVA) and mean performance

4.1.1 Analysis of variance (ANOVA)

The mean sum of squares for yield and yield attributing traits *i.e.*, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, test weight, seed yield per plant along with the disease parameters *Alternaria* leaf spot, phyllody and *Cercospora* leaf spot were presented in table 4.1.

Among all the traits highest variance is observed for phyllody (1401.92) followed by plant height (898.37). This indicates 133 genotypes of sesame were studied to assess their genetic potential exhibited highest variability for phyllody followed by plant height. The mean sum of squares was highly significant for days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, seed yield per plant, phyllody (% incidence) *Alternaria* PDI and *Cercospora* PDI were highly significant. While for test weight it is non-significant. All the genotypes displayed considerable amount of differences in their mean performance with respect to all the traits studied, which indicates that the genotypes under study were genetically diverse.

4.1.2 Mean performance:

4.1.2.1 Days to 50 per cent flowering:

Overall mean for days to 50 per cent flowering was seen as 53 days with a wide variation between the earliest 38 days and late 69 days. 188 RK was earliest to flower while 50KRE8-1 was late followed by 30KRDS-1-2. These two genotypes 188 RK and 10 KRE8-1 are having early flowering and maturity character which provides the seasonal shift and better adoption to changing climatic conditions. Hence, these genotypes can be used as parents in the development of early maturing cultivars which increases the yield.

4.1.2.2 Days to maturity:

Maturity duration varied from 71 days to 113 days with mean of 85 days. Genotypes 10KRE8-1, 188 RK and CPD local-2016 matured early while Rajeswari matured late.

4.1.2.3 Plant height (cm):

Plant height varied from 47.20 to 132.70 cm with an overall mean of 94.68 cm. Among all the genotypes 30KRDS-1-14 (47.20) was dwarf, while AT-332 (132.70) was the tallest. Genotypes 30KRDS-1-14 and 82 RK (56.5) have shown dwarf nature which can withstand the lodging effect during adverse environmental conditions

4.1.2.4 Number of branches per plant:

Number of branches varied from 2 to 8 with overall mean of 4.93 branches per plant. 82 RK, 162 RK (2) were with less branching type, while SDSN-15-16 and SDSN-15-61 (8) were profuse branching type. Genotypes with profuse branching can be used as parents in breeding programmes in development of cultivars with more amount of source-sink relation thereby increasing the yield.

4.1.2.5 Number of capsules per plant:

Range of variation from 6 to 61 was observed for this trait with an overall mean of 19.31 capsules per plant. II IBL Local (1), II IBL Local (7) and TKG-22 (6.00) produced very less number of capsules, while SDSN-15-14 had more number of capsules (61.00) per plant.

4.1.2.6 Test weight (g):

The average test weight was 2.22 g with a range varying from 1.04 to 3.23 g. 30KRDS-1-26 had lighter seeds (1.04 g) while GT-10 had recorded heavier seed (3.23 g).

4.1.2.7 Seed yield per plant (g):

Seed yield per plant exhibited a wide amount of variation varying from 0.26 to 9.40 g per plant. The overall mean was 2.75g. II IBL Local (5) was poor seed yielder (0.26 g), while YLM-66 recorded maximum seed yield per plant (9.40 g) followed by SDSN-15-97 (8.66 g). These genotypes can be used as parents in the improvement breeding programmes in improving the seed yield character for the low yielding cultivars especially during *kharif*.

4.1.2.8 Phyllody (% incidence):

The overall mean for the disease is 74.63. The variation exhibited by the genotypes is between 6.33 and 100.00. SDSN-15-98 is recorded low (6.33) and SGPS-15-17 (9.33). SDSN-15-98 and SGPS-15-17 were to be confirmed and can be used as donors for resistance trait in the breeding programme in the development of elite recombinants against phyllody disease.

4.1.2.9 *Alternaria* leaf spot (PDI):

The overall mean for the disease is 89.03 per cent. The variation exhibited by the genotypes is between 56.66 and 100.00 per cent. TKG-506 is recorded low (56.66) followed by TKG-511 (58.50) which can be used in the resistance breeding for development of *Alternaria* resistance.

4.1.2.10 *Cercospora* leaf spot (PDI):

The overall mean for the disease is 93.98 per cent. The variation exhibited by the genotypes is between 63.33 and 100.00 per cent. YLM-11 (63.33) and YLM-66 (65.33) has recorded low. For the purpose of avoiding high cultivation cost these genotypes can be used for the development if innate resistance against diseases which is more effective.

Note: There were certain risks for natural field evaluation for diseases are as follows (Kulkarni and Chopra, 1989):

i. When environmental conditions are not favourable, selection for disease resistant segregants in field will be difficult.

ii. Proper planting should be present i.e., insufficient insect number or pathogen severity to cause adequate damage or occur at an appropriate phenological stage of crop.

iii. Unmanaged and non-random distribution of pathogen or insect density in field and their occurrence differences over years or locations.

iv. Screening for resistance to a specific disease or target insect may be influenced by other diseases or non-target insects.

It is relatively easier to screen segregating material in field against diseases which occur regularly i.e., in the areas where the disease is endemic or hotspot (for insects). With this view, artificial screening was not conducted as the area of experiment, Jagtial is hotspot which made the advantage to maintain optimum insect or disease density : damage ratio allowing maximum difference among the resistant and susceptible genotypes (www.icrisat.com). The susceptible variety was planted as infector row in regular intervals in the field enhancing the sufficient disease pressure avoiding to go for artificial screening.

All the promising genotypes and their mean values accordingly for the characters were depicted in the table 4.1a.

Table 4.1. Analysis of Variance for yield and yield attributing traits in sesame at RARS, Polasa, Jagtial during *kharif*, 2017.

Source of Variation	df	Mean Sum of Squares									
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Test weight (g)	Seed yield per Plant (g)	Phyllody (% incidence)	*Alternaria* leaf spot PDI (%)	*Cercospora* leaf spot PDI (%)
Replications	2	1.10	1.31	52.36	2.21	2.92	0.20	0.42	276.68	8.72	145.46
Genotypes	132	148.15**	178.38**	898.37**	6.49**	299.47**	0.73	8.21**	1401.92**	204.24**	170.13**
Error	264	1.39	1.35	45.59	0.75	11.57	0.13	0.15	93.21	38.19	56.96
Total	398	150.64	181.04	996.35	9.45	303.96	1.06	8.78	1771.81	251.15	372.55

*- Significance at 5% level of probability (1.43)

** - Significance at 1% level of probability (1.65)

Table. 4.1a. Mean performance of promising genotypes for all the yield and yield contributing characters and diseases.

S. No	Character	Genotypes	Mean value	Range	Overall mean
1.	Days to 50 per cent flowering	188 RK	38.00	38.00-69.00	53.26
2.	Days to maturity	10 KRE8-1	71.00	71.00-113.00	85.22
3.	Plant height (cm)	30 KRDS-1-14	47.20	47.20 – 132.70	94.68
		82 RK	56.50		
4.	Number of branches per plant	82 RK, 162 RK	2.00	2.00 – 8.00	4.93
		E840KR-2, SDSN-15-16, SDSN-15-61	8.00		
5.	Number of capsules per plant	SDSN-15-14	61.00	6.00- 61.00	19.31
6.	Test weight (g)	GT-10	3.23	1.04 – 3.23	2.22
7.	Seed yield per plant	YLM-66	9.40	0.26 – 9.40	2.75
8.	Phyllody (% incidence)	SDSN-15-98	6.33	6.33 – 100.00	74.63
		SGPS-15-17	9.33		
9.	*Alternaria* leaf spot (PDI)	TKG-506	56.66	56.66 – 100.00	89.03
		TKG-511	58.50		
8.	*Cercospora* leaf spot (PDI)	YLM-11	63.33	63.33 – 100.00	93.98
		YLM-66	65.33		

4.2 Genetic variability, heritability and genetic advance as per cent of mean.

An assessment of heritable and non-heritable components in the total variability observed was indispensable in adopting suitable breeding procedure. The heritable portion of the overall observed variation can be ascertained by studying the components of variation such as coefficients of genotypic and phenotypic variability, heritability and predicted genetic advance. The range, mean, phenotypic and genotypic coefficients of variability, heritability estimates in broad sense and genetic advance as per cent of mean for the above parameters is presented in table 4.2. The phenotypic and genotypic coefficient of variation was represented in fig.4.1. whereas heritability and genetic advance as per cent of mean were represented in fig.4.2.

All the sesame genotypes exhibited a significant amount of variability (PCV and GCV) for all the yield and yield contributing characters and disease parameters *i.e.,* days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, seed yield per plant, phyllody (% incidence), *Alternaria* PDI and *Cercospora* PDI were evidenced significant by "F" test at p (0.01) level of significance. This type of wide range of variation provides ample scope of selection for desired genotypes and further improvement.

4.2.1 Days to 50 per cent flowering

Genotypic and phenotypic coefficients of variation were moderate with 13.13 and 13.31 per cent respectively. These results were in accordance with Vanishree *et al*. (2013). While high GCV and PCV was observed by Narayanan and Murugan (2013b) and low by Tripathy *et al*. (2016). This wide range of variation provides shifting the seasonal timing of reproduction and produce novel varieties that are better adopted to local environment and change in climatic conditions.

This character had high heritability (97.22 per cent) with genetic advance (14.20) and high genetic advance per cent of mean of 26.67 per cent. Works of Anitha and Manivannan (2014) and Tripathy *et al.* (2016) revealed the same results. While moderate for Jadhav and Mohrir (2012), high and low by Thirumala Rao *et al*. (2013), high and moderate by Saxena and Bisen (2017). High heritability and GAM suggested that this character is predominantly controlled by complex gene interaction and this also indicated importance of additive genetic effects for control of this character.

4.2.2 Days to maturity

Low genotypic and phenotypic coefficients of variation were observed (9.01 and 9.11 per cent respectively) which were in accordance with Sumathi and Muralidharan (2010) and Monpara (2016), except moderate GCV was reported by Jadhav and Mohrir (2012). Variation in days to maturity provides ample scope for selection of early and late maturing plants for further improvement.

This trait has recorded high heritability (97.76 per cent) coupled with genetic advance (15.65). The per cent mean of genetic advance was moderate (18.36 per cent). These results were collinear with Monpara (2016) and Tripathy *et al.* (2016). Irrespective of these recordings moderate heritability recorded by Abate *et al.* (2015) and it was low for Saxena and Bisen (2017) while low GAM was reported by Bindu *et al*. (2014) and Bharathi *et al*. (2014). High heritability and moderate GAM of this trait indicated that environmental control of the character.

4.2.3 Plant height (cm)

Genotypic and phenotypic coefficients of variation were 17.80 and 19.18 per cent respectively which were moderate. The same results were also observed by Thirumala Rao *et al*. (2013) and Bindu *et al*. (2014). High GCV and PCV were recorded by Sandipan *et al*. (2010) while low by Rajani Bisen *et al*. (2013).

This trait exhibited high heritability (86.18 per cent) with expected genetic advance (32.24). The per cent mean of genetic advance was also high (34.05 per cent) which were on par with Sandipan *et al.* (2010), Jadhav and Mohrir (2012) while moderate results were given by Rajani Bisen *et al*. (2013) and low GAM by Abate *et al*. (2015). This trait is governed by complex gene interaction important for control of additive genetic effects for the control of this character which indicates response to selection.

4.2.4 Number of branches per plant

High genotypic and phenotypic coefficients of variation 28.01 and 33.05 per cent respectively were recorded. These recordings were in line with Gayatree *et al.* (2011), Revathi *et al*. (2012) and Fadia *et al*. (2013). Presence of high variability for genotypes evaluated facilitates genetic improvement.

This trait recorded high heritability (71.81 per cent) with genetic advance (2.41). The per cent mean of genetic advance was high with 48.90 per cent Sandipan *et al.* (2010) and Gayatree *et al.* (2011) revealed the similar findings. Irrespective of these results moderate heritability was given by Ahadu Menzir (2012), low GAM was observed by Thirumala Rao *et al*. (2013). Results indicated possible scope for improvement through selection of this character and breeder may have reliable benefits in next generation with respect to this character.

4.2.5 Number of capsules per plant

Genotypic and phenotypic coefficients of variation were high *i.e.,* 50.72 and 53.69 per cent respectively. Similar result reported by Sumathi and Muralidharan (2010), Khairnar and Monpara (2013) and Thirumala Rao *et al*. (2013). In contrast to these results moderate GCV and PCV were reported by Monpara (2016), while moderate GCV by Abate *et al*. (2015) and moderate PCV by Tripathy *et al.* (2016).

This trait recorded high heritability (89.24 per cent) with genetic advance of 19.06. The per cent mean of genetic advance was also high (98.70 per cent). These reports were in collinear with findings of Thirumala Rao *et al.* (2013) and Bharathi *et al.* (2014). With respect to these results other reports like moderate heritability and GAM was given by Abate *et al.* (2015) and Tripathy *et al.* (2016). Presence of high heritability and GAM for this trait reveals the additive gene effect and can be effectively used in selection procedure.

4.2.6 Test weight (g)

Moderate genotypic coefficient of variation (19.98 per cent) and high phenotypic coefficient of variation (25.91 per cent) were observed which were in accordance with Bharathi *et al.* (2014). With deviation to these results Vanishree *et al.* (2011) reported moderate for both GCV and PCV, whereas low reported by Bindu *et al.* (2014), Saxena and Bisen (2017) and low and moderate GCV and PCV respectively by Abate *et al.* (2015).

This trait recorded moderate heritability (59.48 per cent) with genetic advance (0.70) and the per cent mean of genetic advance was high (31.75 per cent). These recordings were on par with reports of Rajani Bisen *et al*. (2013) and Bharathi *et al.* (2014). In contrast, moderate results are given by Abate *et al*. (2015) and high

by Jadhav and Mohrir (2012), moderate heritability and low GAM by Bindu *et al*. (2014). This trait is controlled by dominant genes and can be improved through heterosis breeding.

4.2.7 Seed yield per plant (g)

The genotypic and phenotypic coefficients of variation were 59.46 and 61.15 per cent which were high respectively, which were in line with Hamouda *et al*. (2016) while deviating from these results high recordings were given by moderate by Tripathy *et al*. (2016).

The heritability was high (94.54 per cent) with genetic advance (3.28). The per cent mean of genetic advance was high (119.10 per cent) agreeing with the works done by Tripathy *et al*. (2016) and Monpara (2016). Irrespective of these results moderate recordings were given by Abate *et al*. (2015). Though seed yield was influenced by yield contributing characters high heritability and GAM indicates, this trait is controlled by additive gene effect and phenotypic selection of this character would fasten the varietal improvement period.

4.2.8 Phyllody (% incidence)

The genotypic and phenotypic coefficients of variation were 27.98 and 30.83 per cent respectively which were high.

The heritability (82.39 per cent) and the per cent mean of genetic advance were high (52.32 per cent). The genetic advance of the disease is 39.05. High heritability and GAM of this trait indicates that it is less controlled by environment and additive gene action plays important role which reveals response to selection is high.

4.3.9 *Alternaria* leaf spot PDI (%)

The genotypic and phenotypic coefficients of variation were low (8.35) and moderate (10.86) per cent respectively. On par with the results by Shobharani and Ravikumar (2002) in *Alternaria* PDI in sunflower while deviating from these studies high GCV and PCV was recorded by Maheswari (2011) and Sujatha and Nadaf in sunflower (2013).

The heritability was moderate (59.17 per cent) with genetic advance (11.79). The per cent mean of genetic advance was moderate (13.24 per cent). In support of

these results moderate heritability was reported by Shobharani and Ravikumar (2003) in sunflower, Harish Babu *et al.* (2005) in safflower. In contradiction to the results obtained, moderate heritibility and low GAM was reported by Abubakar and Ado (2013) in onion, Sujatha and Nadaf (2013) in sunflower. This parameter is controlled both by additive and dominant gene effects which can be improved by recurrent selection.

4.2.10 *Cercospora* leaf spot PDI (%)

The genotypic and phenotypic coefficients of variation were low (6.53 per cent) and moderate (10.35 per cent) respectively. Moderate GCV was reported by Patro and Sankar (2004) in Okra, Kumari (2008) and Adana and Abel (2017) in groundnut. Contradictory to these results high GCV and PCV were reported by Vishnuvardhan *et al.* (2012) in groundnut where as high PCV and moderate GCV by Kumari (2008) in groundnut.

The heritability was moderate (39.84 per cent) coupled with the low per cent mean of genetic advance (8.49 per cent) and the genetic advance is 7.98. Deviating from the results obtained, findings by Patro and Sankar (2004) revealed high heritability and GAM in Okra, Vishnuvardhan *et al*. (2012) and Adana and Abel (2017) in groundnut. However moderate GAM was reported by Khedikar (2008) in groundnut. Moderate heritability coupled with low GAM emphasises that this parameter is highly influenced by environment and controlled by both additive and dominant gene effects. This parameter may be improved by heterosis breeding.

In the present study high PCV observed for all the parameters reveals the influence of environment on the manifestation of these parameters. Hence the difference between PCV and GCV was high for test weight (5.93) followed by number of branches per plant (5.04), number of capsules per plant (2.97), seed yield per plant (1.69) and plant height (1.38). This indicates test weight and number of branches per plant were influenced more by environment followed by seed yield per plant and plant height compared to other yield and yield contributing traits. This study also reveals days to 50 per cent flowering and days to maturity were least effected by environment.

Fig 4.1. Genotypic and phenotypic coefficients of variation for yield and yield attributing traits in sesame genotypes at RARS, Jagtial during *kharif*, 2017.

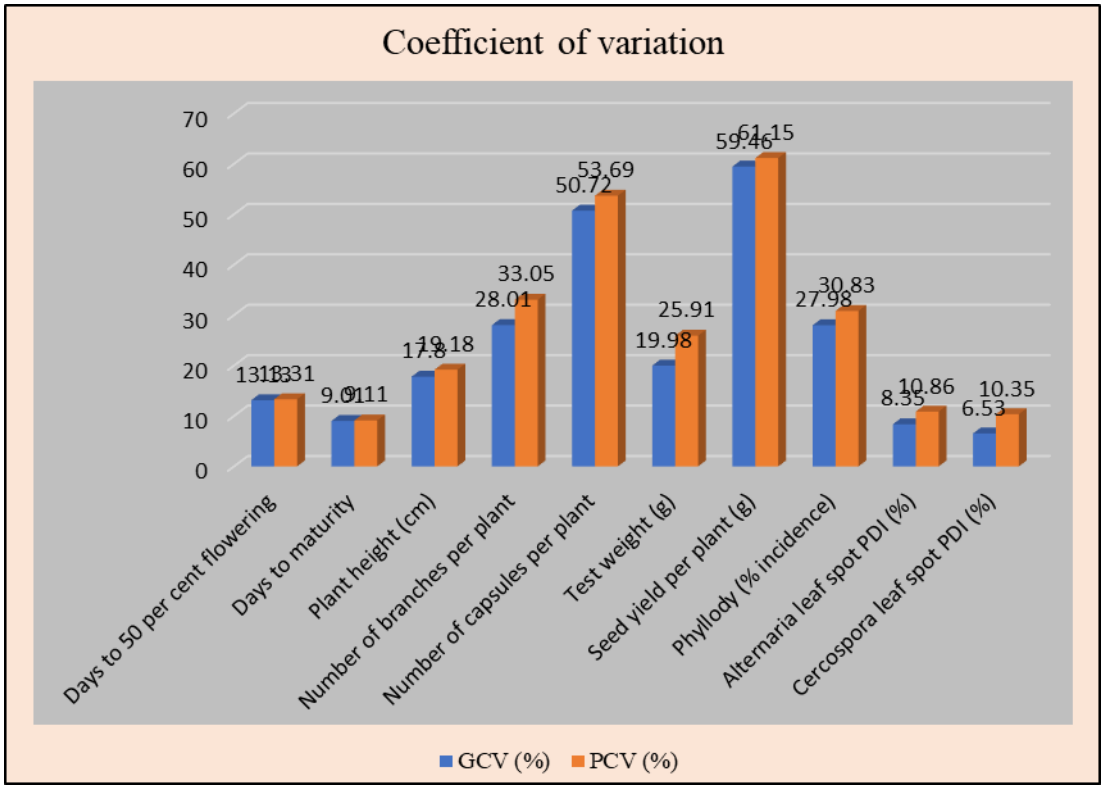

Fig 4.2. Heritability and Genetic advance as per cent of mean for yield and yield attributing traits in sesame genotypes at RARS, Jagtial during *kharif*, 2017.

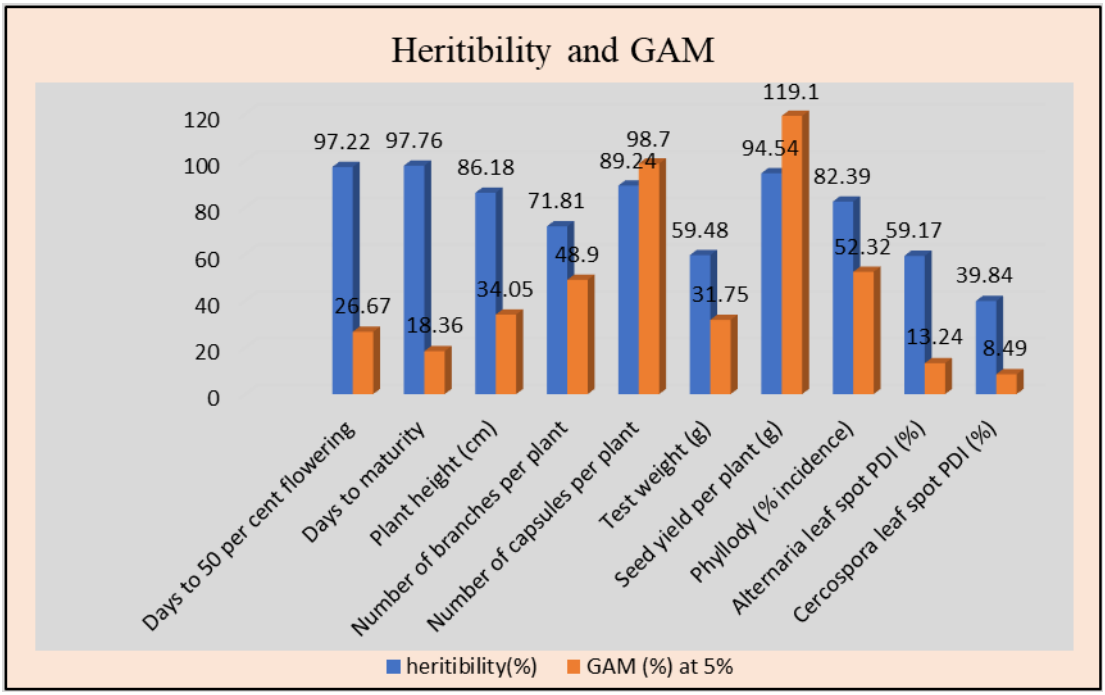

Table 4.2. Genetic parameters for yield and yield attributing traits in sesame at RARS, Polasa, Jagtial during *kharif*, 2017.

Trait	Range		Mean ± SEm	Variance		Coefficient of Variation		h^2 (%)	Genetic Advance (GA) at 5%	GAM (%) at 5%
	min	max		genotypic	Phenotypic	GCV (%)	PCV (%)			
Days to 50 per cent flowering	38.00	69.00	53.26± 0.68	48.92	50.31	13.13	13.31	97.22	14.20	26.67
Days to maturity	71.00	113.00	85.22± 0.67	59.01	60.36	9.01	9.11	97.76	15.65	18.36
Plant height (cm)	47.20	132.70	94.68± 3.89	284.26	329.85	17.80	19.18	86.18	32.24	34.05
Number of branches per plant	2.00	8.00	4.93± 0.50	1.91	2.66	28.01	33.05	71.81	2.41	48.90
Number of capsules per plant	6.00	61.00	19.31± 1.96	95.96	107.54	50.72	53.69	89.24	19.06	98.70
Test weight (g)	1.04	3.23	2.22± 0.21	0.19	0.33	19.98	25.91	59.48	0.70	31.75
Seed yield per plant (g)	0.26	9.40	2.75± 0.22	2.68	2.84	59.46	61.15	94.54	3.28	119.10
Phyllody (% incidence)	6.33	100.00	74.63± 5.57	436.23	529.45	27.98	30.83	82.39	39.05	52.32
***Alternaria* leaf spot PDI (%)**	56.66	100.00	89.03± 3.56	55.35	93.54	8.35	10.86	59.17	11.79	13.24
***Cercospora* leaf spot PDI (%)**	63.33	100.00	93.98± 4.35	37.72	94.69	6.53	10.35	39.84	7.98	8.49

An estimated heritability values alone is less reliable as these values are prone to alter with change in the environment and experimental material (Swarup and Chaugle, 1962). Hence, the use of high heritability coupled with high genetic advance is preferred and observed only for days to 50 per cent flowering, plant height, number of branches per plant, number of capsules per plant and seed yield. Thus, these traits are most probably controlled by additive gene action which may respond to selection.

Among disease parameters, high heritability coupled with high GAM was observed for phyllody and moderate was observed for *Alternaria* PDI and *Cercospora* PDI.

4.3 Genetic divergence through D^2 analysis.

The accurate information about genetic divergence is necessary for effective breeding programme to be carried out. In the present study genetic divergence was assessed by using Mahalanobis D^2 statistics is found to be useful tool in quantifying the degree of divergence between biological population at genotypic level. This can narrow the problem of selection of parents for hybridization programme, if one can identify the characters responsible for discrimination between populations.

4.3.1 Clustering pattern

Based on the D^2 values, the distribution patterns of breeding lines done into nineteen clusters are presented in table 4.3. The diagrammatic representation of nineteen clusters consisting of different advanced breeding lines is shown in fig. 4.3. Among the nineteen clusters, cluster I was the largest comprising of 54 lines followed by cluster II with 28 lines, cluster III with 16 lines, cluster IV with 16 lines, clusters IX and XIV each with 3 lines. Remaining clusters V, VI, VII, VIII, X, XI, XII, XIII, XV, XVI, XVII, XVIII and XIX were solitary. Solitary clusters may be of distinct recombinant or rare segregants. More number of cluster formation is an indication of higher diversity.

4.3.2 Cluster distance

The average D^2 values of intra and inter cluster distances are presented in table 4.4. The maximum intra cluster distance was recorded for cluster IV (38.32) followed by cluster IX (37.61). Because of solitary nature clusters V, VI, VII, VIII,

X, XI, XII, XIII, XV, XVI, XVII, XVIII and XIX recorded zero were in conformity with Venkatesh *et al.* (2011) and Ahadu Menzir (2012).

The inter cluster distance ranged from 14.81 and 392.03. The highest distance is between clusters XIV and XV, while lowest is between X and XI. Results were in line with Jadhav and Mohrir (2012).

The inter cluster distances were higher than intra cluster distances indicating the presence of wider genetic diversity between clusters than within clusters. The highest intra cluster distance for cluster IV depicts that it has maximum divergence among the genotypes present in that cluster and can be made use by recombination breeding in yield improvement. The maximum inter-cluster distances suggest that the genotypes belonging to these clusters if chosen for hybridization are likely to produce maximum amount of heterosis. The greater the distance between clusters wider is the diversity between genotypes.

4.3.3 Cluster mean

The cluster means in respect of 10 traits across nineteen clusters are presented in table 4.5.

In case of days to 50 per cent flowering, cluster means ranged between 42.73 (cluster II) followed by 42.67 (cluster IX) and 69.33 days (cluster XII). Genotypes of cluster II and IX showed characteristic early flowering habit with mean number of days to flowering being 42 days, while, genotypes of cluster XII had late flowering habit with 69 days.

For days to maturity, cluster mean ranged between 80.00 and 110.33 days. Genotypes under cluster V was of early maturity type with number of days to mature being 80.00 days. While, that under cluster XIV were of late maturity types (110.33 days).

With regard to plant height, the genotypes of cluster XI exhibited the highest mean plant height (120.20 cm). Cluster VI comprised of genotypes with a lowest mean plant height (56.50 cm). The mean values of remaining clusters were intermediate.

For number of branches per plant, cluster mean ranged between 1.67 and 7.33. Sesame genotypes under cluster VI had less number of branches per plant and those in cluster XIV had more number of branches per plant.

In case of number of capsules per plant, cluster means ranged between 11 (cluster V) followed by 11.11 (cluster XIV) and 61.00 (cluster XVII). Genotypes under cluster V and XIV had less number of capsules per plant and those in cluster XVII had more number of capsules per plant.

With respect to test weight, cluster XI had the highest mean value (2.99 g) and cluster V had lowest test weight (1.06 g).

Cluster mean for seed yield varied from as low as 0.26 g to as high as 9.40 g. Genotypes in cluster V showed lowest and those in cluster XIX has highest seed yield per plant.

Cluster V (100.00) was with highest mean for phyllody while the lowest was for cluster XV (9.83). Cluster XVII has highest mean for *Alternaria* leaf spot (100.00 per cent) while cluster XIX has lowest mean (71.67 per cent). Clusters V, VII, VIII, XII, XIII, XIV, XVI, XVII have highest mean (100.00 per cent), Cluster XIX has lowest mean 65.33 per cent for *Cercospora* leaf spot.

Genotypes SDSN-15-98 and SGPS-17-15 were grouped into two clusters IV and XV depicting more amount of diversity among them. Therefore, their confirmation for resistance may help in making them to be used as donors in resistance breeding programme and they were found promising showing resistance in field conditions. For seed yield YLM-66 is having highest mean which can be crossed with promising genotypes for development of high yielding and resistant lines.

4.3.4 Relative contribution of different traits towards divergence

The per cent contribution towards genetic divergence by all the yield traits and diseases is presented in table 4.6. and fig. 4.4. The maximum contribution towards genetic divergence was by days to 50 per cent flowering (42.74 per cent), followed by seed yield per plant (16.61 per cent), number of capsules per plant (9.44 per cent), days to maturity (8.58 per cent), plant height (8.07 per cent), phyllody

(8.03 per cent), number of branches per plant (2.98 per cent), *Alternaria* leaf spot (1.81 per cent), *Cercospora* leaf spot (1.15 per cent) and test weight (0.62 per cent)

Figure 4.3 Clustering pattern of sesame genotypes based on Tocher's method.

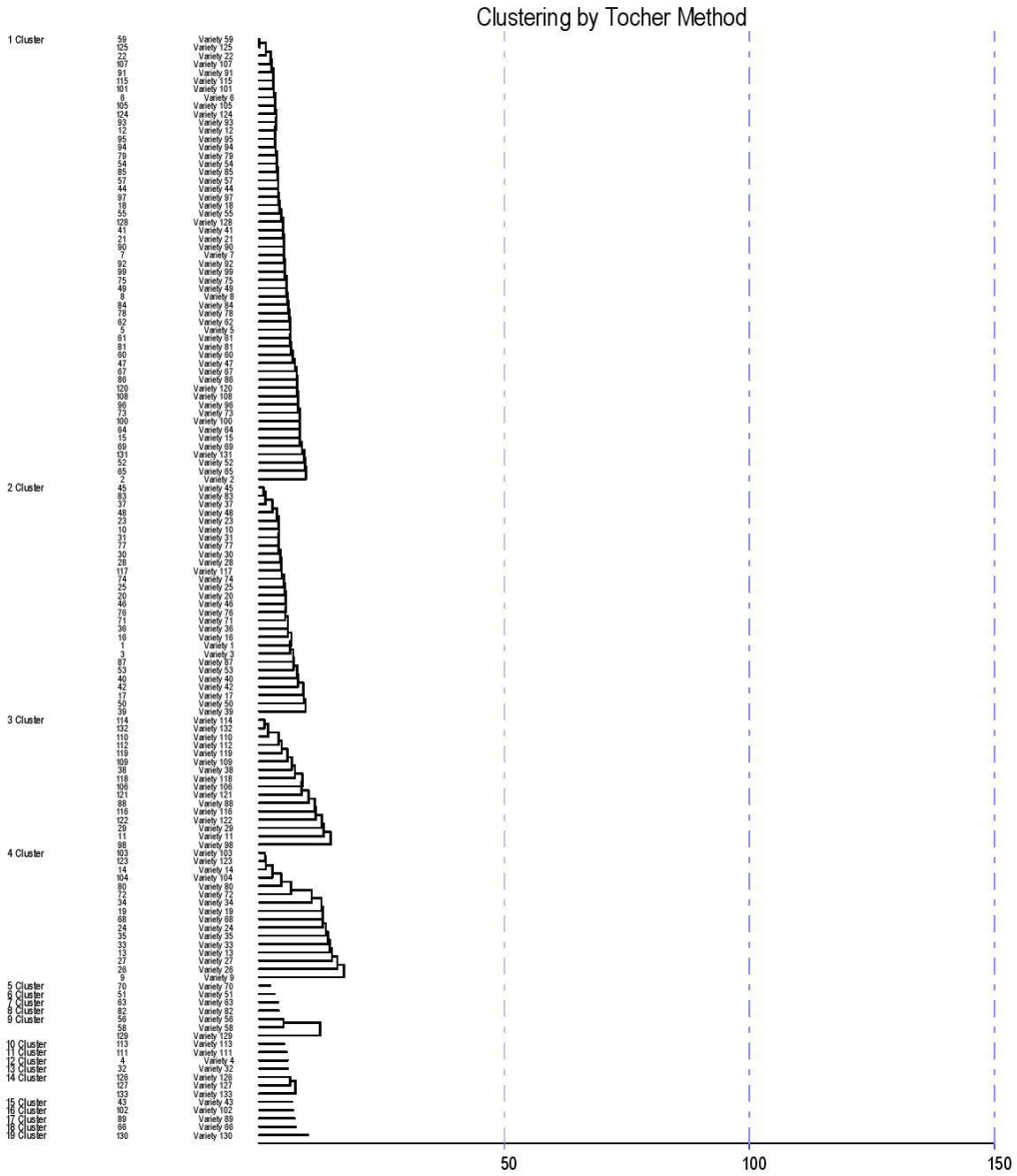

Table 4.3. Clustering pattern of sesame genotypes based on D^2 values at RARS, Polasa, Jagtial during *kharif*, 2017.

Cluster	No. of Genotypes	Genotypes
Cluster I	54	10KRE8-2, OSE-560-1, JCS-3280, 30KRDS-1-23, SDSN-15-115, SDSN-15-58, MT-2014-14, SDSN-15-84, 50KRE8-3, SDSN-15-109, JCS-2698, SDSN-15-65, 30KRDS-1-6, SDSN-15-72, SDSN-15-70, Rajasthan Kishore, 196 RK, RIL-82, Mall-1, R6127-8, SDSN-15-77, 30KRDS-1-16, 223 RK, JLT-408, IISL-3, 30KRDS-1-22, SDSN-15-16, 30KRDS-1, SDSN-15-61, SDSN-15-81, L-3-2, RS Black-108, 30KRDS-1-1, RIL-38, Mall White, OSC-79, SSD-22, 50KRE8-2, Indi Talulk-1, SSD-7, RS Black VRI-1, RIL-198, IVTS-2017-02, RT-376, SDSN-15-76, L-2, SDSN-15-83, DS-1, 30KRDS-1-10, II IBL Local (4), TKG-22, 162 RK and DSS-9
Cluster II	28	R6134, RIL-32, E840KR-3, RS I-Black, 30KRDS-1-25, 30KRDS-1-3, 60KRE8-1-3, RCR-L, 60KRE8-1-2, 30KRDS-1-31, JTS-8, L-3-1, 30KRDS-1-27, 30KRDS-1-20, R6135-7, L-7, II IBL Local (6), E840KR-2, 30KRDS-1-11, 10KRE8-1, 10KRE8-3, CPD Local-2016, 188 RK, IISL-2, IISL-4, 30KRDS-1-14, 73 RK and IISL
Cluster III	16	30KRDS-1-5, 30KRDS-1-71, V-72, SDSN-15-03, SDSN-15-79, SDSN-15-114, RT-378, JLS-710, AT-332, TKG-511, GT-10, TKG-506, PT-10, IVTS-2017-11, JCS-2454 and Pragathi
Cluster IV	16	30KRDS-1-2, 30KRDS-1-7, 30KRDS-1-8, 30KRDS-1-18, 30KRDS-1-26, 30KRDS-1-28, 30KRDS-1-29, 60KRE8-1-5, 60KRE8-1-7, 60KRE8-1-9, II IBL Local (1), L-2, Kanakapur Local, SDSN-15-98, SDSN-15-99 and JCS-2696
Cluster V	1	II IBL Local (5)
Cluster VI	1	82 RK
Cluster VII	1	SC-50
Cluster VIII	1	Indi Taluk-2
Cluster IX	3	N-8, Mall-2 and YLM-11
Cluster X	1	DS-46
Cluster XI	1	AT-314
Cluster XII	1	50KRE8-1
Cluster XIII	1	60KRE8-1-4
Cluster XIV	3	Hima, Rajeswari and Swetha til ©
Cluster XV	1	SGPS-17-15
Cluster XVI	1	SDSN-15-97
Cluster XVII	1	SDSN-15-14
Cluster XVIII	1	RT-273
Cluster XIX	1	YLM-66

Table 4.4. Average intra (diagonal) and inter cluster distances of sesame genotypes at RARS, Poalsa, Jagtial during *kharif*, 2017.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX
I	**17.93**	74.22	35.82	45.85	40.80	26.93	41.20	52.18	79.10	90.43	96.81	103.99	37.51	175.54	85.61	134.06	94.98	105.12	160.21
II		**18.42**	91.99	163.05	35.94	72.17	101.70	69.09	76.84	140.07	150.66	299.45	113.42	362.99	36.06	190.11	154.91	93.45	145.94
III			**30.10**	62.83	84.43	59.57	43.70	51.61	79.84	52.06	60.08	135.11	46.55	200.00	88.81	98.22	75.67	83.73	122.49
IV				**38.32**	106.01	67.42	63.64	101.72	134.54	121.95	131.42	60.44	59.22	130.63	158.59	170.34	129.63	171.01	216.07
V					**0.00**	30.29	94.26	78.72	93.02	166.02	166.08	185.99	74.88	266.29	77.81	209.91	151.46	136.20	214.25
VI						**0.00**	52.52	66.42	101.71	124.16	124.03	115.70	46.88	222.26	89.77	153.85	120.02	116.35	186.42
VII							**0.00**	30.34	99.10	62.60	100.84	148.59	69.13	231.22	68.64	91.90	94.55	56.22	102.19
VIII								**0.00**	68.31	39.07	63.74	209.61	53.45	264.18	51.54	52.65	42.45	19.89	75.87
IX									**37.61**	107.49	129.30	238.90	110.44	206.62	82.50	161.02	137.58	103.01	82.10
X										**0.00**	14.81	216.07	65.79	280.90	110.92	18.34	27.56	33.94	71.19
XI											**0.00**	208.09	48.47	286.01	142.84	32.46	19.14	69.67	130.11
XII												**0.00**	105.05	85.40	319.46	250.22	197.33	306.37	363.68
XIII													**0.00**	183.58	127.86	92.03	44.47	107.11	189.07
XIV														**25.21**	392.03	337.67	272.92	382.37	359.03
XV															**0.00**	160.70	152.32	60.28	90.82
XVI																**0.00**	21.43	38.74	104.68
XVII																	**0.00**	62.00	149.11
XVIII																		**0.00**	47.86
XIX																			**0.00**

Table 4.5. Cluster means for yield and yield attributing traits using Tocher's method in sesame genotypes at RARS, Polasa, Jagtial during *kharif*, 2017.

	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Test weight (g)	Seed yield per plant (g)	Phyllody (% incidence)	*Alternaria* leaf spot PDI (%)	*Cercospora* leaf spot PDI (%)
Cluster I	55.41	86.71	90.62	4.82	16.52	2.16	2.21	79.88	90.28	95.44
Cluster II	42.73	74.13	86.71	4.57	17.09	2.08	2.40	78.18	90.81	94.84
Cluster III	55.83	86.21	117.30	5.28	24.35	2.70	3.94	74.43	81.46	88.00
Cluster IV	61.92	93.40	96.43	5.31	16.56	2.10	2.12	55.15	89.94	94.16
Cluster V	48.33	80.00	66.00	4.00	11.00	1.06	0.26	100.00	98.00	100.00
Cluster VI	54.00	84.67	56.50	1.67	13.67	2.61	1.84	90.67	80.67	90.00
Cluster VII	57.67	86.33	81.60	5.67	14.00	2.95	5.26	57.67	90.00	100.00
Cluster VIII	51.33	84.33	72.80	6.67	36.00	2.47	5.60	64.67	98.67	100.00
Cluster IX	42.67	86.11	113.20	5.56	20.89	2.54	4.18	60.11	85.89	87.78
Cluster X	55.67	86.33	118.70	5.67	49.00	2.56	7.49	67.33	78.00	84.00
Cluster XI	56.33	86.33	120.20	5.00	58.67	2.99	6.12	84.33	73.00	85.00
Cluster XII	69.33	102.67	92.50	2.00	12.00	1.72	0.82	92.00	97.50	100.00
Cluster XIII	57.67	89.67	76.85	6.00	42.00	1.79	2.57	84.67	75.00	100.00
Cluster XIV	60.89	110.33	120.17	7.33	11.11	1.96	1.29	81.00	94.44	100.00
Cluster XV	44.00	74.00	85.90	4.00	21.67	2.90	4.38	9.83	94.00	98.00
Cluster XVI	57.00	87.67	93.10	3.67	57.00	2.53	8.66	90.67	95.00	100.00
Cluster XVII	57.33	88.67	90.00	6.00	61.00	2.50	5.97	94.33	100.00	100.00
Cluster XVIII	49.33	79.67	82.05	5.00	39.67	2.29	7.94	68.67	89.67	91.00
Cluster XIX	43.33	83.00	115.50	4.67	32.00	2.65	9.40	22.67	71.67	65.33

Fig 4.4. Relative contribution (%) of yield and yield attributing traits in sesame genotypes at RARS, Jagtial during *kharif*, 2017

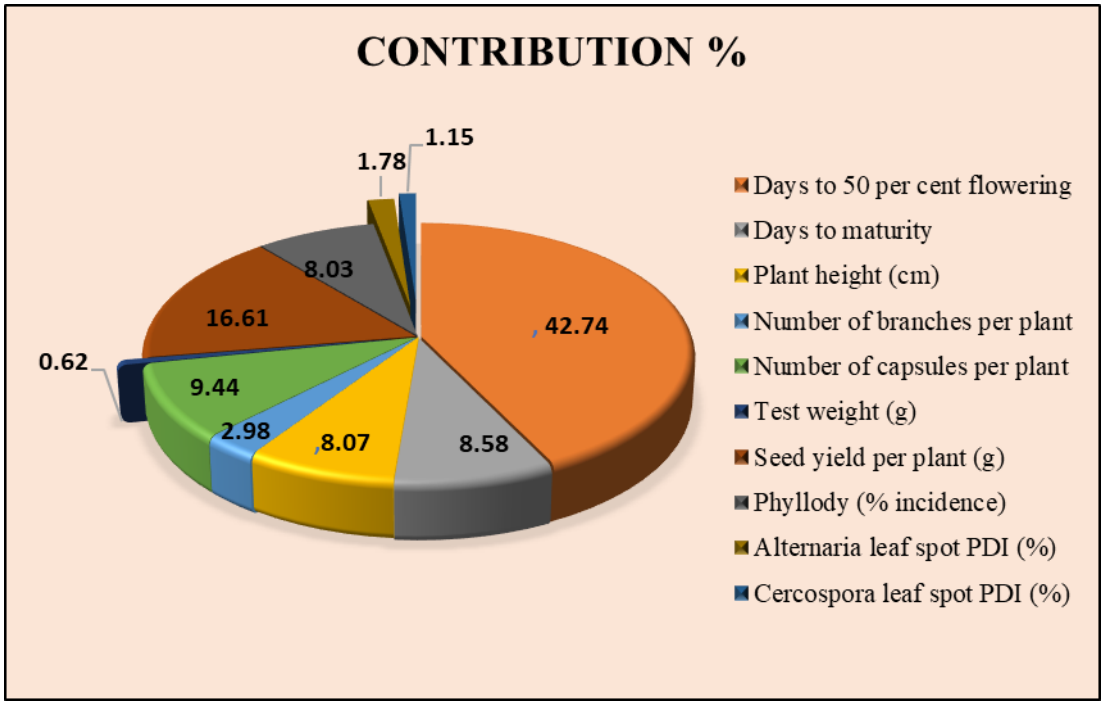

Table 4.6. Relative contribution (%) of yield and yield attributing traits in sesame genotypes at RARS, Polasa, Jagtial during *kharif*, 2017

Character	Times ranked 1st	Contribution %
Days to 50 per cent flowering	3752	42.74
Days to maturity	754	8.58
Plant height (cm)	708	8.07
Number of branches per plant	259	2.98
Number of capsules per plant	829	9.44
Test weight (g)	55	0.62
Seed yield per plant (g)	1457	16.61
Phyllody (% incidence)	704	8.03
Alternaria leaf spot PDI (%)	159	1.78
Cercospora leaf spot PDI (%)	101	1.15

were in similarity with the results of Narayanan and Murugan (2013a) and Rajani Bisen *et al*. (2013) for yield contributing traits.

In breeding programmes, parents having high yield potential with wide genetic diversity are likely to yield superior transgressive segregants within short period (Maurya and Singh, 1977).

4.4 Character association of yield and yield contributing characters and disease parameters.

Knowledge of association between yield and its components is useful to make simultaneous selection for more than one trait. The correlation analysis helps in determining the direction and number of traits to be considered in improving the yield. In this study the genotypic correlations are higher than phenotypic correlations. This indicated that though there was a strong inherent association between characters studied, their expression was influenced by environment. The results were given in table 4.7. The letters 'G' and 'P' in the parenthesis indicates genotypic and phenotypic correlation coefficients respectively.

4.4.1. Association of seed yield among yield contributing characters

Seed yield per plant found highest positive significant association with number of capsules per plant (0.69-G; 0.66-P), test weight (0.59-G; 0.47-P), plant height (0.28-G; 0.26-P) and number of branches per plant (0.18-G; 0.14-P) at both phenotypic and genotypic level. Such high significance with these traits recorded was on par with the results by Goudappagoudr *et al*. (2011), Abate *et al.* (2015) and Abhijatha *et al*. (2017). In deviation from these recordings positive non-significant association with seed yield was given by Sandipan *et al*. (2010) for plant height and number of branches per plant while for number of capsules per plant and test weight was given by Saxena and Bisen (2016).

Highest positive significance between seed yield and number of capsules indicated increased capsule number per plant increases seed yield. Hence during selection more emphasis should be given to this character among all the traits. Further test weight also one of the important components of seed yield and selection for test weight will increase yield. Overall number of capsules and test weight are most reliable traits for yield improvement in sesame.

Positive significant association with plant height and number of branches per plant reveals that taller genotypes will have many internodes, there by more number of branches, results in accommodation of more capsules ultimately giving higher seed yield per plant. Thus, it would be desirable to select sesame plant type having more number of internodes and branches.

Days to 50 per cent flowering (-0.09-G; -0.09-P) exhibited non-significant negative correlation with seed yield which is in accordance with Abate *et al.* (2015), Monapara and Kairnar (2016) and Teklu *et al.* (2017). It would be desirable to select plant with early flowering. Usually in sesame, plant height and number of branches increases after flowering only. Hence these findings reveal that early flowering types may have more chance of increase in plant growth improving the source and sink relationship, which paves way for more number of capsules and seed yield. In contrary to these results workers like Ibrahim and Khidir (2012), Thirumala Rao *et al.* (2013) and Bamrotiya *et al.* (2016) gave positive significant association while positive non-significant was given by Goudappagoudr *et al.* (2011), Yirgalem *et al.* (2013) and Abhijatha *et al.* (2017) and negative significant given by Yol *et al.* (2010) and Kindeya (2017).

Among disease parameters highest negative significant association was observed between *Cercospora* PDI and seed yield per plant (-0.44-G; -0.29-P) followed by with *Alternaria* PDI (-0.26-G; -0.21-P) and phyllody (-0.18-G; -0.17-P). These results were in accordance with Patro and Sankar (2004) for *Cercospora* incidence in Okra and Sujatha and Nadaf (2013) and Shobharani and Ravikumar (2003) in sunflower for *Alternaria* leaf spot. This indicates among foliar diseases *Cercospora* leaf spot is more devastating compared to *Alternaria* leaf spot. Even though phyllody (% incidence) was less negatively correlated compared to *Cercospora* and *Alternaria* leaf spots the stage of occurrence of disease is very important. These diseases can be controlled by pesticides but it is uneconomical to the farmer and resistance breeding involving back cross method will be the ultimate source for improving high yielding genotypes coupled with resistance.

4.4.2. Associated among other yield contributing characters

In general, positive association between days to 50 per cent flowering and days to maturity (0.88-G; 0.87-P) reveals early flowering types mature early and late

flowering types will take more number of days for maturity. In oilseed crops plant growth will be increased after flowering only. Therefore, early flowering types will be benefited with more improvement in yield contributing characters and increase in yield. These results are in accordance with Teklu *et al.* (2014), Abate *et al*. (2015) and Saxena and Bisen (2016). In contrast, negative correlation between the traits plant height, days to maturity and number of branches per plant were reported by Yol *et al*. (2010). However, Abate and Mekbib (2015a) reported negative relation with days to maturity. Non-significant association with number of capsules per plant was given by Abate *et al.* (2015) and Teklu *et al.* (2017) and with test weight was given by Bharathi *et al.* (2015) and Saxena and Bisen (2016).

Days to maturity showed positive significant association with plant height (0.29-G; 0.26-P) and number of branches per plant (0.24-G; 0.21-P) was similar to the findings given by Vanishree *et al.* (2011) and Agrawal *et al.* (2017). In contrast to these results negative significant association was reported by Sabiel *et al*. (2015). The same trait is showing negative non-significant association with number of capsules (-0.02-G; -0.01-P) and test weight (-0.05-G; -0.04-P) which reveals increase in maturity period may not influence the capsule number and test weight which is on par with Abate and Mekbib (2015a), Bamrotiya *et al*. (2016) and Kindeya (2017) while in contrast to these results positive non-significant association was reported by Godappagoudr *et al*. (2011), Abate *et al*. (2015) and Iqbal *et al*. (2016).

Plant height showed positive significant association with number of ranches per plant (0.39-G; 0.30-P) followed by test weight (0.33-G; 0.25-P) was similar to the findings of Yol *et al*. (2010), Ismaila and Usman (2014) and Sabiel *et al*. (2015). This association will increase the active leaf area which increases the source-sink capacity, photosynthates accumulation and increases the test weight. In contrast to these, negative association was reported by Chandramohan (2011) and Teklu *et al*. (2017).

Similarly, same results can be accompanied for positive significance between number of branches per plant with test weight (0.25-G; 0.17-P) and with number of capsules per plant (0.82-G; 0.01-P). These were in accordance with Yol *et al.* (2010). Irrespectively other results, negative association was given by Bilmez and Sogut (2017).

Number of capsules per plant had positive significant association with test weight (0.29-G; 0.22-P), which was collinear to the results of Yol *et al*. (2010), Bamrotiya *et al*. (2016) and Abhijatha *et al.* (2017). Usually high input, irrigation and soil fertility management conditions will increase test weight. In contradiction to these results negative association was given by Vanishree *et al*. (2011), Ismaila and Usman (2014) and Abate and Mekbib (2015a).

4.4.3. Association of disease parameters

Negative significant association of phyllody was observed with test weight (-0.18-G; -0.16-P) where as non-significant negative association with number of capsules per plant (-0.03-G; -0.06-P) and plant height (-0.03-G; -0.02-P). This is mostly due to delayed appearance of phyllody during mid growth period of crop. By this stage plant height and number of capsules per plant might have reached actual genetic potentiality of genotype. But due to incidence of diseases at capsule formation stage is also affect the seed development stage. Seeds which are formed prior to incidence will have actual genetic potential for test weight while which are formed later will become chaffy seed. It was observed positive non-significant association with days to 50 per cent flowering (0.00-G; 0.02-P) and number of branches per plant (0.03-G; 0.02-P) which indicated that days to flowering and number of branches might have already reached as per the inherent capacity of genotype. Incidence of phyllody did not have any significant effect on these traits.

Highest negative significant association is observed between *Alternaria* PDI and plant height (-0.43-G; -0.29-P) followed by test weight (-0.25-G; -0.15-P), number of branches per plant (-0.15-G; -0.21-P) and number of capsules per plant (-0.19-G; -0.17-P). These results are on par with Shabana (2000), Shobharani and Ravikumar (2003) in sunflower. Usually *Alternaria* incidence will start from early growth stages in sesame. Disease is associated with reduction in active leaf area and in regular sesame attains growth after flowering. Here as plant height is more influenced by disease, number of internodes decreases, there by branches and capsule number also decreases. Reduction in net leaf area is associated with deviation of source sink relationship resulting in low test weight was on par with the report by Laxmi (2004). Positive non-significant association of *Alternaria* with days to maturity indicates disease incidence delays maturity of plant to some extent but

Table 4.7. Genotypic and phenotypic correlation coefficients for yield and yield attributing traits in sesame genotypes at RARS, Polasa, Jagtial during *kharif*, 2017.

TRAITS		Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of Capsules per Plant	Test weight (g)	Phyllody (% incidence)	*Alternaria* leaf spot PDI (%)	*Cercospora* leaf spot PDI (%)	Seed yield per plant (g)
Days to 50 per cent flowering	**G**	1.00	0.88**	0.21**	0.15**	0.04	0.01	0.00	-0.03	0.08	-0.09
	P	1.00	0.87**	0.19**	0.14**	0.04	0.01	0.02	-0.02	0.04	-0.09
Days to maturity	**G**		1.00	0.29**	0.24**	-0.02	-0.05	0.00	0.03	0.08	-0.01
	P		1.00	0.26**	0.21**	-0.01	-0.04	0.00	0.02	0.06	-0.09
Plant height (cm)	**G**			1.00	0.39**	0.11*	0.33**	-0.03	-0.43**	-0.49**	0.28**
	P			1.00	0.30**	0.08	0.25**	-0.02	-0.29**	-0.27**	0.26**
Number of branches per plant	**G**				1.00	0.82**	0.25**	0.03	-0.15**	-0.10*	0.18**
	P				1.00	0.10*	0.17**	0.02	-0.21**	-0.19**	0.14**
Number of capsules per plant	**G**					1.00	0.29**	-0.03	-0.19**	-0.32**	0.69**
	P					1.00	0.22**	-0.06	-0.17**	-0.25**	0.66**
Test weight (g)	**G**						1.00	-0.18**	-0.25**	-0.31**	0.59**
	P						1.00	-0.16**	-0.15**	-0.11**	0.47**
Phyllody (% incidence)	**G**							1.00	0.04	0.22**	-0.18**
	P							1.00	0.03	0.17**	-0.17**
***Alternaria* leaf spot PDI (%)**	**G**								1.00	0.46**	-0.26**
	P								1.00	0.54**	-0.21**
***Cercospora* leaf spot PDI (%)**	**G**									1.00	-0.44**
	P									1.00	-0.29**

*- significance at 5% level (0.098) **- significance at 1% level (0.128)

not greatly influenced. In contrast to these results Shobharani (1999) reported negative association with days to maturity in sunflower. Negative non-significant association with days to 50 per cent flowering shows if the appearance of disease is early, it results in delayed flowering to some extent.

Cercospora leaf spot is having high negative significant correlation with plant height (-0.49-G; -0.27-P) followed by number of capsules per plant (-0.32-G; -0.25-P), test weight (-0.31-G; -0.11-P) and number of branches per plant (-0.10-G; -0.19-P) which were on par with findings of Rangaswami and Mahadevan (2001). Similar to *Alternaria* disease reduction in plant height is ultimately associated with decrease in number of branches per plant thereby number of capsules. Further negative significance is associated with reduced test weight which indicates reduction in active photosynthetic leaf area.

4.5. Path coefficient analysis of yield and yield contributing characters and disease parameters.

The correlation coefficient measures the relationship existing between pairs of traits. But a dependent trait is an interaction product of many mutually associated component traits and change in any one component will disturb whole network of cause and effect system. The path coefficient analysis is a statistical device developed by Wright (1921) and Dewey and Lu (1959), takes into account the cause and effect relation between the variables which is unique in partitioning the association into direct and indirect effect through other independent variables. The direct and indirect effects of various yield components and diseases at phenotypic level on the seed yield are tabulated in table 4.8. Phenotypic path diagram shown the influences of 10 different components on yield in 133 breeding lines of sesame are presented in fig. 4.5.

4.5.1. Direct effects:

Highest positive direct effect on seed yield was recorded with number of capsules per plant (0.5738) followed by test weight (0.2868), plant height (0.1488), days to maturity (0.0460) and number of branches per plant (0.0020). This reveals that number of capsules per plant has substantial positive and direct contribution to seed yield per plant.

Direct effect on seed yield by number of capsules per plant (0.5738) was in accordance with the findings of Goudappagoudr *et al*. (2011), Gidey *et al*. (2013), Teklu *et al.* (2014) and Saxena and Bisen (2016). This indicates that if other factors are held constant, an increase in number of capsules per plant will also contribute to increase in total number of seeds per plant and reflect increased seed yield. In contrast to these results others like Sivaprasad and Yadavalli (2012), Bharathi *et al.* (2015) and Bamrotiya *et al*. (2016) reported negative direct effect.

Test weight (0.2868) had positive direct effect on seed yield which is in accordance with many workers Teklu *et al.* (2014), Bharathi *et al.* (2015), Saxena and Bisen (2016) and Agrawal *et al*. (2017). This reveals increased test weight will increase total seed weight per plant in particular genotype which ultimately results in yield improvement.

Plant height (0.1488) has shown direct effect on seed yield which is on par with the works of Parameshwarappa *et al*. (2009), Sandipan *et al*. (2010), Sivaprasad and Yadavalli (2012), Teklu *et al*. (2014) and Saxena and Bisen (2016). As increase in plant height is associated with increase in the internodes, branches, leaf area and there by seed yield. Contradictory to the results negative effect was reported by Thiyagu *et al*. (2007), Gidey *et al.* (2013), Bharathi *et al.* (2015), Bamrotiya *et al*. (2016) and Teklu *et al.* (2017)

Days to maturity (0.0460) had direct effect with seed yield were colinear with results given by Parameshwarappa *et al*. (2009), Agrawal *et al*. (2017) and Teklu *et al.* (2017). The noticed results in the present investigation reveals that late maturing genotypes of sesame will have advantage of increased number of internodes, number of branches per plant and number of capsules in turn will have possible duration for seed filling and maturity, which results in the trait days to maturity alone contributed to the increased seed yield. In deviation from these results negative direct effect reported by Goudappagoudr *et al.* (2011), Bharathi *et al*. (2015), Bamrotiya *et al.* (2016) and Saxena and Bisen (2016).

Among yield attributing parameters highest negative direct effect was seen with days to 50 per cent flowering (-0.1820), these results were similar to that of Sivaprasad and Yadavalli (2012), Bharathi *et al*. (2015), Bamrotiya *et al*. (2016) and Teklu *et al*. (2017). This indicates that usually sesame attains growth after flowering.

Therefore, early flowering paves way for maximum duration of plant growth. Hence, increase in vegetative and reproductive stages is associated with seed yield. Overall if other factors are held constant reduction in number of days taken for flowering will influence crop yield.

Phyllody (-0.0746), *Cercospora* leaf spot (-0.0300) and *Alternaria* leaf spot (-0.0114) exhibited negative direct effect on seed yield.

Highest negative direct association with phyllody (% incidence) which reveals that even initial occurrence of disease during crop growth period ultimately effect the plant growth morphology, capsule development and seed development. This disturbance in physiological stages of crop growth decreases inherent genetic potentiality of genotype in expressing actual yield.

Among foliar diseases, compared to *Alternaria* leaf spot (-0.2103), *Cercospora* leaf spot (-0.2944) had high negative direct effect on seed yield. These results were on par with Sujatha and Nadaf (2013) and Shabana (2000) in sunflower. This is mainly due to *Cercospora* leaf spot influence both vegetative and reproductive stages of plant while maximum in vegetative stages. In turn the former disease will cause more reduction in yield. In contrast to these results positive direct effect was observed by Patro and Sankar (2004). Hence from this investigation it reveals development of seedling resistance is required for *Alternaria* leaf spot while both seedling and adult plant resistance are required for *Cercospora* leaf spot.

4.5.2. Indirect effects:

Highest positive indirect effect was seen with traits test weight *via* number of capsules per plant (0.1259) followed by plant height *via* test weight (0.0724), number of capsules per plant *via* test weight (0.0629) and plant height *via* number of capsules per plant (0.0458).

Indirect effect on seed yield by test weight *via* number of capsules per plant (0.1259) followed by *via* plant height (0.0376). These results were in line with Bamrotiya *et al*. (2016). Plant height *via* test weight (0.0724) followed by via number of capsules per plant (0.0458) has shown indirect influence on seed yield. These results were on par with findings of Agrawal *et al*. (2017). Number of capsules per plant has shown it’s indirect effect on seed yield *via* test (0.0629) in

Figure 4.5 Phenotypic path diagram of sesame genotypes for yield and yield contributing traits and disease parameters.

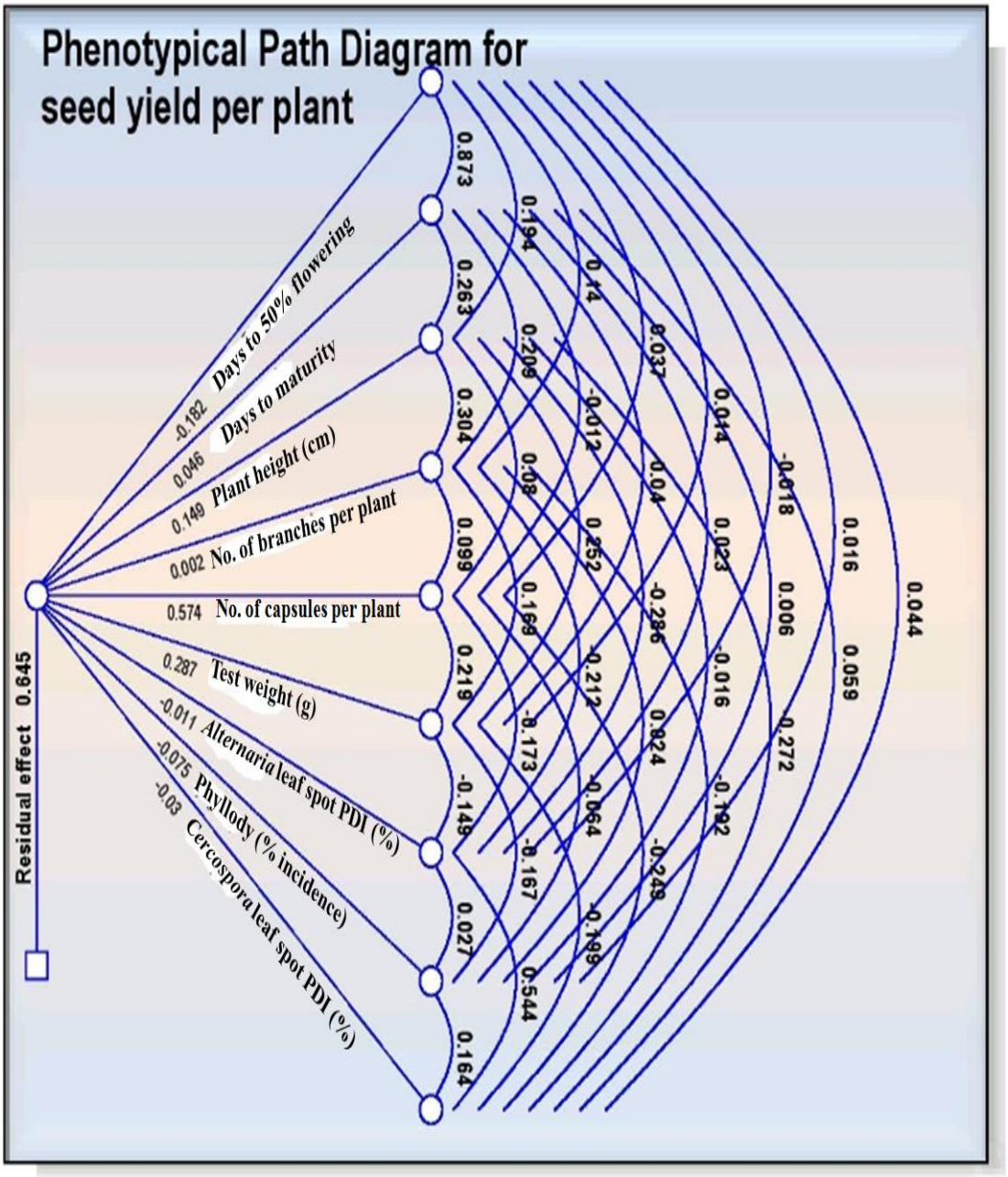

Table 4.8. Direct and Indirect effects of yield and yield attributing traits in sesame genotypes at RARS, Polasa, Jagtial during *kharif*, 2017

Trait	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Test weight (g)	Phyllody (% incidence)	*Alternaria* leaf spot PDI (%)	*Cercospora* leaf spot PDI (%)	Seed yield per plant (g)
Days to 50 per cent flowering	**-0.1820**	0.0402	0.0289	0.0003	0.0211	0.0041	-0.0012	0.0002	-0.0013	-0.0898
Days to maturity	-0.1589	**0.0460**	0.0392	0.0004	-0.0070	-0.0114	-0.0005	-0.0003	-0.0018	-0.0942
Plant height (cm)	-0.0354	0.0121	**0.1488**	0.0006	0.0458	0.0724	0.0012	0.0033	0.0082	0.2569**
Number of branches per plant	-0.0256	0.0096	0.0452	**0.0020**	0.0570	0.0486	-0.0018	0.0024	0.0057	0.1432**
Number of capsules per plant	-0.0067	-0.0006	0.0119	0.0002	**0.5738**	0.0629	0.0048	0.0020	0.0075	0.6558**
Test weight (g)	-0.0026	-0.0018	0.0376	0.0003	0.1259	**0.2868**	0.0124	0.0017	0.0060	0.4662**
Phyllody (% incidence)	-0.0029	0.0003	-0.0024	0.0000	-0.0366	-0.0479	**-0.0746**	-0.0003	-0.0049	-0.1692**
***Alternaria* leaf spot PDI (%)**	0.0032	0.0011	-0.0426	-0.0004	-0.0992	-0.0426	-0.0020	**-0.0114**	-0.0163	-0.2103**
***Cercospora* leaf spot PDI (%)**	-0.0080	0.0027	-0.0405	-0.0004	-0.1428	-0.0571	-0.0122	-0.0062	**-0.0300**	-0.2944**

Residual effect R = 0.6447

*- significance at 5% level (0.098) **- significance level at 1% (0.128)

agreement with the results given by Saxena and Bisen (2016) and followed by plant height (0.0119), which is collinear with Bharathi *et al*. (2015). With increase in plant height there will be increase in source-sink ratio thereby increase in the number of capsules per plant which ultimately increases the seed yield.

Highest negative indirect effect was seen with traits days to maturity *via* days to 50 per cent flowering (-0.1589), *Cercospora* leaf spot PDI via number of capsules per plant (-0.1428) and *Alternaria* leaf spot PDI *via* number of capsules per plant (-0.0992).

Days to maturity has shown indirect effect on seed yield *via* days to 50 per cent flowering (-0.1589) followed by *via* test weight (-0.0114). These results were in line with the findings of Goudappagoudr *et al*. (2011) and Teklu *et al*. (2017). Other traits *Cercospora* PDI has shown indirect influence *via* number of capsules per plant (-0.1428) followed by *via* test weight (-0.0571). With the incidence of disease which occurs on both vegetative and reproductive parts of the plant, there will be less number of capsules and less weight of the grain formed. *Alternaria* leaf spot PDI has shown indirect effect *via* number of capsules per plant (-0.0992) followed by plant height and test weight (-0.0426). This disease occurs on the vegetative parts and also genotypes with more height are prone to highest duration of existence of the pathogen which decreases the source-sink relation thereby decreasing the test weight and ultimately seed yield and also the persistence of disease is favoured by plants with more height.

4.6 Screening of genotypes of sesame against phyllody, powdery mildew, *Alternaria* and *Cercospora* leaf spot under natural field conditions.

The management of the disease through host plants resistance has been the best choice in all the crop improvement programmes. Utilization of resistant cultivars in farming system is the most simple, effective and economical method in the management of diseases. Besides, resistant cultivars conserve natural resources and reduces the cost, time and energy when compared to the other methods of disease management (Badwal, 1975). Therefore, an attempt was made to identify sources of resistance which can be used in disease resistance breeding programmes to mitigate loss in farmer’s field.

Keeping this fact in view, the present study disease scoring was done for phyllody, powdery mildew, *Alternaria* and *Cercospora* leaf spot. Due to climatic conditions prevailed during experimental period there was no incidence of powdery mildew.

4.6.1 Reaction of genotypes of sesame for phyllody.

Among the major constraints, phyllody is a very serious disease in most sesame growing regions, especially in warm climates (Salehi and Izadpanah, 1992). Dry weather, moderate temperature, low humidity and low rainfall are favourable conditions for development of phyllody occurrence. Phyllody is not seed borne. In nature, disease is mainly spread by leafhopper *Orosius albicinctus* and survives in alternate hosts (Akhtar *et al*., 2009). It transmits the disease causing organism mycoplasma like organism called phytoplasma, being a major hindrance for the successful production of sesame worldwide (Akhtar *et al*., 2013).The major symptoms are phyllody (production of leafy structures of floral parts),flower virescence (colour change to green), witches' broom, shoot tip fasciation, flattening of the shoot apex, intense leaf and flower bud proliferation and cracking of seed capsules (Salehi and Izadpanah., 1992., Selvanarayanan and Selvamuthukumaran., 2000., Akhtar *et al*., 2009., Catal *et al.*, 2013 and Nabi *et al*., 2015). In addition to this, infected plants exhibit reduction of inter-node distance and of leaf size (Akhtar *et al*., 2009). Both the phyllody (conversion of floral parts into leaf like structure) and witches' broom (dense mass of younger shoots grown from a single point) were the two major symptoms (Rao *et al*., 2015). Sesame is vulnerable to infection by a number of pathogens that cause considerable yield losses. Among the major diseases, phyllody is a very serious disease, which can inflict up to 80% yield loss (Kumar and Mishra, 1992 and Salehi and Izadpanah, 1992).

The severity of the disease is estimated by 0-5 scale (AICRP system). The scale showed different degrees of severity with 1-10 % infection (resistant), 11-25 % infection (moderately resistant), 26-50 % (moderately susceptible), 51-75 % (susceptible) and >75 % (highly susceptible). The results of the experiment were as follows:

The per cent disease incidence for phyllody ranged between 6.33 (SDSN-15-98) to 100.00. Two (SGPS-17-15, SDSN-15-98) genotypes showed resistant

Table 4.9. Classification of sesame genotypes based on per cent incidence of phyllody at RARS, Jagtial during *kharif*, 2017.

S.No	Disease reaction	Score	Sesame Genotypes
1.	Immune	0	----------
2.	Resistant	1-10	SGPS-17-15, SDSN-15-98
3.	Moderately resistant	11-25	30KRDS-1-18, 60KRE8-1-7, SDSN-15-79, SDSN-15-99, JCS-2696, YLM-11, YLM-66
4.	Moderately susceptible	26-50	10KRE8-3, 30KRDS-1-10, DS-1, II IBL Local (4), Kanakapur Local, SDSN-15-83, JCS-2454
5.	Susceptible	51-75	10KRE8-1, 10KRE8-2, 50KRE8-2, 30KRDS-1, 30KRDS-1-5, 30KRDS-1-26, 30KRDS-1-28, 30KRDS-1-71, 60KRE8-1-2, IISL, IISL-2, IISL-3, IISL-4, RS Black, SC-50, DSS-9, RT-273, II IBL Local (1), L-3-1, Indi Taluk-2, DS-46, GT-10, PT-10, IVTS-2017-02, IVTS-2017-11
6.	Highly susceptible	>75	10KRE8-3, 50KRE8-1, 50KRE8-3, 30KRDS-1-1, 30KRDS-1-2, 30KRDS-1-3, 30KRDS-1-6, 30KRDS-1-11, 30KRDS-1-14, 30KRDS-1-16, 30KRDS-1-18, 30KRDS-1-20, 30KRDS-1-22, 30KRDS-1-23, 30KRDS-1-25, 30KRDS-1-27, 30KRDS-1-29, 30KRDS-1-31, 60KRE8-1-3, 60KRE8-1-4, 60KRE8-1-5, 60KRE8-1-9, E840KR-2, E840KR-3, V-72, SGPS-17-15, R6127-8, R6134, R6135-7, RS I-Black, RS Black-108, 73 RK, 82 RK, 162 RK, 188 RK, 196 RK, 223 RK, N-8, Mall-1, Mall-2, OSE-560-1, SSD-7, SSD-22, OSC-79, VRI-1, II IBL Local (5), II IBL Local (6), II IBL Local (7), L-2, L-3-2, L-7, RCR-L, Mall White, Rajasthan Kishore, Indi Taluk-1, RIL-32, RIL-38, RIL-82, RIL-198, CPD Local-2016, SDSN-15-14, SDSN-15-16, SDSN-15-61, SDSN-15-65, SDSN-15-70, SDSN-15-72, SDSN-15-76, SDSN-15-77, SDSN-15-81, SDSN-15-84, SDSN-15-97, SDSN-15-109, SDSN-15-114, SDSN-15-115, RT-273, RT-376, JLS-710, AT-314, AT-332, MT-2014-14, JTS-8, JCS-2698, JCS-3280, Hima, Rajeswari, JLT-408, TKG-22, Pragathi, Swetha til ©.

reaction. Seven (30KRDS-1-18, 60KRE8-1-7, SDSN-15-79, SDSN-15-99, JCS-2696, YLM-11, YLM-66) genotypes have shown moderately resistant reaction. Seven (10KRE8-3, 30KRDS-1-10, DS-1, II IBL Local (4), Kanakapur Local, SDSN-15-83, JCS-2454) genotypes showed moderately susceptible. Twenty six genotypes have shown susceptible reaction while remaining 91 expressed highly susceptible reaction. Local check (Swetha til) was found to be with highly susceptible reaction.

From the table 4.9. it can be concluded that no entry has shown immune reaction. From the present study, two lines (SGPS-17-15 and SDSN-15-98) were found resistant to phyllody under field conditions. Rest of the entries were categorized into different reaction levels based on their performance. These results obtained were in accordance with Mirza and Aslam (1994), Gopal *et al.* (2005), Sarwar and Haq (2006), Gayatree *et al.* (2011) and Shobharani *et al.* (2016). The resistant genotypes would be useful in sesame phyllody resistant breeding programme.

4.6.2 Reaction of genotypes of sesame for *Alternaria* leaf spot.

Alternaria leaf spot of sesame caused by *Alternaria sesame* or *Alternaria sesamicola* is a major fungal disease distributed throughout the sesame growing areas of India. Symptoms of disease are the appearance of spots on leaves which are brown circular to irregular in shape and often have concentric rings which causes seed rot, pre and post-emergence death of seedlings and infect all the above ground parts resulting in considerable yield loss both qualitatively and quantitatively (Naik *et al*., 2003). Symptoms on the capsules started with minute watersoaked lesions later turned to black circular and finally such capsules drop off. The pathogen *A. sesami* also causes considerable damage to sesame capsules (Berry, 1960). Yield losses ranging from 18 to 55% were attributed to the fungus (Barboza *et al*., 1966). Occasionally, seedlings and young plants are killed exhibiting pre and post emergence damping-off and losses of 55 to 59% have been attributed to the fungus (Yu *et al*., 1987).

The favourable environment for the prevalence of disease is moderate to warm temperature and extended period of leaf wetness. The environment report was obtained from meteorology department Regional Agricultural Research Station, Polasa, Jagtial. The temperature ranges are between 20.1^0 C to 34.2^0 C and relative

humidity ranged between 53.0 to 91.9 %. The weather data is in line with the reports given by the optimum temperature for *A. alternata* was 25^0C as reported by Prashanthi and Kulkarni (2003). Sidalauskiene *et al.* (2003) reported that favourable temperatures for growing pure monocultures of *Alternaria* genus are 25^0C to 30^0C. Rodriguez *et al.* (1991) studied the intensity and dynamics of *A. porri* at relative humidity levels from 76 to 100% and observed that the minimum threshold for relative humidity was between 76 and 78%. Severity of *Alternaria* blight disease of *Brassica* was positively correlated with maximum and minimum temperature and relative humidity (Chattopadhyay *et al.*, 2005). Weather factors like temperature, wind velocity, relative humidity and sunshine were considered as critical weather factors for development of *Alternaria* blight of broad bean (Dubey, 2005). Thus, from these it can be inferred that the environmental conditions were in favour of disease preponderance at the correct age of the plant which led to the susceptible reaction. Further very severe incidence (56.66 to 100.00 %) on national, zonal and local checks indicates the sufficient disease pressure in the trial. The location may be considered as "hot spot" for evaluation of genotypes for disease resistance.

The severity of the disease is estimated by 0-5 scale (AICRP system). The scale describes the severity of the incidence in the population by estimating the per cent of the infection. Here, the plants infected in the range of 51-75 % were ranked as susceptible genotypes while > 75% given the status of highly susceptible genotypes. Further based on disease grades or rating scales, PDI was calculated. The results of the experiment were as follows:

The per cent disease index for *Alternaria* blight ranged from 56.66 (TKG-506) to 100.00. Three entries have shown susceptible reaction while remaining 130 genotypes showed highly susceptible reaction. The check for the experiment used Swetha til also showed highly susceptible reaction.

From the table 4.10. it can be seen that none of the lines found resistant to *Alternaria* leaf spot. Three lines have shown susceptible reaction while remaining were found as highly susceptible to *Alternaria* leaf spot. These results were in line with the works by Basavaraj *et al.* (2007), Marri *et al.* (2012), Pawar *et al.* (2013) and Goudapagoudr *et al.* (2013). From this study there is a need for the germplasm collection from different regions showing inherent resistance character in all the

Table 4.10. Classification of sesame genotypes based on per cent infection of *Alternaria* leaf spot at RARS, Jagtial during *kharif*, 2017.

S. No	Disease reaction	Score	Sesame Genotypes
1.	Immune	0	--------
2.	Resistant	1	-------
3.	Moderately resistant	2	-------
4.	Moderately susceptible	3	---------
5.	Susceptible	4	TKG-511, TKG-506, IVTS-2017-02
6.	Highly susceptible	5	10KRE8-1, 10KRE8-2, 10KRE8-3, 50KRE8-1, 50KRE8-2, 50KRE8-3, 30KRDS-1, 30KRDS-1-1, 30KRDS-1-2, 30KRDS-1-3, 30KRDS-1-5, 30KRDS-1-6, 30KRDS-1-7, 30KRDS-1-7, 30KRDS-1-10, 30KRDS-1-11, 30KRDS-1-14, 30KRDS-1-16, 30KRDS-1-18, 30KRDS-1-20, 30KRDS-1-22, 30KRDS-1-23, 30KRDS-1-25, 30KRDS-1-26, 30KRDS-1-27, 30KRDS-1-28, 30KRDS-1-29, 30KRDS-1-31, 30KRDS-1-71, 60KRE8-1-2, 60KRE8-1-3, 60KRE8-1-4, 60KRE8-1-5, 60KRE8-1-7, 60KRE8-1-9, E840KR-2, E840KR-3, V-72, IISL, IISL-2, IISL-3, IISL-4, SGPS-17-15, R6127-8, R6134, R6135-7, RS Black, RS I-Black, RS Black-108, 73 RK, 82 RK, 162 RK, 188 RK, 196 RK, 223 RK, N-8, Mall-1, Mall-2, OSE-560-1, SSD-7, SSD-22, OSC-79, SC-50, DS-1, DSS-9, RT-273, VRI-1, II IBL Local (1), II IBL Local (4), II IBL Local (5), II IBL Local (6), II IBL Local (7), L-2, L-3-1, L-3-2, L-7, RCR-L, Mall White, Rajasthan Kishore, Kanakapur Local, Indi Taluk-1, Indi Taluk-2, RIL-32, RIL-38, RIL-82, RIL-198, CPD Local-2016, SDSN-15-03, SDSN-15-14, SDSN-15-16, SDSN-15-58, SDSN-15-61, SDSN-15-65, SDSN-15-70, SDSN-15-72, SDSN-15-76, SDSN-15-77, SDSN-15-79, SDSN-15-81, SDSN-15-83, SDSN-15-84, SDSN-15-97, SDSN-15-98, SDSN-15-99, SDSN-15-109, SDSN-15-114, SDSN-15-115, RT-273, RT-376, JLS-710, AT-314, AT-332, DS-46, GT-10, MT-2014-14, JTS-8, PT-10, IVTS-2017-11, JCS-2454, JCS-2696, JCS-2698, JCS-3280, Hima, Rajeswari, JLT-408, YLM-11, YLM-66, TKG-22, Pragathi, Swetha til ©.

environmental conditions and verify for the resistant lines which can be used in hybridization programme using back cross method. As there is lack of resistance in germplasm it may be improved by mutation breeding approach and somaclonal variations.

4.6.3 Reaction of genotypes of sesame for *Cercospora* leaf spot.

Symptoms of the disease are, first appears as small, angular brown leaf spots of 3mm diameter and may increase upto 10 mm with grey center and dark margin delimited by veins. Stage of crop at which disease appears is 4-6 leaf stage of crop and continues till maturity (Status Paper on Oilseeds, 2014). Capsule shows more or less circular, brown to black lesions ranging upto 7 mm with deformed and shrivelled seeds. *Cercospora* leaf spot (CLS) is considered to be one of the most prevalent diseases of sesame that could lead to about 22 to 53% reduction in yield (Enikuomehin *et al*., 2002).

The favourable conditions for CLS are leaf wetness of >11 hours, relative humidity 70 to 90 % and temperature 25^0 C to 28^0 C. Since leaf wetness is not actually measured relative humidity is substituted. All the factors present simultaneously begin and progress the disease (Harveson, 2013). Collinear to these reports, temperatures and relative humidity prevailed during the experimental period was in range between 20.1^0 C to 34.2^0 C and 53.0 to 91.9 % respectively. *Cercopora* leaf spot severity on sesame had significant reaction and was positively correlated with rainfall (Poswal and Misari, 1994). The prescribed conditions were present during the experimentation period because of that severe incidence of disease was observed. The genotypes with late maturity showed less severity of disease while that for early maturity showed 100 % severity. Late maturing types were less affected by the disease than the early maturing and unbranched types (Poswal and Misari, 1994). The severity of disease is very high that it recorded that all the genotypes showed susceptible reaction similar to the results of *Alternaria* leaf spot.

The severity of the disease is estimated by 0-5 scale (AICRP system). The scale describes the severity of the incidence in the population by estimating the per cent of the infection. Here, the plants infected in the range of 51-75 % were ranked

as susceptible genotypes while > 75% given the status of highly susceptible genotypes. The results of the experiment were as follows:

According to the severity index three genotypes showed susceptible reaction (SDSN-15-03, YLM-11, YLM-66) while remaining genotypes have shown highly susceptible reaction. The check for the experiment used Swetha til also showed highly susceptible reaction.

From the table 4.11. it can be seen that no entry shown resistant reaction. These results were supported by Nahunnaro and Tanwari (2012), Vishnuvardhan *et al.* (2012) in groundnut. In contrast to these results sesame cultivars like IS4, IS15, IS29 were reported as resistant (Kushwaha and Kaushal, 1970 and Vyas, 1981) and accessions from Adana and Ndok was reported resistant by Udo *et al.* (2017). Identification of sources of resistance to CLS is important for development of *Cercospora* resistant varieties.

Table 4.11. Classification of sesame genotypes based on per cent infection of *Cercospora* leaf spot at RARS, Jagtial during *kharif*, 2017.

S.No	Disease reaction	Score	Sesame Genotypes
1.	Immune	1	----------
2.	Resistant	2	----------
3.	Moderately resistant	3	----------
4.	Moderately susceptible	4	----------
5.	Susceptible	5	SDSN-15-03, YLM-11, YLM-66.
6.	Highly susceptible	6	10KRE8-1, 10KRE8-2, 10KRE8-3, 50KRE8-1, 50KRE8-2, 50KRE8-3, 30KRDS-1, 30KRDS-1-1, 30KRDS-1-2, 30KRDS-1-3, 30KRDS-1-5, 30KRDS-1-6, 30KRDS-1-7, 30KRDS-1-7, 30KRDS-1-10, 30KRDS-1-11, 30KRDS-1-14, 30KRDS-1-16, 30KRDS-1-18, 30KRDS-1-20, 30KRDS-1-22, 30KRDS-1-23, 30KRDS-1-25, 30KRDS-1-26, 30KRDS-1-27, 30KRDS-1-28, 30KRDS-1-29, 30KRDS-1-31, 30KRDS-1-71, 60KRE8-1-2, 60KRE8-1-3, 60KRE8-1-4, 60KRE8-1-5, 60KRE8-1-7, 60KRE8-1-9, E840KR-2, E840KR-3, V-72, IISL, IISL-2, IISL-3, IISL-4, SGPS-17-15, R6127-8, R6134, R6135-7, RS Black, RS I-Black, RS Black-108, 73 RK, 82 RK, 162 RK, 188 RK, 196 RK, 223 RK, N-8, Mall-1, Mall-2, OSE-560-1, SSD-7, SSD-22, OSC-79, SC-50, DS-1, DSS-9, RT-273, VRI-1, II IBL Local (1), II IBL Local (4), II IBL Local (5), II IBL Local (6), II IBL Local (7), L-2, L-3-1, L-3-2, L-7, RCR-L, Mall White, Rajasthan Kishore, Kanakapur Local, Indi Taluk-1, Indi Taluk-2, RIL-32, RIL-38, RIL-82, RIL-198, CPD Local-2016, SDSN-15-14, SDSN-15-16, , SDSN-15-58, SDSN-15-61, SDSN-15-65, SDSN-15-70, SDSN-15-72, SDSN-15-76, SDSN-15-77, SDSN-15-79, SDSN-15-81, SDSN-15-83, SDSN-15-84, SDSN-15-97, SDSN-15-98, SDSN-15-99, SDSN-15-109, SDSN-15-114, SDSN-15-115, RT-273, RT-376, JLS-710, AT-314, AT-332, DS-46, GT-10, MT-2014-14, TKG-511, JTS-8, TKG-506, PT-10, IVTS-2017-02, IVTS-2017-11, JCS-2454, JCS-2696, JCS-2698, JCS-3280, Hima, Rajeswari, JLT-408, TKG-22, Pragathi, Swetha til ©.

Plate 1. Overall experimental plot view at RARS, Polasa, Jagtial during *kharif*, 2017

Plate 2. Symptom of phyllody disease in field.

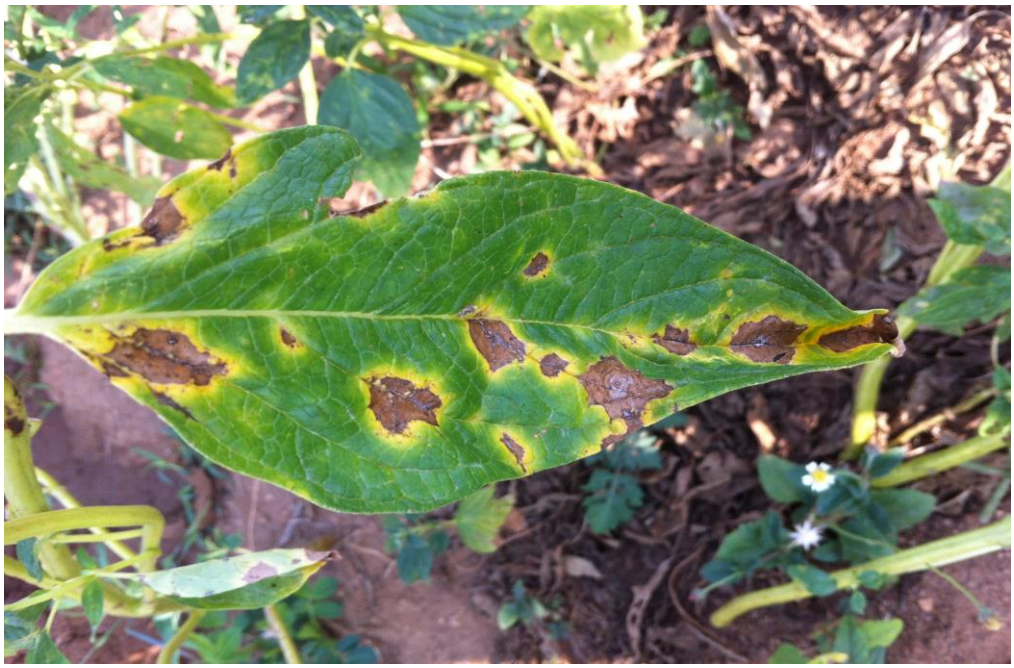

Plate 3. Symptom of *Alternaria* leaf spot in field.

Plate 4. Symptom of *Cercospora* leaf spot in field.

Plate 5. Resistant genotypes for phyllody (SGPS-17-15 and SDSN-15-98)

SDSN-15-98

SGPS-17-15

Plate 6. Moderately Resistant genotypes for Phyllody (30KRDS-1-18, YLM-11, YLM-66)

30 KRDS-1-18

YLM-11

YLM-66

Chapter V

SUMMARY AND CONCLUSIONS

Sesame is an important oil seed crop cultivated in India and called as "**Queen of oilseed crops**" by virtue of its excellent quality. The presence of variability in a crop is important for genetic studies and consequent use for improvement and selection. India has second highest acreage, production and exporter of sesame seeds globally. Yet with low productivity small and marginal farmers are growing this crop unscientifically. The main reason for the low productivity of this crop is due to the attack of various fungal and phytoplasmal diseases. Powdery mildew, *Alternaria* and *Cercospora* leaf spot and phytoplasma disease such as phyllody are major yield reducing biotic factors in sesame. Development of resistant varieties against these diseases is one of the thrust areas identified in sesame improvement programmes. There is ample scope for improving the productivity of this important oil seed crop through varietal improvement and development.

In the present investigation entitled "Studies on genetic diversity in advanced mutant breeding lines of sesame (*Sesamum indicum* L.)" 133 genotypes were evaluated in randomized block design to find out the extent of genetic variability for yield and yield attributing traits, disease reaction, their association and genetic divergence with seed yield. The observations were recorded as mean values on seven quantitative characters along with three disease parameters and were subjected to genetic variability, correlation, path analysis and genetic divergence. Also, the reaction pattern of phyllody, *Alternaria* and *Cercospora* leaf spot was studied to identify the sources of resistance. The results of the study and conclusions drawn from the experiment are summarized below.

Breeding lines differed highly significant for days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, seed yield per plant (g). In case of diseases phyllody, *Alternaria* and *Cercospora* leaf spot were significant. Non-significant results observed for test weight (g) as evidenced by "F" test of ANOVA.

Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were high for characters number of branches per plant, number of capsules per plant, seed yield per plant and phyllody (% incidence). Moderate PCV

and GCV were recorded for days to 50 per cent flowering, plant height and low for days to maturity. Other characters *Alternaria* PDI (%) and *Cercospora* PDI (%) had shown moderate PCV and low GCV, while test weight showed high PCV and moderate GCV. This type of wide range of variation provides ample scope of selection for desired genotypes and further improvement.

High heritability coupled with high genetic advance as per cent of mean was observed for days to 50 per cent flowering, plant height, number of branches per plant, number of capsules per plant, seed yield per plant and phyllody (% incidence) suggesting that, these characters were controlled by additive gene action. This type of characters could be improved by simple phenotypic selection. Moderate heritability associated with low GAM was observed for test weight which suggests the role of dominant gene action and can be improved using heterosis breeding.

The 133 breeding lines were distributed into 19 clusters based on the D^2 values. Among the nineteen clusters, cluster I was the largest comprising of 54 breeding lines followed by cluster II with 28 breeding lines, cluster III with 16 lines, cluster IV with 16 lines, clusters IX and XIV each with 3 lines. Remaining clusters V, VI, VII, VIII, X, XI, XII, XIII, XV, XVI, XVII, XVIII and XIX were solitary. Cluster analysis indicates the presence of large amount of heterogeneity among the genotypes. The highest inter cluster distance (392.03) is between clusters XIV and XV while lowest (14.81) is between X and XI. The genotypes in these clusters if used in hybridization programme produce useful segregants for yield improvement in recombination breeding programmes.

The maximum contribution towards genetic divergence was by the character days to 50 per cent flowering (42.74 per cent), followed by seed yield per plant (16.61 per cent), number of capsules per plant (9.44 per cent), days to maturity (8.58 per cent), plant height (8.07 per cent), phyllody (8.03 per cent), number of branches per plant (2.98 per cent), *Alternaria* leaf spot (1.81 per cent), *Cercospora* leaf spot (1.15 per cent) and test weight (0.62 per cent). Five characters *i.e.*, days to 50 per cent flowering, days to maturity, plant height, number of capsules per plant, seed yield per plant contributed more than 80% towards genetic divergence. This diversity paves way for further improvement in breeding programmes.

A significant positive correlation was recorded between seed yield and number of capsules per plant, test weight, plant height and number of branches per plant at both phenotypic and genotypic level. Whereas, negative significant association of seed yield with disease incidence phyllody (% incidence), *Alternaria* PDI (%) and *Cercospora* PDI (%). Days to 50 per cent flowering showed negative non-significant association with seed yield at both levels. It refers that selection of these characters *i.e.*, number of capsules per plant, test weight, plant height and number of branches per plant ultimately result in the higher seed yield.

Highest positive direct effect on seed yield was recorded with character number of capsules per plant followed by test weight, plant height, days to maturity and number of branches per plant. Therefore, these traits may be considered as the principle traits, while selecting for seed yield. Selection indices may be formed by considering all these five characters for improvement of seed yield.

In disease screening under natural epiphytotic conditions, two entries SGPS-17-15 and SDSN-15-98 have shown resistance reaction against phyllody while seven genotypes were moderately resistant. These resistant genotypes identified during the experimental period should be confirmed and further can be used as donors in resistance breeding through back cross programme for the development of new resistant varieties. All the genotypes have shown susceptible reaction to *Alternaria* and *Cercospora* leaf spots. None of the entry has shown immune reaction to all the three diseases. So, there is a need for development of resistant lines by exploring the wild relatives, germplasm accessions, mutational breeding and somaclonal variants.

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*- Original is not seen

Appendix A. List of genotypes significantly superior for yield and their traits with mean performances including diseases.

S.No	Genotype	Seed yield per plant (g)	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Test weight (g)	Phyllody (% incidene)	*Alternaria* leaf spot (PDI)	*Cercospora* leaf spot (PDI)
1	YLM-66	9.40	43.33	83.00	115.50	4.67	32.00	2.65	71.67	22.67	65.33
2	SDRN-15-97	8.66	57.00	87.67	93.10	3.67	57.00	2.53	95.00	90.67	100.00
3	RT-273	7.94	49.33	79.67	82.05	5.00	39.66	2.29	89.66	68.67	91.00
4	DS-46	7.48	55.67	86.33	118.70	5.67	49.00	2.56	78.00	67.33	84.00
5	YLM-11	6.15	42.67	82.33	115.90	4.67	32.66	2.56	76.67	24.33	63.33
6	AT-314	6.12	56.33	86.33	120.20	5.00	58.67	2.99	73.00	84.33	85.00
7	SDRN-15-14	5.97	57.33	88.67	90.00	6.00	61.00	2.50	100.00	94.33	100.00
8	SDRN-15-03	5.81	56.33	86.67	113.30	7.66	35.67	2.58	90.00	83.33	68.67
9	Indi Taluk-2	5.60	51.33	84.33	72.80	6.67	36.00	2.47	98.67	64.67	100.00
10	SGPS-17-15	4.38	44.00	74.00	85.90	4.00	21.66	2.90	94.00	9.83	98.00
11	SDRN-15-98	2.51	56.33	86.67	92.00	4.00	15.00	2.35	91.00	6.33	91.00

Appendix B. Means of genotypes with yield and disease reaction.

S. No	Genotypes	Seed yield per plant (g)	Phyllody (% incidence)		*Alternaria* leaf spot		*Cercospora* leaf spot	
1	10KRE8-1	1.31	57.33	S	97.50	HS	96.00	HS
2	10KRE8-2	3.96	63.33	S	96.00	HS	98.00	HS
3	10KRE8-3	1.23	44.33	MS	98.00	HS	98.00	HS
4	50KRE8-1	0.82	92.00	HS	97.50	HS	100.00	HS
5	50KRE8-2	3.31	70.33	S	98.00	HS	90.00	HS
6	50KRE8-3	2.06	87.67	HS	89.00	HS	90.00	HS
7	30KRDS-1	3.41	54.67	S	89.50	HS	90.00	HS
8	30KRDS-1-1	2.96	80.67	HS	90.00	HS	82.50	HS
9	30KRDS-1-2	3.17	77.33	HS	90.00	HS	90.00	HS
10	30KRDS-1-3	2.78	83.17	HS	91.00	HS	96.00	HS
11	30KRDS-1-5	3.64	70.67	S	86.00	HS	90.00	HS
12	30KRDS-1-6	1.75	89.67	HS	97.50	HS	100.00	HS
13	30KRDS-1-7	1.21	95.33	HS	86.50	HS	84.83	HS
14	30KRDS-1-8	2.10	14.83	HS	81.50	HS	90.00	HS
15	30KRDS-1-10	1.81	29.00	MS	86.50	HS	93.50	HS
16	30KRDS-1-11	3.47	72.00	HS	83.50	HS	72.67	HS
17	30KRDS-1-14	3.08	85.00	HS	93.00	HS	95.00	HS
18	30KRDS-1-16	2.66	86.67	HS	88.00	HS	92.50	HS
19	30KRDS-1-18	2.15	88.33	MR	98.50	HS	100.00	HS
20	30KRDS-1-20	3.12	85.33	HS	93.00	HS	98.00	HS
21	30KRDS-1-22	3.35	72.00	HS	95.50	HS	93.00	HS
22	30KRDS-1-23	2.19	89.67	HS	80.50	HS	100.00	HS
23	30KRDS-1-25	2.54	77.33	HS	89.50	HS	100.00	HS
24	30KRDS-1-26	1.17	63.00	S	95.50	HS	96.33	HS
25	30KRDS-1-27	1.80	92.33	HS	89.50	HS	89.00	HS
26	30KRDS-1-28	4.58	68.33	S	88.50	HS	92.67	HS
27	30KRDS-1-29	4.28	88.67	HS	95.50	HS	100.00	HS
28	30KRDS-1-31	2.44	75.33	HS	95.00	HS	86.00	HS
29	30KRDS-1-71	2.73	65.67	S	83.00	HS	100.00	HS
30	60KRE8-1-2	3.06	66.00	S	75.00	HS	88.00	HS
31	60KRE8-1-3	3.52	88.67	HS	88.00	HS	92.00	HS
32	60KRE8-1-4	2.57	84.67	HS	75.00	HS	100.00	HS
33	60KRE8-1-5	2.82	93.67	HS	82.00	HS	100.00	HS
34	60KRE8-1-7	1.74	24.17	MR	88.00	HS	92.00	HS
35	60KRE8-1-9	0.73	92.00	HS	80.00	HS	81.67	HS
36	E840KR-2	1.74	92.00	HS	88.50	HS	92.00	HS
37	E840KR-3	1.84	94.67	HS	89.50	HS	100.00	HS
38	V-72	3.12	85.67	HS	74.00	HS	88.00	HS
39	IISL	1.12	61.00	S	85.00	HS	91.33	HS

40	IISL-2	1.42	70.33	S	85.00	HS	98.00	HS
41	IISL-3	2.57	54.33	S	96.00	HS	91.67	HS
42	IISL-4	2.86	53.33	S	90.50	HS	96.00	HS
43	SGPS-17-15	4.38	9.83	R	94.00	HS	98.00	HS
44	R6127-8	2.09	84.33	HS	89.00	HS	100.00	HS
45	R6134	1.34	92.67	HS	95.50	HS	100.00	HS
46	R6135-7	3.63	75.33	HS	92.00	HS	100.00	HS
47	RS Black	3.35	63.67	S	96.50	HS	100.00	HS
48	RS I-Black	2.10	80.33	HS	86.50	HS	100.00	HS
49	RS Black-108	1.69	85.67	HS	97.00	HS	100.00	HS
50	73 RK	4.77	76.00	HS	81.50	HS	100.00	HS
51	82 RK	1.84	90.67	HS	80.50	HS	90.00	HS
52	162 RK	1.38	92.33	HS	92.50	HS	100.00	HS
53	188 RK	2.26	87.00	HS	97.00	HS	100.00	HS
54	196 RK	2.24	87.67	HS	92.00	HS	100.00	HS
55	223 RK	1.24	90.00	HS	89.50	HS	90.00	HS
56	N-8	3.29	81.33	HS	86.00	HS	100.00	HS
57	Mall-1	1.91	86.00	HS	100.00	HS	100.00	HS
58	Mall-2	3.09	74.67	HS	95.00	HS	100.00	HS
59	OSE-560-1	1.96	80.00	HS	75.00	HS	100.00	HS
60	SSD-7	3.81	84.67	HS	88.50	HS	100.00	HS
61	SSD-22	1.13	91.67	HS	98.50	HS	100.00	HS
62	OSC-79	2.76	76.00	HS	72.00	HS	100.00	HS
63	SC-50	5.26	57.67	S	90.00	HS	100.00	HS
64	DS-1	2.25	35.83	MS	82.50	HS	78.00	HS
65	DSS-9	4.48	68.67	S	94.50	HS	92.50	HS
66	RT-273	7.94	68.67	S	89.50	HS	91.00	HS
67	VRI-1	4.01	81.67	HS	82.00	HS	100.00	HS
68	II IBL Local (1)	0.74	52.67	S	96.00	HS	96.00	HS
69	II IBL Local (4)	0.66	48.83	MS	96.50	HS	100.00	HS
70	II IBL Local (5)	0.26	100.00	HS	98.00	HS	100.00	HS
71	II IBL Local (6)	1.15	92.33	HS	99.00	HS	98.00	HS
72	II IBL Local (7)	1.13	49.67	HS	97.00	HS	100.00	HS
73	L-2	0.96	97.67	HS	97.00	HS	100.00	HS
74	L-3-1	2.29	53.67	S	97.50	HS	100.00	HS
75	L-3-2	3.39	78.67	HS	95.50	HS	100.00	HS
76	L-7	1.50	85.67	HS	96.50	HS	100.00	HS
77	RCR-L	3.54	72.67	HS	91.50	HS	100.00	HS
78	Mall White	1.87	82.00	HS	90.00	HS	90.00	HS
79	Rajasthan Kishore	1.30	90.00	HS	93.50	HS	96.00	HS
80	Kanakapur Local	1.51	34.00	MS	85.50	HS	100.00	HS
81	Indi Taluk-1	1.53	77.33	HS	91.50	HS	100.00	HS

82	Indi Taluk-2	5.60	64.67	S	98.50	HS	100.00	HS
83	RIL-32	0.84	89.67	HS	97.50	HS	100.00	HS
84	RIL-38	1.10	92.00	HS	95.50	HS	100.00	HS
85	RIL-82	2.56	81.33	HS	97.00	HS	100.00	HS
86	RIL-198	0.99	87.67	HS	97.00	HS	100.00	HS
87	CPD Local-2016	3.23	92.67	HS	89.50	HS	80.50	HS
88	SDRN-15-03	5.81	83.33	HS	90.00	HS	68.67	S
89	SDRN-15-14	5.97	94.33	HS	100.00	HS	100.00	HS
90	SDRN-15-16	2.85	83.00	HS	94.00	HS	92.00	HS
91	SDRN-15-58	2.95	91.00	HS	72.50	HS	81.33	HS
92	SDRN-15-61	3.26	95.67	HS	87.00	HS	88.33	HS
93	SDRN-15-65	1.59	92.00	HS	93.50	HS	94.00	HS
94	SDRN-15-70	1.77	98.67	HS	94.00	HS	94.33	HS
95	SDRN-15-72	1.33	100.00	HS	94.00	HS	92.33	HS
96	SDRN-15-76	0.96	80.00	HS	84.50	HS	93.33	HS
97	SDRN-15-77	1.20	83.00	HS	91.00	HS	96.00	HS
98	SDRN-15-79	4.21	24.33	MR	95.50	HS	96.00	HS
99	SDRN-15-81	3.65	85.67	HS	93.50	HS	100.00	HS
100	SDRN-15-83	3.13	34.67	MS	95.00	HS	100.00	HS
101	SDRN-15-84	1.73	83.00	HS	94.00	HS	100.00	HS
102	SDRN-15-97	8.66	90.67	HS	95.00	HS	100.00	HS
103	SDRN-15-98	2.51	6.33	R	91.00	HS	91.00	HS
104	SDRN-15-99	1.05	17.00	MR	88.00	HS	92.00	HS
105	SDRN-15-109	2.29	97.67	HS	90.00	HS	92.67	HS
106	SDRN-15-114	3.15	98.00	HS	96.00	HS	98.33	HS
107	SDRN-15-115	2.98	92.00	HS	90.00	HS	98.67	HS
108	RT-376	1.69	96.67	HS	84.50	HS	92.00	HS
109	RT-378	2.95	85.00	HS	82.00	HS	84.67	HS
110	JLS-710	4.42	94.33	HS	90.00	HS	89.67	HS
111	AT-314	6.12	84.33	HS	73.00	HS	85.00	HS
112	AT-332	3.56	92.33	HS	76.50	HS	88.67	HS
113	DS-46	7.48	67.33	S	78.00	HS	84.00	HS
114	GT-10	5.09	70.00	S	87.00	HS	90.00	HS
115	MT-2014-14	2.32	89.33	HS	84.00	HS	87.67	HS
116	TKG-511	1.71	84.83	HS	58.50	S	84.67	HS
117	JTS-8	3.31	93.00	HS	85.00	HS	89.00	HS
118	TKG-506	4.70	90.00	HS	56.50	S	86.67	HS
119	PT-10	5.59	56.00	S	84.50	HS	87.33	HS
120	IVTS-2017-02	1.71	55.67	S	74.50	S	83.33	HS
121	IVTS-2017-11	3.76	70.67	S	75.00	HS	78.67	HS
122	JCS-2454	3.29	39.33	MS	86.00	HS	84.00	HS
123	JCS-2696	3.09	17.00	MR	95.00	HS	100.00	HS
124	JCS-2698	1.91	86.00	HS	100.00	HS	100.00	HS

125	JCS-3280	1.96	80.00	HS	75.00	HS	100.00	HS
126	Hima	1.60	81.00	HS	84.50	HS	100.00	HS
127	Rajeswari	1.69	73.67	HS	98.50	HS	100.00	HS
128	JLT-408	0.89	93.67	HS	79.50	HS	100.00	HS
129	YLM-11	6.15	24.33	MR	76.50	HS	63.33	S
130	YLM-66	9.40	22.67	MR	71.50	S	65.33	S
131	TKG-22	0.67	74.00	HS	91.50	HS	100.00	HS
132	Pragathi	5.33	80.67	HS	82.00	HS	92.67	HS
133	Swetha til ©	0.56	88.33	HS	100.00	HS	100.00	HS

Appendix C. Genotypes in the clusters with concerned mean performance of traits for yield contributing characters and diseases.

S. No	Character	Cluster	Mean	Genotypes
1.	Days to 50 per cent flowering	IX	42.67	N-8, Mall-2 and YLM-11
2.	Days to maturity	XV	74.00	SGPS-17-15
3.	Plant height (cm)	XIV	120.20	Hima, Swetha and Rajeswari
4.	Number of branches per plant	XIII and XVII	6.00	60KRE8-1-4 and SDSN-15-14
5.	Number of capsules per plant	XVII	61.00	SDSN-15-14
6.	Test weight (g)	VII	2.95	SC-50
7.	Seed yield per plant (g)	XIX	9.40	YLM-66
8.	Phyllody (% incidence)	XV	9.83	SGPS-17-15
9.	*Alternaria* and *Cercospora* leaf spot (PDI)	XIX	65.33	YLM-66