

Genetic Assessment for Seed Yield and Quality Traits in Sesame (*Sesamum indicum* L.)

THESIS

Submitted to

Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur

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for the Degree of**

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In

**AGRICULTURE
(GENETICS AND PLANT BREEDING)**

By

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2021

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This is to certify that the thesis entitled “**Genetic Assessment for Seed Yield and Quality Traits and in Sesame (*Sesamum indicum* L.)**” submitted in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE IN AGRICULTURE (Genetics and Plant Breeding)** of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur is a record of the bonafide research work carried out by **Sakshi Seth**, I.D. No. 190116012 under my guidance and supervision. The subject of the thesis has been approved by the student’s Advisory Committee and the Director of Instructions.

All the assistance and help received during the course of the investigation has been acknowledged by her.

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LIST OF ABBREVIATIONS

%	-	Percentage
$\sqrt{\quad}$	-	Square root
Σ	-	Summation
$^{\circ}\text{C}$	-	Degree Celsius
<i>et al.</i>	-	And coworkers
i.e.	-	That is
%	-	Percentage
Max	-	Maximum
Min	-	Minimum
CD	-	Critical difference
d.f	-	Degree of freedom
g	-	Gram
SE	-	Standard error
DFI	-	Days to flower initiation
DFF	-	Days to 50% flowering
DM	-	Days to maturity
PH	-	Plant height
NPB	-	Number of primary branches per plant
NSB	-	Number of secondary branches per plant
SYP	-	Seed yield per plant
OC	-	Oil content
NCP	-	Number of capsules per plant
NSPC	-	Number of seeds per capsule
CL	-	Capsule length
PCV	-	Phenotypic coefficient of variation

GCV	-	Genotypic coefficient of variation
CC	-	Corolla color
CoH	-	Corolla hairiness
BP	-	Branching pattern
SH	-	Stem hairiness
LH	-	Leaf hairiness
LS	-	Leaf shape
BLM	-	Basal leaf margin
CaH	-	Capsule hairiness
CA	-	Capsule arrangement
PGT	-	Plant growth type
PGH	-	Plant growth habit
MSC	-	Main stem colour
BH	-	Branching habit
LIBL	-	Lobe incision of basal leaf
PC	-	Petiole colour
NFPLA	-	No. of flowers per leaf axil
NLPC	-	No. of locules per capsule
CDC	-	Colour of dry capsule
TCB	-	Type of capsule beak
SCC	-	Seed coat colour
OA	-	Oxalic Acid

Chapter – I

INTRODUCTION

INTRODUCTION

Sesame (*Sesamum indicum* L.) is a self-pollinated Pedaliaceae family member that grows as a short day, erect herbaceous annual plant. It is widely grown in tropical, subtropical and temperate climates around the world, but mostly in Asia, Africa, and South America (Anilakumar *et al.*, 2010). Despite the fact that the crop originated in Africa, India is regarded to be a key centre of genetic variation (Maiti *et al.*, 2012). The crop is drought tolerant, grows well on most well-drained soils and in a variety of agroclimatic regions, and is well-suited to varied rotations.

Sesame is one of the world's oldest cultivated oilseed crops. It is mostly farmed for its seed, which contains oil (48-55 percent) and is a good source of protein (20-28 percent) and carbohydrates (23 percent). Its seed additionally has calcium, potassium, tryptophan, and methionine. Its exceptional stability is ascribed to the presence of antioxidant lignans (sesamin, sesamolin and sesaminol (Kiruthika *et al.*, 2018), for which sesame seeds are known as "The seed of immortality". Sesame oil includes fatty acids such as oleic acid (43 percent), linoleic acid (35 percent), palmitic acid (11 percent), and stearic acid (7 percent). Sesame has earned the title of "Queen of Oilseeds" due to its high quality oil.

After groundnut, rapeseed-mustard, sunflower and soybean, sesame is India's fifth most important edible oil crop. Sesame seed is processed into oil and meal for around 70% of the world's supply. It is used in the creation of sweets as condiments, as well as in culinary and confectionery applications. Paints, scented oils, and medications all employ sesame oil in their manufacturing processes. It possesses bacteriocidal and insecticidal properties, as well as antioxidant properties that help prevent cholesterol absorption and synthesis in the liver.

Sesame is grown over 1625 thousand hectares in India, with a production of 812 thousand tonnes and a productivity of 500 kg/ha (Anonymous, 2020-21). Madhya Pradesh is placed second in area and output, with 315 thousand ha and a production of 126 thousand tonnes and a productivity of 400 kg/ha.

In sesame, genetic variation exists for agronomically important traits, yet productivity remains low in India. Low yields are due to a lack of wider adaptability, non synchronous maturity, the presence of pre and post fertilisation barriers, as well as lack of superior high yielding varieties with built in resistance to biotic and abiotic stresses. In contrast to cereals, this crop's under development is due to a lack of proper research. Climate, nutrients, water availability, inter and intraspecific competitors, pests and diseases, as well as sociocultural and socioeconomic factors, all have an impact on crop performance. Since India has a lot of genetic diversity in *Sesamum* species, taking advantage of that diversity will help improve the crop's genetic background. There is a need to take advantage of sesame's genetic variability in order to generate high yielding cultivars that can adapt and produce in a changing environment.

Yield, on the other hand, is a product of yield components and is controlled by several genes interacting with the environment. Selecting parents only on the basis of yield can be deceiving. For intelligent breeding processes to evolve high yielding varieties, it is vital to understand the mode of inheritance of the yield components, their correlation, and the relationship between each component and yield (Robinson *et al.*, 1951 and Johnson *et al.*, 1955). It allows for the estimate of the interrelationship among two desired features and aids in the mutual enhancement of both desirable traits through a common selection programme. Path coefficient analysis aids in indirect selection for genetic enhancement of yield in sesame, which is a low heritable trait. Estimating heritability and genetic advance also aids a breeder in comprehending the magnitude, nature, and interaction of genotype and environmental variation of traits.

The study of genetic divergence aids breeders in selecting genetically diverse parents for a hybridization programme. Principal Component Analysis (PCA) and D^2 can be used to identify superior lines in a diverse breeding population by measuring the extent of genetic distance between lines for producing high yielding good quality cultivars and finding yield contributing factors.

The presence of oxalic acid is one of the biggest barriers to sesame seed consumption. Oxalic acid, calcium (9.75 g 100 g⁻¹), phosphorus (4.29 g 100 g⁻¹), and other minerals are abundant in the seed coat of sesame. The presence of oxalic acid (14.3 g 100 g⁻¹) renders the calcium and phosphorus in the seed unavailable and imparts an unpleasant flavour. It may bind with calcium forming calcium oxalate, which contributes to kidney stone formation. As a result of the development of sesame lines with minimal anti-nutritional components, considerable amounts of calcium and phosphorus will be available for human consumption (Pathak *et al.*, 2014).

The present investigation was therefore conducted to evaluate different germplasm lines of sesame with following objectives.

Objectives of investigation

1. Characterization of genotypes based on morphological traits
2. To estimate genetic variability, character association and direct and indirect effects of various traits on seed yield
3. To quantify the extent of genetic divergence (D^2 statistics) and rank genotypes based on Principal Component Analysis
4. To identify putative lines for low oxalic acid and high oil content

Chapter – II

REVIEW OF LITERATURE

REVIEW OF LITERATURE

Sesame is considered as one of the most important oilseed crop because of high nutritional value and oil content. But requisite attention has been lacking for its genetic improvement. Thus, an attempt has been made in the present investigation to evaluate sesame genotypes through yield performance and by estimating genetic variability and genetic divergence for developing high yielding varieties.

The relevant literature pertaining to the present investigation is briefly reviewed under the following heading.

- 2.1 Morphological Characterization
- 2.2 Genetic variation
 - 2.2.1 Genotypic and phenotypic coefficient of variation
 - 2.2.2 Heritability and genetic advance
- 2.3 Association analysis
 - 2.3.1 Correlation coefficient analysis
 - 2.3.2 Path coefficient analysis
- 2.4 Genetic divergence using Mahalanobis D^2 analysis
- 2.5 Principal Component Analysis
- 2.6 Identification of putative lines with low oxalic content

2.1 Morphological Characterization

For an effective breeding program for crop variety development through hybridization, the analysis of genetic diversity is one of the useful tools and plays a fundamental role in identification of parents. Moreover, better knowledge on genetic diversity could help to achieve long-term selection gain. As a traditional method, morphological traits are used to assess genetic divergence and classify existing germplasm materials. However, this technique, a low level but powerful taxonomic tool, has been utilized for the preliminary grouping of germplasm prior to their characterization using more precise marker technologies. Moreover, this

technique is easier, cost effective, and easy to score and requires less time and finally it does not need any technical knowledge.

Nura *et al.* (2013) studied sesame mutants on the basis of morphological traits such as height at maturity, anthesis period, number of leaves per plant, leaf area, internodes length, number of capsules per plant, length of capsules, number of seeds per capsule and 1000 seeds weight. The results revealed highly significant difference ($p \leq 0.01$) in the morphological traits of the mutants when compared with the controls. They further characterized the mutants as early flowering with tall stature having larger leaves which produced large number of capsules with numerous seeds.

Kiranmayi *et al.* (2016) characterized twenty three accessions of sesame for morphological characterization and found a wide variation in flower color, seed color and capsule bearing capacity.

Singh *et al.* (2017) characterized 83 sesame varieties and revealed that maximum variation was recorded in almost all the morphological traits. On the basis of frequency distribution, majority of sesame varieties were found to possess early with light purple petal colour, sparse petal hairiness, basal branching pattern, medium plant height, medium plant branching, sparse stem hairiness, medium leaf size, slightly lobed leaf, strong leaf serration, sparse capsule hairiness, broad oblong capsule shape, alternate capsule arrangement and medium capsule length.

Aye *et al.* (2018) evaluated 40 sesame germplasm and observed wide range of variability for stem, leaf and flower traits, and also yield and yield component traits.

Bhoot *et al.* (2019) evaluated thirty genotypes of sesame for various plant and seed morphological traits and found that the genotypes of sesame can be distinguished and identified by plant morphological characters. These differences in morphological traits were useful in identification of individual sesame.

Pavani *et al.* (2020) characterized thirty sesame genotypes and revealed the presence of significant variation for days to 50% flowering, plant height, branching, stem hairiness, leaf lobes, capsule hairiness, capsule

length, days to maturity, seed coat colour, thousand seed weight and oil content indicating variations due to genetic makeup of the lines and these descriptors can be utilized in genotype identification, characterization and maintenance.

2.2 Genetic variation

2.2.1 Genotypic and phenotypic coefficient of variation

The success of selection depends on the availability of wide variability. Phenotypic and genotypic coefficients are genetic parameters of variation which compare the variability observed among different characters. The findings of different workers on genetic variability in sesame are listed here.

Tripathi *et al.* (2013) assessed 100 sesame accessions and revealed that seed yield per plant followed by number of secondary branches, thousand seed weight and number of primary branches showed high PCV and GCV estimates and moderate for days to 50 per cent flowering, oil content and plant height. Days to maturity and capsule length indicated low estimates of GCV and PCV.

Bharathi *et al.* (2014) evaluated fifty sesame accessions and observed that the magnitude of PCV and GCV were moderate to high for seed yield per plant, number of capsules per plant and number of branches per plant.

Desawi *et al.* (2014) reported that number of capsules per plant and seed yield per ha had high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

Bamrotiya *et al.* (2016) assessed 40 sesame genotypes and recorded high values of GCV and PCV for number of capsules per leaf axil followed by seed yield per plant, number of capsules per plant and height to first capsule.

Saxena and Bisen (2016) evaluated twenty six advanced varietal lines of sesame and observed high values of PCV and GCV for seed yield per plant, number of capsules per plant and number of secondary branches.

Soury *et al.* (2016) studied seven sesame genotypes for days to 50% flowering, days to maturity, plant height, number of capsules per plant, seed

yield per plant (g) and seed yield (kg per ha) and observed a wide range of variability among the genotypes for all characters.

Parveen *et al.* (2017) investigated sesame germplasm to assess the variability for six characters. The analysis of variance revealed significant differences among the genotypes for all the characters. The difference between PCV and GCV was high for seed yield, number of branches per plant and number of capsules per plant indicating the influence of environment on these characters.

Saxena and Bisen (2017) evaluated fourteen advanced varietal lines of sesame genotypes and recorded high PCV and GCV for traits *viz.*, seed yield per plant, number of primary branches per plant, oil content and seeds per capsule whereas moderate GCV and PCV were exhibited by plant height, number of secondary branches per plant, number of capsules per plant and days to maturity.

Gokulakrishnan *et al.* (2018) assessed thirty genotypes of sesame and reported that the genotypes exhibited significant differences for all the traits under study. A wide range of variability along with high estimates of PCV and GCV were observed for seed yield per plant, number of capsules per plant and number of branches per plant.

Patil and Ioksha (2018) evaluated 100 sesame advanced breeding lines and revealed that seed yield/plant followed by distance from ground to first capsule and number of capsules/plant showed high PCV and GCV estimates and moderate PCV and GCV were obtained for the characters *viz.*, plant height, number of branches per plant, number of seeds per capsule, capsule weight and test weight.

Shanmugam *et al.* (2018) studied 53 genotypes and found that PCV and GCV were high for number of secondary branches, number of primary branches, base leaf area, top leaf area, mid leaf area, top petiole length, mid petiole length and base petiole length for the plant characters with respect to yield attributes. However, the genetic variability was found to be moderate in days to 50 per cent flowering, thousand seed weight, number of capsules per

plant, number of seeds per capsule, plant height, days to maturity, capsule length, single plant yield and capsule width.

Singh *et al.* (2018) studied seventy five sesame genotypes and recorded high values of PCV and GCV for traits viz., number of secondary branches per plant, number of primary branches per plant, seed yield per plant, number of seeds per capsule, number of capsules per plant and days to flower initiation.

Kalaiyarasi *et al.* (2019) recorded high PCV and GCV for number of branches per plant, seed yield per plant and total number of capsules per plant in fifteen sesame genotypes.

Takele *et al.* (2019) assessed forty nine sesame genotypes and observed high significant differences among the genotypes for all quantitative traits. Branches per plant, capsule per plant, biomass yield, harvest index, thousand seed weight showed medium phenotypic and genotypic coefficient of variations.

Umamaheswari *et al.* (2019) obtained high GCV and PCV for number of branches per plant in 30 genotypes.

Kehie *et al.* (2020) evaluated 25 genotypes and observed highest genotypic coefficient of variation for seed yield per plant, while the highest phenotypic coefficient of variation was recorded for stem height from base to first branch.

Teklu *et al.* (2021) evaluated one hundred sesame germplasm and revealed high GCV and PCV for number of primary branches, number of secondary branches, thousand seed weight, seed yield per hectare and oil yield per hectare.

2.2.2 Heritability and genetic advance

Heritability of a trait is the relative amount of heritable portion of variation that is transferred to the progeny. Its magnitude is of paramount significance because high heritability makes the selection process a straight forward job. However, the use of heritability alone is not adequate to bring significant improvement through selection if not accompanied with sufficient

amount of genetic advance. Genetic advance or response to selection is a measure of how much gain one may get from phenotypic selection for a trait. Heritability and genetic advance are important to plant breeders as they not only serve as predictive function of crop performance in a succeeding generation but also guide the breeder in selection. The review on heritability and genetic advance studies on sesame is given below.

Tripathi *et al.* (2013) evaluated 100 sesame accessions and recorded high heritability combined with high genetic advance for seed yield/plant, number of secondary branches/plant and thousand seed weight.

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

Bharathi *et al.* (2014) reported high heritability combined with high genetic advance for seed yield per plant, number of capsules per plant and number of branches per plant.

Bindu *et al.* (2014) recorded high heritability and genetic advance as per cent of mean for plant height, number of branches, number of capsules per plant, oil content and yield except days to 50% flowering and thousand seed weight.

Desawi *et al.* (2014) studied that the highest heritability was observed for days to 50% flowering. Traits like number of capsules per plant and seed yield per ha had moderately high heritability (h^2) and genetic advance as a percentage of mean.

Rani (2014) observed that the characters seed yield per plant, number of secondary branches, number of capsules per plant and number of seeds per capsule exhibited high heritability accompanied by high genetic advance over the environments.

Abate *et al.* (2015) observed high heritability coupled with high genetic advance for number of branches per plant, capsule number per plant and seed yield indicating the important role of additive gene action for these traits.

Bamrotiya *et al.* (2016) reported high genetic advance for seed yield per plant, height to first capsule, number of seeds per capsule, number of capsules per plant, length of capsule, number of capsules per leaf axil, plant height and number of branches per plant in 40 sesame genotypes.

Soury *et al.* (2016) assessed seven sesame genotypes and observed high heritability coupled with low genetic advance for days to 50% flowering, days to maturity and plant height while low to moderate heritability with high genetic advance was recorded for the yield and its components.

Bhagasara *et al.* (2017) evaluated 1700 germplasm lines for nine quantitative characters and reported that genetic gain was high for seeds per capsule and heritability for thousand seed weight.

Saxena and Bisen (2017) evaluated fourteen advanced varietal lines of sesame genotypes and recorded high heritability combined with high genetic advance for seeds per capsule followed by oil content, yield per plant, harvest index, days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, plant height, days to maturity, capsule length, thousand seed weight and number of capsules per plant and moderate heritability for number of primary branches per plant.

Aye *et al.* (2018) found that the number of primary branches per plant, number of capsules per plant and seed yield per plant showed high heritability with high genetic advance.

Maibam *et al.* (2018) assessed sesame entries and reported that plant height, number of pods per plant, thousand seed weight and yield per plant exhibited high heritability coupled with high genetic advance.

Patil and Loksha (2018) in a study of 100 sesame advanced breeding lines revealed that high heritability coupled with high genetic advance was observed for plant height and distance from ground to first capsule.

Shanmugam *et al.* (2018) reported that days to 50 per cent flowering, days to maturity, number of primary branches, number of secondary branches, basal leaf area, basal petiole length, mid leaf area, mid petiole length, top leaf area, top petiole length, number of capsules per plant, capsule

length, number of seeds per capsule, 1000 seed weight and oil content showed high heritability coupled with high genetic advance in 53 genotypes.

Singh *et al.* (2018) recorded high heritability coupled with moderate genetic advance for oil content and days to 50% flowering in 75 sesame accessions.

Gogoi and Sarma (2019) evaluated thirty three sesame genotypes and observed significant differences for all the characters studied except for number of branches per plant. High heritability coupled with high genetic advance as a percent of mean was observed for yield per plant followed by 1000 grain weight.

Kalaiyarasi *et al.* (2019) studied fifteen sesame genotypes and observed high heritability and genetic advance for characters number of branches per plant, number of capsules per plant, seed yield per plant, plant height, plot yield, thousand seed weight and number of seeds per capsule.

Takele *et al.* (2019) studied forty nine sesame genotypes and observed that seed yield, biomass yield, capsule per plant, and branches per plant showed moderately high heritability with high genetic advance as a percent of mean. Thousand seed weight showed high heritability with moderate genetic advance as a percent of mean.

Umamaheswari *et al.* (2019) obtained high heritability coupled with high genetic advance as percent of mean for plant height at maturity, number of branches per plant, number of capsules per plant, length of the capsule, number of seeds per capsule, thousand seed weight and seed yield per plant and moderate heritability for capsule length in 30 sesame genotypes .

Kehie *et al.* (2020) evaluated 25 genotypes and observed high heritability coupled with high genetic advance as per cent mean for number of capsules per plant, seeds per capsule, thousand seed weight, days to 50 per cent flowering and oil content and moderate heritability for capsule length.

Patidar *et al.* (2020) evaluated twenty seven elite lines of sesame and reported that heritability in broad sense were high for characters *viz.*, internode length, oil content and number of seeds per capsule. The genetic

advance as a percent of mean were high in internode length followed by number of seeds per capsule and seed yield per hectare.

Teklu *et al.* (2021) evaluated one hundred sesame germplasm and the findings revealed high high heritability and genetic advance for number of primary branches, number of secondary branches, thousand seed weight, seed yield per hectare and oil yield per hectare.

2.3 Association analysis

2.3.1 Correlation analysis

Yield is a quantitative trait that is dependent upon a number of other traits. An understanding of association between yield and yield contributing characters will help to make simultaneous selection for more characters. Correlation studies help to know the association between highly heritable traits with the most economic trait, the yield. Works done by various authors in this line are reviewed here.

Abate *et al.* (2015) assessed 49 sesame genotypes and revealed that biomass per plant, harvest index and thousand seed weight exhibited highly significant and positive correlation with seed yield per plant.

Bharathi *et al.* (2015) evaluated 54 sesame genotypes and revealed that seed yield exhibited significant positive association with number of capsules per plant, number of seeds per capsule, test weight and plant height.

Fazal *et al.* (2015) evaluated 13 sesame genotypes and revealed that yield per plant had highly significant positive correlation with traits *viz.*, plant height, capsules per plant, number of branches, number of seeds per capsule and thousand seed weight.

Sabiel *et al.* (2015) observed highly significant and positive association of seed yield (kg per ha) with biomass (yield kg per ha), thousand seed weight and plant height. However, it had significant negative association with days to flowering.

Bamrotiya *et al.* (2016) reported that seed yield per plant was found to be significantly and positively correlated with days to flowering, days to maturity, plant height, number of seeds per capsule and harvest index.

Saxena and Bisen (2016) revealed positive correlation of days to flower initiation, days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, number of capsules per plant, capsule length, seeds per capsule, 1000-seed weight, oil content and harvest index with seed yield whereas plant height was negatively correlated in sesame genotypes.

Agrawal *et al.* (2017) reported that days to maturity, number of branches per plant, number of capsules per plant, number of seeds per capsule, thousand seed weight and protein content showed significant positive association with seed yield per plant.

Kindeya (2017) studied seventeen sesame genotypes and revealed that seed yield had a significant and positive correlation with number of branches and number of capsules and negative significant association with days to maturity and flowering time.

Abate (2018) assessed eightyone mid altitude sesame accessions and observed that the traits *viz.*, number of capsules, biomass yield, harvest index and thousand seed weight showed highly significant and highly positive correlation with seed yield. Plant height and number of seeds per capsule showed highly significant but moderately positive correlation with seed yield.

Aye *et al.* (2018) reported that days to first flowering, days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant and capsule length were found to be the main yield contributing traits in sesame production.

Iqbal *et al.* (2018) analysed 205 genotypes and revealed that capsule number and thousand seed weight had a strong relation with seed yield.

Lalpantluangi and Shah (2018) evaluated twenty one sesame genotypes and revealed significant positive association of seed yield per plant with days to 80 percent maturity, number of capsules per plant and thousand seed weight.

Patil and Loksha (2018) studied 100 sesame advanced breeding lines and observed that number of capsules per plant, number of branches per

plant, capsule length, number of seeds per capsule, capsule weight and test weight had strong and significant positive association with seed yield per plant at both genotypic and phenotypic levels.

Sasipriya *et al.* (2018) evaluated forty-five sesame genotypes and observed that the seed yield showed positive significant correlation with number of branches per plant, number of capsules per plant, capsule length, number of seeds per capsule and thousand seed weight both at genotypic as well as phenotypic levels. The trait number of capsules per plant showed the highest phenotypic and genotypic correlation with seed yield followed by thousand seed weight.

Singh *et al.* (2018) revealed that the characters *viz.*, plant height, number of secondary branches/plant, number of seeds/capsule and oil content have significant positive correlation with seed yield in 75 sesame accessions.

Vinoth *et al.* (2018) evaluated 12 sesame genotypes and the correlation analysis revealed that there was a positive significant association of seed yield with number of capsule per plant.

Kalaiyarasi *et al.* (2019) evaluated thirteen sesame genotypes and revealed that the characters *viz.*, number of seeds/capsule and plant height have positive direct effect along with significant positive correlation with seed yield whereas, the character days to 50% flowering showed significant negative association with seed yield.

Manjeet *et al.* (2019) assessed twenty-four genotypes and observed positive, significant and strong correlation of seed yield per plant with number of branches per plant, number of capsules per plant, number of seeds per capsules, thousand seeds weight, biological yield per plant and harvest index. At the same time seed yield per plant was negatively and significantly correlated with days to 50% flowering and plant height.

Navaneetha *et al.* (2019) studied thirty sesame hybrids and reported that the characters *viz.*, number of capsules on main stem and number of capsules per plant had the highest positive correlation with seed yield per

plant followed by plant height, number of seeds per capsule, number of primary branches per plant and height of first capsule.

Umamaheswari *et al* (2019) found that Seed yield per plant showed positive association with number of capsules per plant, number of seeds per capsule, number of branches per plant and thousand seed weight in 30 genotypes.

Kehie *et al.* (2020) evaluated 25 genotypes and observed that the character 1000 seed weight, number of locules per capsule and internodal length showed positive association with seed yield.

Patidar *et al.* (2020) evaluated twenty seven elite lines and revealed highly significant and positive association with seed yield per plot and number of seeds per capsule.

2.3.2 Path coefficient analysis

The path coefficient analysis is a useful tool for assessing both direct and indirect causes of correlation, and it allows for critical analysis of the specific characteristics that result in a particular outcome correlation. It provides information about magnitude and direction of direct and indirect effect of the yield components.

The review on path coefficient studies in sesame by many authors is given below.

Abate *et al.* (2015) observed that highest positive direct effect on seed yield was exhibited by biomass per plant followed by harvest index and thousand seed weight, while negative direct effect on seed yield was exhibited by days to maturity in 49 sesame genotypes.

Bharathi *et al.* (2015) assessed 54 sesame genotypes and indicated that number of seeds per capsule, number of capsules per plant, number of branches per plant and capsule length had positive direct effect on seed yield, while negative direct effect was exhibited by days to 50% flowering.

Fazal *et al.* (2015) revealed that capsules per plant had highest direct effect on seed yield per plant while, seeds per capsule had highest indirect effect via capsules per plant on seed yield per plant in sesame genotypes.

Bamrotiya *et al.* (2016) assessed 40 genotypes of sesame and observed number of seeds per capsule followed by number of branches per plant and number of capsules per plant exhibited high and positive direct effect on seed yield per plant.

Saxena and Bisen (2016) evaluated twenty six advanced lines of sesame genotypes and reported positive direct effect of number of secondary branches and number of capsules per plant on seed yield per plant.

Agrawal *et al.* (2017) studied forty sesame genotypes and observed that days to maturity, capsule length, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, number of seed per capsule and thousand seed weight had positive direct effect on seed yield.

Soundharya *et al.* (2017) assessed sixty two sesame genotypes and revealed maximum positive direct effect of number of seeds per capsule on seed yield followed by number of capsules per plant.

Abate (2018) evaluated eighty one mid-altitude sesame accessions and reported maximum positive direct effect on seed yield was exerted by number of capsules, biomass yield, days to maturity and harvest index.

Lalpantluangi and Shah (2018) reported that days to 80 percent maturity, seeds per capsule and number of secondary branches per plant exerted positive direct effect on seed yield and thus may be good selection criteria for seed yield per plant.

Patil and Ioksha (2018) studied 100 sesame advanced breeding lines and revealed that number of seeds per plant followed by number of capsules per plant had positive effect on seed yield whereas days to maturity and capsule length had negative effect.

Sasipriya (2018) evaluated 45 sesame genotypes and reported that 1000-seed weight recorded the highest positive direct effect on seed yield followed by number of capsules per plant and number of seeds per capsules. Number of seeds per capsules, capsule length and plant height are the other traits which showed positive direct effect on seed yield.

Singh *et al.* (2018) revealed that the characters *viz.*, plant height, number of secondary branches/plant, number of seeds/capsule and oil content have positive direct association with seed yield in 75 sesame genotypes.

Tidke *et al.* (2018) reported that days to 50% flowering exerted the highest positive direct effect on seed yield per hectare followed by number of seeds per capsule, number of primary branches per plant and number of capsules per plant in thirty four sesame germplasm.

Gogoi and Sharma (2019) evaluated thirty three sesame genotypes and reported that days to fifty percent flowering and thousand seed weight had high direct effect on seed yield and high indirect effect *via.*, height of first capsule bearing node, branches per plant and seeds per capsule.

Kalaiyarasi *et al.* (2019) evaluated thirteen sesame genotypes and reported that the characters *viz.*, number of seeds per capsule and plant height exhibited positive direct effect on seed yield.

Navaneetha *et al.* (2019) studied thirty sesame hybrids and revealed that the trait number of capsules on main stem had high direct effect on yield followed by capsule length, thousand seed weight and number of seeds per capsule.

Rehab *et al.* (2019) assessed fifteen sesame genotypes and revealed maximum positive direct effect of thousand seed weight per plant, number of seeds per capsule on seed yield followed by seed oil content, capsules weight per plant and plant height.

Umamaheswari *et al.* (2019) revealed that the traits plant height at maturity, number of capsules per plant and number seeds per capsule were directly influencing the seed yield per plant in 30 genotypes under study.

Teklu *et al.* (2021) evaluated one hundred sesame germplasm and reported high direct effects of oil yield per hectare and number of seeds per capsule on seed yield per hectare.

Kehie *et al.* (2020) evaluated 25 genotypes and observed that direct effect on seed yield was contributed by internodal length, capsule length, oil content, seeds per capsule and number of capsules per plant.

Patidar *et al.* (2020) evaluated twenty seven elite lines and revealed direct highly positive and significant effect was exhibited on seed yield by number of seeds per capsule followed by number of capsule/plant, oil content and thousand seed weight.

2.4 Genetic Divergence

In the hybridization programme, genetic divergence or D^2 statistics analysis is a potential method for selecting genetically different parents. It divides genotypes into clusters and evaluates the relative contributions of different variables to total divergence at both the inter- and intra cluster levels. As a result, it is possible to select parents for hybridization. The clustering pattern aids in determining the nature and extent of genotype-to-genotype diversity in order to isolate diverse parents. Superior hybrids and desirable recombinants are expected to result from intercrossing genetically diverse parents. The available genetic diversity literature is presented here.

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

Tripathi *et al.* (2013) grouped 100 sesame accessions into 11 clusters and observed that maximum inter cluster distance was observed between cluster VI and XI followed by clusters V and XI while, lowest divergence was noticed between cluster IV and V. Among the nine characters studied, days to 50% flowering contributed highest towards genetic divergence followed by seed yield per plant. Cluster VI exhibited highest means for days to 50 % flowering, plant height, number of primary and secondary branches per plant and days to maturity.

Chandra Mohan (2014) grouped 280 sesame genotype into 12 clusters and found that highest inter-cluster distance was observed between cluster VI & XII followed by cluster VI & IX .and the traits capsule per plant and plant height contributed maximum for divergence.

Abate *et al.* (2015) grouped forty nine genotypes into seven clusters using Mahalanobis D^2 statistics. The clustering pattern suggested the absence of relationship between geographical diversity and genetic diversity. Harvest index, seed yield, biomass yield and plant height had highest contribution towards genetic divergence.

Baraki *et al.* (2015) grouped thirteen genotypes into four clusters based on agronomic traits and the dendrogram indicated that clusters I, II, III and IV had 9, 1, 1 and 2 number of genotypes and the highest grain yield as well as highest oil content was observed in cluster III. Highest genetic divergence was observed between clusters II and III whereas, the lowest distance was found between clusters I and III.

Kindeya (2017) evaluated seventeen sesame genotypes and based on the cluster analysis, white seeded sesame genotypes were classified into four distinct clusters. Cluster II, III, and IV had high mean yield, oil content and oil yield than the other clusters.

Soundharya *et al.* (2017) evaluated 62 sesame genotypes which were grouped into 6 clusters where, cluster I was largest containing 44 genotypes followed cluster II with twelve genotypes, cluster VI with three genotypes and cluster III, V, VI having solitary genotypes. The inter cluster distance was maximum between cluster IV and VI and minimum between cluster I and III.

Dash *et al.* (2018) assessed forty five sesame genotypes and classified them into five clusters based on Mahalanobis D^2 statistics. Results on inter-cluster distances revealed maximum diversity between genotypes of cluster II and IV. Further, capsule width shared the highest contribution to total divergence followed by thousand seed weight, seed number per capsule, capsule length and seed yield per plant.

Iqbal *et al.* (2018) evaluated 205 genotypes using 8 characters and revealed that the inter cluster distance in most cases was larger indicating

wider diversity among the germplasm of different groups. The maximum inter cluster distance was found between clusters V and III followed by clusters V and II.

Singh *et al.* (2018) studied seventy five sesame genotypes and grouped them into thirteen clusters based on divergence analysis. Clustering pattern indicated that majority of genotypes, i.e. 64 (85%) were genetically close to each other and grouped in 3 clusters, while apparent diversity was mainly noticed due to 11 genotypes (15%) distributed over 10 clusters. Maximum inter cluster divergence was observed between cluster XII and IV followed by cluster XIII and IX indicating that good recombinants can be realized by mating between the genotypes of these clusters in a definite fashion. The traits days to flower initiation, oil content and number of capsules per plant contributed maximum towards genetic divergence.

Masoudi and Ahmadi (2019) studied ninety one sesame genotypes and reported that the evaluated genotypes were classified into five groups based on cluster analysis for all evaluated traits. The results of cluster analysis showed that the grouping of genotypes were not related to geographical distribution of genotypes and most genotypes were grouped based on morphological differences.

Mohanty *et al.* (2020) assessed 30 sesame genotypes and reported that the genotypes displayed marked divergence and were grouped into four clusters. Cluster I had twenty seven genotypes while cluster II, cluster III and cluster IV were mono genotypic. The oil content exhibited maximum contribution towards divergence.

Sirisha *et al.* (2020) evaluated 114 sesame genotypes and recorded maximum intercluster distance between cluster V & cluster XI. Among the relative contribution of the characters under study, the parameters days to maturity, number of branches per plant and number of capsules showed maximum contribution.

2.5 Principal Component Analysis

Principal Component Analysis (PCA) is mostly utilised in exploratory data analysis and in the development of prediction models. After mean

centering the data matrix for each attribute, PCA can be performed using eigen value decomposition of a data covariance (or correlation) matrix. Component scores, also known as factor scores and loadings, are commonly used to describe the results of a PCA. PCA is the most basic eigen vector-based multivariate analysis method. Its operation can be regarded of as revealing the data's internal structure in a way that best explains the data's variation.

Rather going after all the features under study, it is useful for genetic improvement of traits with larger contributions to variability.

Ismaila and Usman (2014) revealed that the variation in PC1 was mainly associated with height at maturity, capsule length and weight of seed per capsules. PC2 was associated with yield per hectare, number of capsules per plant and number of branches per plant in thirteen sesame genotypes.

Baraki *et al.* (2015) observed that out of eight, first three PCs accounted for 88.49% of the total variance and these three PCs were considered as significant.

Shim *et al.* (2016) evaluated 250 germplasm accessions and grouped them on five PCs, which accounted for 82.3% of total variation. The first PC (PC1) was positively correlated with days to flowering, days to maturity, and number of capsules per plant, whereas the second PC (PC2) was negatively correlated with all characteristics except capsule-bearing stem length. The third component (PC3) was highly positively correlated with capsule length and plant height.

Tanwar and Bisen (2017) evaluated ninety six sesame genotypes on the basis of PC scores using principal component analysis (PCA). Only nine PCs exhibited more than 0.5 eigen value and showed 95.19 % total variability among the characters. On the basis of PCA, the germplasm ES-334962, EC-334992-1, ES-424, S-0069, ES-173, G-19 and GRT-8392 were selected with highest PC values for characters plant height, number of capsules, number of primary branches per plant, oil content, days to maturity and seed yield per plant.

Singh *et al.* (2018) evaluated seventy five sesame genotypes and PCA yielded twelve PCs from the twelve agronomic traits of sesame out of which seven PCs showed about 83.193% variability. Results revealed that the genotypes *viz.*, S-0644, KMS-5- 361, T-1-A, NIC-16214, SI-1125, NIC-8080-A had highest PC values for characters number of capsules/plant, number of seeds/capsule, number of primary branches/plant, number of secondary branches/plant, 1000 seed weight and seed yield/plant.

Baraki and Berhe (2019) revealed that PC1 accounted for 38.3% of the variation and it was positively associated with grain yield, branches per plant, length of the pod-bearing zone, plant height, number of pods per plant, number of seeds per pod and thousand seed weight.

2.6 Studies on oxalic acid content in sesame

Sesame seed coat is rich in minerals (22.8 g 100 g⁻¹) including calcium (9.75 g 100 g⁻¹), Phosphorus (4.29 g 100 g⁻¹) and other micronutrients. The presence of oxalic acid (14.3 g 100 g⁻¹) and phytic acid (in traces) in the seed coat renders the calcium and phosphorus into non available form thereby hindering its use in large quantities. Hence, identification of sesame lines low in oxalic acid content will render increased calcium in available form and thereby decrease incidence of kidney stones. Available literature on oxalic acid content in sesame seeds is as follows.

Sahu *et al.* (2016) found that *kharif* season sesame crop had higher amount of oxalic acid in brown sesame (1.63 %) followed by black (1.58%) and white variety (1.52%) than in *Rabi* season.

Thakur *et al.* (2017) studied variation in oxalic acid content of 7 different sesame varieties and observed .highest oxalic acid content in variety GT-10 (1.63±0.2) and lowest value in variety PKVNT-11 (0.15±0.03).

Chapter – III

MATERIAL AND METHODS

MATERIAL AND METHODS

The present investigation entitled “Genetic Assessment for Seed Yield and Quality Traits in Sesame (*Sesamum indicum* L.)” was Breeder Seed Production conducted at Unit (Groundnut), College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh during *Kharif* 2020. The details of the material used and the methods adopted to conduct the experiment are presented in this chapter.

3.1 Experimental material and other details

3.1.1 Experimental site

The experiment was conducted at BSP (Groundnut), Research Farm, JNKVV, Jabalpur (M.P.) during *kharif* 2020. The soil of the experiment is sandy loam with uniform topography and free from water logged conditions.

3.1.2 Climate and Weather

Jabalpur is situated at 23.90° North latitude, 79.58° East longitudes and on an altitude of 411.78 m above the mean sea level. It has a humid subtropical climate with hot and dry summer and cold winter with occasional rain. The average rainfall is about 1200-1400 mm which is mainly received from end of June to end of September. The relative humidity varies from season to season and ranges between 80% to 90% during rainy season, which reduces up to 60% to 70% and 30% to 40% during winter and summer seasons, respectively. The climatic conditions during the crop period were optimum for a normal plant growth (Appendix-III).

3.1.3 Experimental material

The experimental material consisted of 200 sesame accessions with four checks. Details of germplasm and checks used in the study are given in Table 3.1.

Table 3.1: Experimental material

S. No.	Entry Name	S. No.	Entry Name	S. No.	Entry Name	S. No.	Entry Name
1	SI-1687-I	51	G-16	101	ES-303311	151	77-701
2	IC-14331	52	IS-387-2	102	S-0253	152	RJS-9613
3	Oct-81	53	Guj Sel-12	103	BS-10	153	RJS-4-79
4	EC-182832	54	IS-289	104	IC-204997	154	EC-335000-A
5	G-18	55	NIC-7982	105	IS-482-B	155	IC-204630
6	NIC-8033	56	IS-446-1-84	106	IS-261-2	156	NIC-16264
7	SI-805	57	EC-334992-I	107	NIC-16187	157	IC-204137
8	G-2	58	G-19	108	IS-109	158	S-0248
9	G-6	59	EC-310455	109	IC-204167	159	Local-1
10	RJS-185	60	SI-3114	110	KMS-4-238	160	IC-205206
11	NIC-8282	61	EC-334969	111	S-0486	161	Dharand
12	IS-387	62	EC-204704	112	G-9-1	162	Kolenyola
13	G-13	63	EC-334995-I	113	IS-514	163	GRT-8342
14	EC-334955	64	ES-64	114	G-49	164	G-20
15	NCR/82/No/Bo/NS	65	IS-564	115	Murg-1-7	165	NIC-8035
16	IS-205-I	66	S-0210	116	RJS-218	166	IS-475
17	NIC-8062	67	IS-350	117	G-44	167	Chagata local
18	G-8	68	ES-5503	118	NIC-13006	168	IS-24-P
19	SI-1925	69	IC-30884	119	IS-455	169	S-0501
20	EC-35000	70	NIC-8343	120	G-39	170	IS-39-B
21	NIC-9835	71	IS-90	121	ES-3196-I	171	IC-131953
22	IS-77	72	GRT-8359	122	S-0126	172	IS-299
23	EC-334993-I	73	I-68	123	NIC-3351	173	SI-3097
24	ES-110-A	74	IS-686	124	IS-101-213	174	IS-564A
25	GRT-8327	75	78-266-I	125	G-1	175	KMR-78
26	NIC-8055-I	76	S-0281	126	IS-352	176	SI-2143
27	S-0619	77	TMV-12-52	127	IS-101-4	177	KIS-551
28	IS-132295	78	IS-712	128	54-1641	178	GRT-8385
29	ES-131-1-84	79	GRT-83128	129	S-0650	179	TC-326
30	S-0069	80	NIC-16218	130	SI-2561	180	NIC-8020
31	ES-139-2-84	81	KJS-21	131	TC-171	181	78-831
32	RJS-Bo	82	GAD-5	132	NIC-13032	182	NIC-8511
33	S-0627	83	EC-335009	133	S-0021	183	MOHUR-3
34	IC-152485	84	IS-302	134	G-15	184	G-5
35	ES-120-1-84-B	85	NIC-8210	135	EC-310448	185	SI-7619-B
36	ES-173	86	78-20	136	EC-335004-I	186	IS-101-2
37	WLR/92/No/217/Shal	87	ES-560	137	TS-332	187	IS-470
38	G-47	88	Coredbose	138	G-17	188	GRT-8368-I
39	IS-99-A	89	ES-312955	139	RJS-29-I	189	RJS-8316
40	SI-3275	90	IC-14142	140	NIC-8174	190	IS-733
41	IS-436-3-84	91	GRT-8392	141	ES-41	191	B-223
42	IS-449	92	ES-370	142	GRT-8609	192	EC-310425
43	EC-334987	93	NIC-6059	143	NIC-17389	193	NIC-8523
44	IS-199-2-04	94	IS-607-2-04	144	78-505	194	18-Oct
45	EC-334967	95	SI-1873	145	SI-2073	195	IS-445-I
46	IS-156-3-84	96	RJS-61	146	NIC-17301	196	RJS-738-2-84
47	IS-641-2-84	97	NIC-8260	147	GRT-8368	197	IS-431
48	G-40	98	IS-562	148	S-0479	198	EC-334968
49	SI-3315-16	99	IS-424	149	EC-132295	199	SI-7178
50	IC-2621694	100	ES-334962	150	NIC-8590	200	IS-393-1-A
Check-1	TKG-21						
Check-2	TKG-22						
Check-3	JTS-8						
Check-4	GT-10						

3.1.4 Design of experiment

The experiment was laid out in Augmented Block Design (ABD) with 200 genotypes and four checks. The experimental details are as follows:-

Season	<i>Kharif 2020</i>
Experimental Design	Augmented Block Design
Number of genotypes	204 (including 4 checks viz., TKG-21, TKG-22, GT-10, JTS-8)
Number of rows per block	24 lines (20 sesame genotypes + 4 checks)
Row length	3m
Row to row distance	40 cm
Plant to plant distance	10 cm

3.2 Observations recorded

Observations were recorded on five randomly chosen competitive plants which were selected from each genotype and following quantitative and morphological traits were recorded for evaluation of yield and yield contributing traits.

3.2.1 Quantitative traits

3.2.1.1 Days to flower initiation

The period from the date of sowing to the date when first flower of the plants in a plot were in bloom was recorded and expressed in number of days.

3.2.1.2 Days to 50% flowering

The period from the date of sowing to the date when 50% of the flowers of the plants in a plot were in bloom was recorded and expressed in number of days.

3.2.1.3 Plant height (cm)

The height of five plants was measured at maturity in centimeters from the ground level to the tip of the plant and average was calculated.

3.2.1.4 Number of primary branches per plant

The number of branches of five tagged plants from each plot was recorded and mean was calculated.

3.2.1.5 Number of secondary branches per plant

The number of secondary branches of five tagged plants from each plot was recorded and mean was calculated.

3.2.1.6 Number of capsules per plant

The total number of capsule per plant at maturity stage was counted on five plants and mean was calculated.

3.2.1.7 Capsule length (cm)

Five matured capsules were selected randomly from each plant and measured in centimeters from base to the tip of the capsule.

3.2.1.8 Days to maturity

The period from the date of sowing to the date of maturity (when 90% capsules turn (yellow) was recorded and expressed in number of days.

3.2.1.9 Number of seeds per capsule

Total number of seeds present in five randomly selected capsules of selected plant was counted and recorded at maturity.

3.2.1.10 Thousand seed weight (g)

Weight of 1000 normal seeds drawn randomly from each lot was measured in grams.

3.2.1.11 Seed yield per plant (g)

The tagged five plants were harvested and threshed separately. The seed yield of individual plant was weighed in gram.

3.2.2 Qualitative Traits

3.2.2.1 Oil content (%)

The oil content of seeds was estimated by Soxhlet Extraction Method. Oil from known quantity of the seed was extracted using petroleum ether. Then, it was diluted off completely, dried, weighed and percent oil was calculated.

$$\text{Fat \%} = \frac{W_2 - W_1}{W} \times 100$$

3.2.2.2 Oxalic Acid content (%)

The presence of anti-nutritional factors like oxalic acid (14.3g/100g) and phytic acid (in traces) in the sesame seed coat renders the calcium and phosphorus into non-available form and imparts unpleasant taste also. The oxalic acid binds with calcium to form calcium oxalate, which is not utilized by the human body. Oxalic acid may combine with other minerals to form less soluble salts known as oxalates. It is known to interfere with mineral metabolism in the body. Oxalic acid content of the sesame seed for 200 lines was determined according to titration method as described by AOCS, 1980. Following formula was used to calculate the oxalic acid present in the sesame seeds-

$$\text{Oxalic acid \%} = \frac{6.303 \times \text{normality of KMnO}_4 \times \text{reading of buret}}{\text{Weight of seed sample (gm)}}$$

3.2.3 Morphological traits

3.2.3.1 Plant growth type

This trait was observed based on growing pattern of plants whether determinate or indeterminate type.

3.2.3.2 Plant growth habit

This trait was recorded based on the growing habit of plant *i.e.* prostrate, semi-erect or erect.

3.2.3.3 Main stem color

On the basis of presence of pigments on mature plants, stem colour was determined on the older lower part of the stem.

3.2.3.4 Stem hairiness

This trait was recorded on green main stem of plant at flowering.

3.2.3.5 Plant branching habit

This trait was recorded at the maturity stage of plant.

3.2.3.6 Plant branching pattern

This trait was observed at maturity stage of plant.

3.2.3.7 Leaf hairiness

Leaf hairiness was recorded on the ventral surface of bottom leaves.

3.2.3.8 Leaf shape

Leaf shape was recorded for middle and top leaves separately.

3.2.3.9 Basal leaf margin

This characteristic was recorded on fully developed leaves from five plants

3.2.3.10 Lobe incision of basal leaf

This character was recorded on the lower half of the main stem at beginning of flowering based on the most common state.

3.2.3.11 Petiole colour

Petiole colour was observed on fully formed and mature leaves.

3.2.3.12 Number of flowers per leaf axil

This trait was recorded at flowering stage by counting the number of flowers per leaf axil.

3.2.3.13 Corolla hairiness

This character was observed at flowering stage for presence or absence of hair on corolla.

3.2.3.14 Corolla colour

This trait was recorded on fully opened fresh flowers at noon.

3.2.3.15 Number of locules per capsule

Number of locules per capsule was observed on capsules from the middle of main stem.

3.2.3.16 Capsule arrangement

This characteristic was recorded on fully developed capsules of middle capsule of five plants.

3.2.3.17 Capsule hairiness

This characteristic was recorded on green capsules of plant at flowering.

3.2.3.18 Colour of dry capsule

Colour of sun-dried capsule was noted.

3.2.3.19 Type of capsule beak

This trait was noted by observing mature capsules of the fully matured plants.

3.2.3.20 Seed coat colour

Seed coat colour was noted as per the intensity of colour in descending order.

3.3 Statistical analysis

Statistical analysis was performed for following parameters:

3.3.1 Analysis of variance

3.3.2 Parameters of genetic variability

3.3.3 Correlation coefficient analysis

3.3.4 Path coefficient analysis

3.3.5 Genetic divergence using Mahalanobis D^2 analysis

3.3.6 Principal component analysis (PCA)

3.3.7 Screening of sesame germplasm with low oxalic acid content

3.3.1 Analysis of variance

The mean data on five plants were subjected to variance analysis and test of significance as per the method of Sharma (1999).

The data on quantitative characters were statistically analyzed on the basis of model described for Augmented Block Design.

$$Y_{ij} = (\mu + b_i + t_j + e_{ij}) n_{ij}$$

Where,

Y_{ij} = Performance of j^{th} genotype in i^{th} block

M = General mean

b_i = True effect of i^{th} block

t_j = True effect of j^{th} treatment

e_{ij} = Random errors which are supposed to be identically and independently distributed with normal distribution having mean zero and variance σ^2_e .

Table 3.2: Skeleton of ANOVA for Augmented Block Design

Source of Variation	d.f.	Sum of Squares	Mean Squares	F value	Expected mean squares
Blocks	(b-1)	Bss	bMS	bMS/EMS	
Entries	(e-1)	eSS	eMS	eMS/EMS	$\sigma^2_g = \text{MSg} - \text{MSe}/r$
Checks	(c-1)	Css	cMS	cMS/EMS	
Varieties	(v-1)	Vss	vMS	vMS/EMS	
Checks Vs. varieties	1	CvSS	cvMS	cvMS/EMS	
Error	(c-1)(b-1)	ESS	EMS		
Total	(N-1)	TSS			

$$\text{Genotypic variance } (\sigma^2_g) = \frac{M_2 - M_3}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \frac{M_2 - M_3}{r} + M_3$$

$$3. \text{ Environmental variance } (\sigma^2_e) = M_3$$

Where,

R = Number of replications

g = Number of genotypes

M_1 = Mean square due to replications

M_2 = Mean square due to genotypes

M_3 = Mean square due to error

A significant value of F-test at 5% and 1% level indicates that the genotypes differ significantly among themselves, which requires computing the critical difference (CD).

$$\text{Standard error of difference of mean SE (d)} = \sqrt{\frac{2 \text{ EMS}}{r}}$$

$$\text{Critical difference (CD)} = \text{SE}_{(d)} \times t_{\alpha}$$

Where,

t_{α} = t-value at 5% and 1% probability level

EMS = Error mean square from Anova

The significance of the computed mean squares was tested making ratio of respective mean square against error mean square. The calculated value of F (F_c) is compared with table value of F (F_t) at n_1 and n_2 (error d.f.) degrees of freedom. If calculated value is $>F$ tabulated at given probability level is said to be significant.

3.3.2 Parameters of genetic variability

3.3.2.1 Mean

The average of recorded observation was calculated as follows:-

$$\text{Mean } (\bar{X}) = \frac{\sum X_i}{n}$$

Where,

$\sum X_i$ = Summation of all values of observation

n = Number of observed values

3.3.2.2 Range

Range is the difference between the smallest and the greatest term of a series of observation and thus provides the information about the variability present in the genotypes.

3.3.2.3 Phenotypic coefficient of variation (PCV)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

$$\text{P C V} = (\sigma p / \bar{X}) \times 100$$

Where,

$$\sigma p = \sqrt{\sigma^2 p}$$

3.3.2.4 Genotypic Coefficient of Variation (GCV)

$$GCV = (\sigma_g / \bar{X}) \times 100$$

Where,

$$\sigma_g = \sqrt{\sigma^2_g}$$

Where,

σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

σ^2_g = Genotypic variance

σ_g = Genotypic standard deviation

σ^2_e = Environment variance

$\bar{X}$ = General Mean

3.3.2.5 Heritability

Heritability in broad sense was estimated by the following formula given by Hanson (1956):

$$h^2 (bs) \% = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

The range of heritability was categorized as low (below 50 per cent), moderate (50-70 per cent) and high (above 70 per cent) as followed by Johnson *et al.* (1955).

3.3.2.6 Genetic advance

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Johnson *et al.* (1955).

$$G(s) = K \times h^2 \times \sigma_p$$

Where,

K = Selection intensity (value of K at 5% 2.06),

h^2 = Heritability in broad sense, and

σ_p = Phenotypic standard deviation

3.3.2.7 Genetic advance as percentage of mean

It was calculated by the following formula:

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

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

< 10 per cent = low

10-20 per cent = moderate

> 20 per cent = high

3.3.3 Correlation coefficients analysis

Correlation coefficients were calculated for combination of all characters under study at genotypic, phenotypic and environmental levels with the help of formula suggested by Miller *et al.* (1958).

$$r_{ij} = \frac{\text{Cov}(ij)}{\sqrt{(\sigma^2 i)(\sigma^2 j)}}$$

Where,

r_{ij} = Correlation coefficient between i^{th} and j^{th} traits

$\text{Cov}(ij)$ = Covariance between i^{th} and j^{th} traits

$\sigma^2 i$ = Variance of i^{th} trait

$\sigma^2 j$ = Variance of j^{th} trait

To test the significance of phenotypic correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1963) at $n-2$ d.f. at two levels of probability, viz., 5% and 1%.

$$T_{cal.} = \frac{r}{\sqrt{(1-r^2)}} \times \sqrt{n-1} \text{ at } (n-2) \text{ d.f.}$$

3.3.4 Path coefficient analysis

It is a simple standardized partial coefficient method to detect the direct and indirect effects of the independent variable on dependent variable. It permits separation of correlation into components of direct and indirect effects.

The method of path coefficient was developed by Wright (1921) and modified by Dewey and Lu (1959). The following set of simultaneous equations were formed and used for estimation of direct and indirect effects on seed longevity.

Path coefficients were obtained by simultaneous equations which express basic relationship between correlation and path coefficient.

$$r_{1y} = P_1y + P_2yr_{12} + P_3yr_{13} + \dots + P_{(n-1)}y r_{1(n-1)}$$

$$r_{2y} = P_2y + P_1yr_{21} + P_3yr_{23} + \dots + P_{(n-1)}y r_{2(n-1)}$$

$$r_{3y} = P_3y + P_2yr_{32} + P_1yr_{31} + \dots + P_{(n-1)}y r_{3(n-1)}$$

$$y = P_1y + P_2y r_{1(n-1)} + P_3y r_{2(n-1)} + \dots + P_{(n-1)}y r_{1(n-1)}$$

Where,

y = is the dependent variable i.e. yield per plant

r = Genotypic or phenotypic correlation coefficients between a pair of character

n = Total number of characters under study

Apart from these variations, unexplained residual variation is also there, which is an account of residual factor which is calculated by following formula.

Residual effect:

$$1 = R^2 + P_1y^2 + P_2y^2 + \dots + [p_{(n-1)}y]^2 + 2 \{p_1yP_2y r_{12} + P_1y P_3y r_{13} + P_1y P_4y r_{14} + \dots + p_{(n-2)}y p_{(n-1)}y r_{(n-2)}\}$$

$$1 = R^2 + X$$

Where,

X is equal to sum of all terms of right hand side of equation except R^2 .

$$\text{Or } R^2 = (1-X)$$

Therefore,

$$R = \sqrt{(1-X)}$$

Later the path coefficients were rated based on the scales given below (Lenka and Mishra, 1973).

>1.00	=	Very high
0.3-0.99	=	High
0.2-0.29	=	Moderate
0.1-0.19	=	Low
0.0-0.09	=	Negligible

3.3.5 Genetic divergence using Mahalanobis D² analysis

3.3.5.1 Genetic divergence

D² analysis: Mahalanobis (1928) defines D² analysis as follows.

$$D^2P = b_1d_1 + b_2d_2 + \dots \dots \dots b_p d_p$$

A resource for group distance based on multiple characters with X₁, X₂, X₃.....X_p as the multiple measurements available on each individual and d₁, d₂ d_p as x₁₁. x₂₂..... x_{1p}. x_{2p}, respectively is the difference in the means of two populations. The 'P' values are to be estimated that the ratio of variance between the populations to the variance within the populations is maximized. Taking variance and covariance under consideration, the D² value may be estimated by this Formula.

$$D^2 = \sum w_{ij} \sum \left(\frac{1}{\bar{x}} - \frac{2}{\bar{x}} \right) \left(\frac{1}{\bar{x}} - \frac{2}{\bar{x}} \right)$$

Where,

W_{ij} is the inverse of estimated variance and covariance matrix

3.3.5.2 Step to estimate D² value

3.3.5.2.1 Collection of data

Data were collected considering "V" population and "P" characters which have been measured on each individual.

3.3.5.2.2 Test of significance

According to Wilk's criteria, a simultaneous test of difference between mean values of number of correlated variance is done (Rao, 1948).

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

$$A = \begin{vmatrix} W \\ S \end{vmatrix} = \frac{\text{Determination of error matrix}}{\text{Determination of error+ variety matrix}}$$

$$V(\text{State}) = -m \frac{(P+g+1)}{2} \log e = [n] \log e$$

Where

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

P = Number of variance or character

Q = Degree of freedom for population

N = Degree of freedom for error + variety

E = Constant (2.7183)

V (state) is distributed as X^2 with Pq degree of freedom.

The tabulated value of X^2 for Pq degree of freedom at 5% level is compared with the X^2 value for testing the significance.

3.3.5.2.3 Transformation of correlated values

Transformation is done by using pivotal consideration method. The correlated variables are first transformed into uncorrelated once and D^2 values are calculated.

3.3.5.2.4 Computation of D^2 values

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

3.3.5.2.5 Contribution of individual characters towards divergence

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

3.3.5.2.6 Grouping of varieties into various clusters by Ward's method

Under present investigation genetic divergence of 204 sesame genotypes was determined by using both morphological and quantitative characters which were used as a input for UPGMA (unweighted pair group method with arithmetic mean) cluster analysis. The UPGMA is a simple agglomerative (bottom-up) hierarchial clustering method attributed by Sokal and Michener (1958). UPGMA clustering is done using Ward's minimum variance method and Gower's method of genetic distance (Gower, 1971) was derived (for morphological characters) and Euclidean distance (quantitative traits).

Gower's method of genetic distance:

for qualitative data (nominal variables),

$$D_{Gower} (x_1, x_2) = 1 - \left(\frac{1}{p} \sum_{j=1}^p s_j (x_1, x_2) \right)$$

for quantitative data (ordinal variables),

$$D_{Gower} (x_1, x_2) = 1 - \frac{|y_{1j} - y_{2j}|}{R_j}$$

Euclidean method of genetic distance:

$$d(x, y) = \sqrt{\sum_{i=1}^n (y_i - x_i)^2} \text{ where, } x, y \text{ are ordinal variables}$$

3.3.5.2.7 Average intra cluster distance

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

$$\sum D_i^2/n$$

Where,

$\sum D_i^2/n$ is the sum of distance between all possible contributions (n) of the population included in the cluster.

3.3.5.2.8 Average inter-cluster distance

First of all, the distance clusters are measured. The clusters are taken one by one and their distances from other cluster are calculated.

3.4.6 Principal component analysis

PCA is a well-known method of dimension reduction (Massy, 1965; Jolliffe, 1986), which seeks linear combinations of the columns of $\mathbf{X}$ with maximal variance, or equivalently, high information. It is routinely applied in chemometrics with the goal of providing the most compact representation of the data. The original p variables $\mathbf{X} = [\mathbf{x}_1 \dots \mathbf{x}_p]$ are transformed in a new predictor set $\mathbf{T} = [\mathbf{t}_1 \dots \mathbf{t}_k]$, with $k \leq \min(n-1, p)$. The new variables $\mathbf{t}_j$, called *scores*, are a weighted average of the original $\mathbf{X}$ variables. The *principal components* are the eigen vectors, $\mathbf{u}_j$ from the eigen decomposition of $\mathbf{X}'\mathbf{X}$ (and of the sample covariance matrix $\mathbf{S}$, up to a constant). PCA sequentially maximises the variance of a linear combination of the original predictor variables

$$\mathbf{u}_j = \arg \max \text{Var}(\mathbf{X}\mathbf{u}),$$

$$\mathbf{u}'_i \mathbf{S} \mathbf{u}_j = 0 \text{ for all } 1 \leq i < j.$$

Subject to the constraint that $\mathbf{u}'_i \mathbf{S} \mathbf{u}_j = 0$ for all $1 \leq i < j$. This ensures that $\mathbf{t}_j = \mathbf{X}\mathbf{u}_j$ is uncorrelated with all the previous linear combinations $\mathbf{t}_i = \mathbf{X}\mathbf{u}_i$. The principal components are ordered in terms of the amount of variation of the original data they account for. The first principal component direction has the property that $\mathbf{t}_1 = \mathbf{X}\mathbf{u}_1$ has the largest sample variance among all normalized linear combinations of the columns of $\mathbf{X}$. Each subsequent component gives combinations with the largest possible variance which is uncorrelated with those that have been taken earlier.

There are various standard approaches to find the principal components, e.g. taking the singular value decomposition of $\mathbf{X}$. In chemometrics, it is common to estimate the principal components using the nonlinear iterative partial least-squares (NIPALS) algorithm (Wold, 1966). This is because the number of required components is usually much less than the total possible number ($k \ll p$). In fact, the NIPALS algorithm does not calculate all the principal components at once, but it first calculates $\mathbf{t}_1$ and $\mathbf{u}_1$ from the $\mathbf{X}$ matrix. Then the outer product $\mathbf{t}_1 \mathbf{u}_1'$ is subtracted from $\mathbf{X}$ and the residual $\mathbf{X}_2$ is calculated. In turn, this residual can be used to calculate $\mathbf{t}_2$ and $\mathbf{u}_2$.

Chapter – IV

RESULTS

RESULTS

The present study was conducted at BSP (Groundnut) Research Farm, JNKVV, Jabalpur with 204 sesame genotypes including four checks in Augmented Block Design during *Kharif*, 2020.

The purpose of this study was to determine the variability parameters across sesame genotypes in order to develop adequate selection criteria for crop development. Correlation and path coefficient analysis were used to provide information on the relationship between plant traits and seed yield, which is crucial for breeders when selecting desirable genotypes. Divergence analysis was used to determine how genotypes were grouped into different clusters and to choose the best divergent parents for subsequent hybridization. The type of variation present in the selected population was investigated using principal component analysis.

The experimental findings of the present investigation have been organized under following headings.

- 4.1 Characterization
- 4.2 Analysis of variance
- 4.3 Parameters of genetic variability
 - 4.3.1 Mean and range
 - 4.3.2 Genotypic and phenotypic coefficient of variation
 - 4.3.3 Heritability
 - 4.3.4 Genetic advance
- 4.4 Association analysis
 - 4.4.1 Correlation coefficient analysis
 - 4.4.2 Path coefficient analysis
- 4.5 Genetic divergence using Mahalanobis D^2 analysis
- 4.6 Identification of putative lines with low oxalic acid content

4.1 Characterization

A total of twenty morphological traits viz., plant growth type, plant growth habit, main stem colour, stem hairiness, branching habit and branching pattern, leaf hairiness, leaf shape, basal leaf margin, lobe incision of basal leaf, petiole colour, number of flowers per leaf axil, corolla hairiness, corolla colour, number of locules per capsule, capsule arrangement, capsule hairiness, colour of dry capsule, type of capsule beak and seed coat colour were used to characterize sesame germplasm in. Their categorization is presented in Table 4.1.

Table 4.1: Frequency distribution of visual and morphological traits in sesame germplasm

Trait	Classes	Number of genotypes	Frequency (%)
Plant growth type	Indeterminate	204	100
	Determinate	0	0
Plant growth habit	Prostrate	0	0
	Semi-erect	8	3.92
	Erect	196	96.07
Main stem colour	Green	204	100
	Yellow	0	0
	Purplish green	0	0
	Purple	0	0
Stem hairiness	Absent	42	20.58
	Sparse	160	66.66
	Dense	2	0.98
Branching habit	Absent	0	0
	Few	63	30.88
	Medium	112	54.90
	Profuse	29	14.21
Branching pattern	Non branching	0	0
	Basal branching	0	0
	Top branching	204	100
Leaf hairiness	Glabrous	9	4.41
	Sparse	195	95.58
	Medium	0	0
	Strong	0	0
Leaf shape	Linear	0	0
	Lanceolate (top leaves)	204	100
	Elliptic	0	0
	Ovate (middle leaves)	204	100
	Narrowly cordate	0	0

Trait	Classes	Number of genotypes	Frequency (%)
Basal leaf margin	Entire	49	24.01
	Serrate	155	75.98
	Dentate	0	0
Lobe incision of basal leaf	Absent	21	10.29
	Weak	33	16.17
	Medium	118	57.84
	Strong	32	15.68
Petiole colour	Green	0	0
	Greenish purple	204	100
	Purple	0	0
	Pink	0	0
No. of flowers per leaf axil	One	204	100
	More than one	0	0
Corolla hairiness	Absent	0	0
	Sparse	25	12.25
	Dense	179	87.74
Corolla colour	White	0	0
	White with pink shading	136	66.67
	White with deep pink shading	68	33.33
	Pink	0	0
	Light violet	0	0
	Dark violet	0	0
	Purple	0	0
	Red	0	0
	Light maroon	0	0
Capsule shape	Tapered at apex	0	0
	Square	0	0
	Broad Oblong	2	0.98
	Narrow oblong	202	99.01
No. of locules per capsule	Four	203	99.50
	Six	0	0
	Eight	1	0.49
	Mixed	0	0
Capsule arrangement	Monocapsular	204	100
	Multicapsular	0	0
Capsule hairiness	Absent	1	0.49
	Sparse	110	53.92
	Medium	34	16.66
	Dense	95	46.56
Colour of dry capsule	Green	0	0
	Straw	38	18.62
	Brown	166	81.37
	Purple	0	0
Type of capsule beak	Short	114	55.88
	Long	64	31.37
	Curved	62	30.39
	Cleft	0	0
Seed coat colour	White	3	1.47
	Dark brown	200	98.03
	Black	1	0.49

4.1.1 Plant growth type

Based on plant growth type, germplasm were categorized in two groups i.e. determinate and indeterminate. All the germplasm showed indeterminate plant growth type.

4.1.2 Plant growth habit

Based on growth habit, germplasm were categorized in three groups i.e. erect, semi erect and prostrate. Eight germplasm were having semi erect while 196 were having erect plant growth habit and none were prostrate in growth habit.

4.1.3 Main stem colour

Based on the colour of main stem, the germplasm were categorized in green, yellow, purplish green and purple. All the germplasm were having green main stem colour.

4.1.4 Stem hairiness

Based on stem hairiness, germplasms were categorized in three groups *viz.*, absent, sparse and dense. 160 germplasm had sparse, two germplasm had dense stem hairiness and in forty two germplasm stem hairiness was absent.

4.1.5 Branching habit

Based on plant branching habit, germplasm were categorized in four groups i.e. absent, few, medium and profuse branching. Sixty three lines had few branching, 112 genotypes had medium branching and twenty nine had profuse branching.

4.1.6 Branching pattern

Based on plant branching pattern, germplasm were categorized in three groups i.e. basal, top and non branching. All the germplasm were having top branching pattern.

4.1.7 Leaf hairiness

Based on the leaf hairiness, germplasm were categorized in four groups i.e. glabrous, sparse, medium and strong. Nine lines were having glabrous leaves and 195 lines were having sparse leaf hairiness.

4.1.8 Leaf shape

Based on leaf shape, germplasm were categorized in five groups *i.e.* linear, lanceolate, elliptic, ovate and narrowly cordate. All the germplasm were found to possess ovate and lanceolate leaves in their middle and top stem portions, respectively.

4.1.9 Basal leaf margin

On the basis of basal leaf margin, germplasm were categorized in three groups *i.e.* entire, serrate and dentate. Fourty ninegermplam showed entire basal leaf margin whereas, one 155 lines showed serrate basal leaf margin.

4.1.10 Lobe incision of basal leaf

Based on lobe incision of basal leaf, germplasm were categorized in four groups *i.e.* absent, weak, medium and strong lobe incision. In twenty one germplasm, lobe incision was absent, thirty three germplasm had weak lobe incision, 118 germplasm had medium lobe incision and thirty two germplasm had strong lobe incision of basal leaf.

4.1.11 Petiole colour

Based on the colour of petiole, the germplasm were categorized into four groups *i.e.* green, greenish purple, purple and pink. All the germplasm were having greenish purple petiole colour.

4.1.12 Number of flowers per leaf axil

Based on the number of flowers per leaf axil, the germplasm were categorized into two groups *i.e.* one and more than one. All the germplasm were found to have one flower per leaf axil.

4.1.13 Corolla hairiness

On the basis of corolla hairiness, germplasm were categorized in three groups *i.e.* absent, sparse and dense. Twenty five germplasm had sparse corolla hairiness while 179 germplasm lines had dense corolla hairiness.

4.1.14 Corolla colour

Based on corolla color, germplasm were categorized in nine groups *i.e.* white, white with pink shading, white with deep pink shading, pink, light violet,

dark violet, purple, red and light maroon. 136 lines showed white with pink shading corolla color and sixty eight lines showed white with deep pink shading corolla colour.

4.1.15 Number of locules per capsule

On the basis of locule number, germplasm were categorized in four groups i.e. four, six, eight and mixed. 203 germplasm had four locular capsules and one line had eight locular capsules.

4.1.16 Capsule arrangement

On the basis of capsule arrangement, germplasm were categorized in two groups i.e. monocapsular and multicapsular. All the germplasm had monocapsular capsule arrangement.

4.1.17 Capsule hairiness

On the basis of capsule hairiness, germplasm were categorized in four groups i.e. absent, sparse, medium and dense. One germplasm had no capsule hairiness, ninety five had dense capsule hairiness, 110 had sparse capsule hairiness and thirty four lines had medium hairiness.

4.1.18 Color of dry capsule

Based on the color of dry capsule, the germplasm were categorized into four groups i.e. green, straw, brown and purple. Thirty eight germplasm had straw colored capsule whereas, 166 germplasm had brown colored capsule.

4.1.19 Type of capsule beak

Based on the type of capsule beak, the germplasm were classified into four groups i.e. short, long, curved and cleft. 114 germplasm had short capsule beak, sixty four germplasm had long capsule beak and sixty two germplasm had curved capsule beak.

4.1.20 Seed coat color

Based on the seed coat color, the germplasm were categorized into three groups i.e. white, dark brown and black. Three germplasm had white seed coat color, 200 germplasm had dark brown seed coat color and one germplasm had black seed coat color.

Table 4.2: Categorization of sesame genotypes based on morphological traits

Trait	Classes	Genotypes
Plant growth type	Indeterminate (204)	All
	Determinate (0)	None
Plant growth habit	Prostrate (0)	None
	Semi-erect (8)	IS-387, NCR/82/No/Bo/NS, Guj Sel-12, IS-289, SI-3114, EC-334969, Coredbose, IS-482-B
	Erect (196)	SI-1687-I, IC-14331, Oct-81, EC-182832, G-18, NIC-8033, SI-805, G-2, G-6, RJS-185, NIC-8282, G-13, EC-334955, IS-205-I, NIC-8062, G-8, SI-1925, EC-35000, NIC-9835, IS-77, EC-334993-I, ES-110-A, GRT-8327, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, RJS-Bo, S-0627, IC-152485, ES-120-1-84-B, ES-173, WLR/92/No/217/Shal, G-47, IS-99-A, SI-3275, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-156-3-84, IS-641-2-84, G-40, SI-3315-16, IC-2621694, G-16, IS-387-2, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, EC-204704, EC-334995-I, ES-64, IS-564, S-0210, IS-350, ES-5503, IC-30884, NIC-8343, IS-90, GRT-8359, I-68, IS-686, 78-266-I, S-0281, TMV-12-52, IS-712, GRT-83128, NIC-16218, KJS-21, GAD-5, EC-335009, IS-302, NIC-8210, 78-20, ES-560, ES-312955, IC-14142, GRT-8392, ES-370, NIC-6059, IS-607-2-04, SI-1873, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, S-0253, BS-10, IC-204997, IS-261-2, NIC-16187, IS-109, IC-204167, KMS-4-238, S-0486, G-9-1, IS-514, G-49, Murg-1-7, RJS-218, G-44, NIC-13006, IS-455, G-39, ES-3196-I, S-0126, NIC-3351, IS-101-213, G-1, IS-352, IS-101-4, 54-1641, S-0650, SI-2561, TC-171, NIC-13032, S-0021, G-15, EC-310448, EC-335004-I, TS-332, G-17, RJS-29-I, NIC-8174, ES-41, GRT-8609, NIC-17389, 78-505, SI-2073, NIC-17301, GRT-8368, S-0479, EC-132295, NIC-8590, 77-701, RJS-9613, RJS-4-79, EC-335000-A, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, IC-205206, Dharand, kolenyola, GRT-8342, G-20, NIC-8035, IS-475, Chagata local, IS-24-P, S-0501, IS-39-B, IC-131953, IS-299, SI-3097, IS-564A, KMR-78, SI-2143, KIS-551, GRT-8385, TC-326, NIC-8020, 78-831, NIC-8511, MOHUR-3, G-5, SI-7619-B, IS-101-2, IS-470, GRT-8368-I, RJS-8316, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, IS-431, EC-334968, SI-7178, IS-393-1-A, TKG-21, TKG-22, JTS-8, GT-10
Main stem colour	Green (204)	All
	Yellow (0)	None
	Purplish green (0)	None
	Purple (0)	None
Stem hairiness	Absent (42)	SI-1687-I, IC-14331, EC-182832, G-18, NIC-8033, SI-805, NCR/82/No/Bo/NS, G-8, EC-334993-I, ES-110-A, GRT-8327, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, RJS-Bo, WLR/92/No/217/Shal, G-47, IC-2621694, ES-64, G-9-1, G-49, Murg-1-7, NIC-13006, ES-3196-I, IS 101-213, G-1, SI-2561, TC-171, G-15, NIC-8174, GRT-8609, SI-2073, NIC-8590, RJS-4-79, IC-205206, NIC-8035, IS-475, 78-831, MOHUR-3, GRT-8368-I, RJS-8316

Trait	Classes	Genotypes
	Sparse (160)	Oct-81, G-2, G-6, RJS-185, NIC-8282, IS-387, G-13, EC-334955, IS-205-I, SI-1925, EC-35000, NIC-9835, IS-77, NIC-8055-I, S-0619, S-0627, IC-152485, ES-120-1-84-B, ES-173, IS-99-A, SI-3275, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-156-3-84, IS-641-2-84, G-40, SI-3315-16, G-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, SI-3114, EC-334969, EC-204704, EC-334995-I, IS-564, S-0210, IS-350, ES-5503, IC-30884, NIC-8343, IS-90, GRT-8359, I-68, IS-686, 78-266-I, S-0281, TMV-12-52, IS-712, GRT-83128, NIC-16218, KJS-21, GAD-5, EC-335009, IS-302, NIC-8210, 78-20, ES-560, Coredbose, ES-312955, IC-14142, GRT-8392, ES-370, NIC-6059, IS-607-2-04, SI-1873, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, S-0253, BS-10, IC-204997, IS-482-B, IS-261-2, NIC-16187, IS-109, IC-204167, KMS-4-238, S-0486, IS-514, RJS-218, G-44, IS-455, G-39, S-0126, NIC-3351, IS-352, IS-101-4, 54-1641, S-0650, NIC-13032, S-0021, EC-310448, EC-335004-I, G-17, RJS-29-I, ES-41, NIC-17389, 78-505, NIC-17301, GRT-8368, S-0479, EC-132295, 77-701, RJS-9613, EC-335000-A, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, Dharand kolenyola, GRT-8342, G-20, Chagata local, IS-24-P, S-0501, IS-39-B, IC-131953, IS-299, SI-3097, IS-564A, KMR-78, SI-2143, KIS-551, GRT-8385, TC-326, NIC-8020, NIC-8511, G-5, SI-7619-B, IS-101-2, IS-470, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, IS-431, EC-334968, SI-7178, IS-393-1-A, TKG-21, TKG-22, JTS-8, GT-10
	Dense (2)	NIC-8062, TS-332
Branching habit	Absent (0)	None
	Few (63)	EC-182832, G-18, NCR/82/No/Bo/NS, NIC-8062, SI-1925, EC-35000, ES-110-A, NIC-8055-I, S-0069, ES-139-2-84, S-0627, IC-152485, ES-120-1-84-B, G-47, IS-156-3-84, SI-3315-16, EC-334969, IS-686, S-0281, NIC-16218, NIC-8210, 78-20, ES-560, GRT-8392, ES-370, NIC-6059, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, IC-204997, IS-482-B, IS-261-2, IS-109, G-9-1, G-49, Murg-1-7, G-44, NIC-13006, NIC-3351, S-0650, SI-2561, S-0021, G-15, SI-2073, NIC-17301, EC-132295, RJS-9613, RJS-4-79, EC-335000-A, IC-204630, Local-1, IC-205206, Dharand, IS-564A, TC-326, NIC-8020, 78-831, SI-7619-B, IS-445-I, IS-431
	Medium (112)	SI-1687-I, IC-14331, Oct-81, SI-805, G-6, RJS-185, NIC-8282, IS-387, G-13, EC-334955, IS-205-I, IS-77, EC-334993-I, GRT-8327, S-0619, IS-132295, ES-131-1-84, RJS-Bo, ES-173, WLR/92/No/217/Shal, IS-99-A, SI-3275, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-641-2-84, G-40, IC-2621694, G-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, SI-3114, EC-204704, IS-564, S-0210, IS-350, ES-5503, IC-30884, NIC-8343, IS-90, I-68, TMV-12-52, IS-712, EC-335009, IS-302, Coredbose, ES-312955, IC-14142, IS-607-2-04, SI-1873, S-0253, NIC-16187, IC-204167, KMS-4-238, S-0486, RJS-218, IS-455, G-39, ES-3196-I, S-0126, G-1, IS-352, IS-101-4, 54-1641, TC-171, NIC-13032, EC-335004-I, G-17, GRT-8609, 78-505, GRT-8368, S-0479, NIC-8590, 77-701, NIC-16264, IC-204137, kolenyola, GRT-8342, NIC-8035, IS-475, Chagata local, IS-24-P, IS-39-B, IS-299, SI-3097, SI-2143, GRT-8385, NIC-8511, MOHUR-3, G-5, IS-101-2, IS-470, RJS-8316, IS-733, NIC-8523, 18-Oct, RJS-738-2-84, EC-334968, SI-7178, IS-393-1-A, TKG-21, TKG-22, JTS-8, GT-10.
	Profuse (29)	NIC-8033, G-2, G-8, NIC-9835, EC-334995-I, ES-64, GRT-8359, 78-266-I, GRT-83128, KJS-21, GAD-5, BS-10, IS-514, IS-101-213, EC-310448, TS-332, RJS-29-I, NIC-8174, ES-41, NIC-17389, S-0248, G-20, S-0501, IC-131953, KMR-78, KIS-551, GRT-8368-I, B-223, EC-310425

Trait	Classes	Genotypes
Branching pattern	Non branching (0)	None
	Basal branching (0)	None
	Top branching (204)	All
Leaf hairiness	Glabrous (9)	78-20, IS-514, EC-310448, RJS-9613, IS-24-P, TKG-21, TKG-22, JTS-8, GT-10
	Sparse (195)	SI-1687-I, IC-14331, Oct-81, EC-182832, G-18, NIC-8033, SI-805, G-2, G-6, RJS-185, NIC-8282, IS-387, G-13, EC-334955, NCR/82/No/Bo/NS, IS-205-I, NIC-8062, G-8, SI-1925, EC-35000, NIC-9835, IS-77, EC-334993-I, ES-110-A, GRT-8327, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, RJS-Bo, S-0627, IC-152485, ES-120-1-84-B, ES-173, WLR/92/No/217/Shal, G-47, IS-99-A, SI-3275, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-156-3-84, IS-641-2-84, G-40, SI-3315-16, IC-2621694, G-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, SI-3114, EC-334969, EC-204704, EC-334995-I, ES-64, IS-564, S-0210, IS-350, ES-5503, IC-30884, NIC-8343, IS-90, GRT-8359, I-68, IS-686, 78-266-I, S-0281, TMV-12-52, IS-712, GRT-83128, NIC-16218, KJS-21, GAD-5, EC-335009, IS-302, NIC-8210, ES-560, Coredbose, ES-312955, IC-14142, GRT-8392, ES-370, NIC-6059, IS-607-2-04, SI-1873, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, S-0253, BS-10, IC-204997, IS-482-B, IS-261-2, NIC-16187, IS-109, IC-204167, KMS-4-238, S-0486, G-9-1, G-49, Murg-1-7, RJS-218, G-44, NIC-13006, IS-455, G-39, ES-3196-I, S-0126, NIC-3351, IS-101-213, G-1, IS-352, IS-101-4, 54-1641, S-0650, SI-2561, TC-171, NIC-13032, S-0021, G-15, EC-335004-I, TS-332, G-17, RJS-29-I, NIC-8174, ES-41, GRT-8609, NIC-17389, 78-505, SI-2073, NIC-17301, GRT-8368, S-0479, EC-132295, NIC-8590, 77-701, RJS-4-79, EC-335000-A, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, IC-205206, Dharand, kolenyola, GRT-8342, G-20, NIC-8035, IS-475, Chagata local, S-0501, IS-39-B, IC-131953, IS-299, SI-3097, IS-564A, KMR-78, SI-2143, KIS-551, GRT-8385, TC-326, NIC-8020, 78-831, NIC-8511, MOHUR-3, G-5, SI-7619-B, IS-101-2, IS-470, GRT-8368-I, RJS-8316, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, IS-431, EC-334968, SI-7178, IS-393-1-A
	Medium (0)	None
	Strong (0)	None
Leaf shape	Linear (0)	None
	Lanceolate (top leaves) (204)	All
	Elliptic (0)	None
	Ovate (middle leaves) (204)	All
	Narrowly cordate (0)	None

Trait	Classes	Genotypes
Basal leaf margin	Entire (49)	RJS-Bo, IC-152485, ES-120-1-84-B, G-47, IS-99-A, SI-3275, IS-641-2-84, G-40, IC-2621694, G-16, SI-3114, EC-204704, ES-64, IS-564, IS-350, EC-335009, IS-302, 78-20, ES-560, Coredbose, IS-109, IC-204167, S-0486, G-9-1, G-49, RJS-218, G-44, G-39, S-0126, NIC-3351, G-1, SI-2561, TC-171, EC-310448, NIC-8174, NIC-17389, 77-701, IC-205206, Dharand, IS-24-P, IC-131953, IS-299, IS-564A, KMR-78, NIC-8020, IS-445-I, IS-431, EC-334968, IS-393-1-A
	Serrate (155)	SI-1687-I, IC-14331, Oct-81, EC-182832, G-18, NIC-8033, SI-805, G-2, G-6, RJS-185, NIC-8282, IS-387, G-13, EC-334955, NCR/82/No/Bo/NS, IS-205-I, NIC-8062, G-8, SI-1925, EC-35000, NIC-9835, IS-77, EC-334993-I, ES-110-A, GRT-8327, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, S-0627, ES-173, WLR/92/No/217/Shal, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-156-3-84, SI-3315-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, EC-334969, EC-334995-I, S-0210, ES-5503, IC-30884, NIC-8343, IS-90, GRT-8359, I-68, IS-686, 78-266-I, S-0281, TMV-12-52, IS-712, GRT-83128, NIC-16218, KJS-21, GAD-5, NIC-8210, ES-312955, IC-14142, GRT-8392, ES-370, NIC-6059, IS-607-2-04, SI-1873, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, S-0253, BS-10, IC-204997, IS-482-B, IS-261-2, NIC-16187, KMS-4-238, IS-514, Murg-1-7, NIC-13006, IS-455, ES-3196-I, IS-101-213, IS-352, IS-101-4, 54-1641, S-0650, NIC-13032, S-0021, G-15, EC-335004-I, TS-332, G-17, RJS-29-I, ES-41, GRT-8609, 78-505, SI-2073, NIC-17301, GRT-8368, S-0479, EC-132295, NIC-8590, RJS-9613, RJS-4-79, EC-335000-A, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, kolenyola, GRT-8342, G-20, NIC-8035, IS-475, Chagata local, S-0501, IS-39-B, SI-3097, SI-2143, KIS-551, GRT-8385, TC-326, 78-831, NIC-8511, MOHUR-3, G-5, SI-7619-B, IS-101-2, IS-470, GRT-8368-I, RJS-8316, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, RJS-738-2-84, SI-7178, TKG-21, TKG-22, JTS-8, GT-10
	Dentate (0)	None
Lobe incision of basal leaf	Absent (21)	G-47, IC-2621694, SI-3114, EC-204704, ES-64, IS-564, IS-109, NIC-3351, TS-332, NIC-17389, 78-505, SI-2073, GRT-8368, 77-701, IC-205206, Dharand, IS-24-P, IS-299, IS-564A, SI-2143, IS-431
	Weak (33)	NIC-8282, IS-387, ES-110-A, GRT-8327, RJS-Bo, S-0627, IC-152485, ES-120-1-84-B, WLR/92/No/217/Shal, IS-99-A, SI-3275, G-16, EC-334969, KJS-21, GAD-5, KMS-4-238, G-1, SI-2561, TC-171, GRT-8609, S-0479, EC-335000-A, IC-204137, IS-475, Chagata local, SI-3097, KMR-78, TC-326, NIC-8020, MOHUR-3, EC-334968, SI-7178, IS-393-1-A
	Medium (118)	SI-1687-I, IC-14331, Oct-81, EC-182832, G-18, NIC-8033, G-6, RJS-185, G-13, EC-334955, IS-205-I, G-8, SI-1925, EC-35000, NIC-9835, IS-77, EC-334993-I, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, ES-173, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-156-3-84, IS-641-2-84, G-40, IS-387-2, Guj Sel-12, NIC-7982, EC-334992-I, EC-310455, EC-334995-I, IS-350, ES-5503, I-68, TMV-12-52, IS-712, GRT-83128, NIC-16218, EC-335009, IS-302, NIC-8210, 78-20, ES-560, Coredbose, IC-14142, GRT-8392, ES-370, RJS-61, ES-334962, BS-10, IS-482-B, IS-261-2, NIC-16187, IC-204167, S-0486, G-9-1, IS-514, G-49, Murg-1-7, RJS-218, G-44, NIC-13006, IS-455, G-39, ES-3196-I, S-0126, IS-352, 54-1641, S-0650, NIC-13032, S-0021, G-15, EC-310448, EC-335004-I, G-17, RJS-29-I, NIC-8174, ES-41, NIC-17301, EC-132295, NIC-8590, IC-204630, NIC-16264, S-0248, Local-1, kolenyola, GRT-8342, G-20, NIC-8035, S-0501, IS-39-B, IC-131953, GRT-8385, 78-831, NIC-8511, G-5, SI-7619-B, IS-101-2, IS-470, GRT-8368-I, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, TKG-21, TKG-22, JTS-8, GT-10

Trait	Classes	Genotypes
	Strong (32)	SI-805, G-2, NCR/82/No/Bo/NS, NIC-8062, SI-3315-16, IS-289, IS-446-1-84, G-19, S-0210, IC-30884, NIC-8343, IS-90, GRT-8359, IS-686, 78-266-I, S-0281, ES-312955, NIC-6059, IS-607-2-04, SI-1873, NIC-8260, IS-562, IS-424, ES-303311, S-0253, IC-204997, IS-101-213, IS-101-4, RJS-9613, RJS-4-79, KIS-551, RJS-8316
Petiole colour	Green (0)	None
	Greenish purple (204)	All
	Purple (0)	None
	Pink (0)	None
No. of flowers per leaf axil	One (204)	All
	More than one (0)	None
Corolla hairiness	Absent (0)	None
	Sparse (25)	EC-334987, IS-156-3-84, SI-3315-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, S-0210, IC-30884, NIC-8343, IS-686, S-0281, TMV-12-52, ES-560, SI-1873, RJS-61, IS-562, ES-303311, IC-204997, IS-261-2, G-9-1, GRT-8609, NIC-17389
	Dense (179)	SI-1687-I, IC-14331, Oct-81, EC-182832, G-18, NIC-8033, SI-805, G-2, G-6, RJS-185, NIC-8282, IS-387, G-13, EC-334955, NCR/82/No/Bo/NS, IS-205-I, NIC-8062, G-8, SI-1925, EC-35000, NIC-9835, IS-77, EC-334993-I, ES-110-A, GRT-8327, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, RJS-Bo, S-0627, IC-152485, ES-120-1-84-B, ES-173, WLR/92/No/217/Shal, G-47, IS-99-A, SI-3275, IS-436-3-84, IS-449, IS-199-2-04, EC-334967, IS-641-2-84, G-40, IC-2621694, G-16, G-19, EC-310455, SI-3114, EC-334969, EC-204704, EC-334995-I, ES-64, IS-564, IS-350, ES-5503, IS-90, GRT-8359, I-68, 78-266-I, IS-712GRT-83128 NIC-16218 KJS-21 GAD-5 EC-335009 IS-302 NIC-8210 78-20 Coredbose ES-312955 IC-14142 GRT-8392 ES-370 NIC-6059 IS-607-2-04, NIC-8260, IS-424, ES-334962, S-0253, BS-10, IS-482-B, NIC-16187, IS-109, IC-204167, KMS-4-238, S-0486, IS-514, G-49, Murg-1-7, RJS-218, G-44, NIC-13006, IS-455, G-39, ES-3196-I, S-0126, NIC-3351, IS-101-213, G-1, IS-352, IS-101-4, 54-1641, S-0650, SI-2561, TC-171, NIC-13032, S-0021, G-15, EC-310448, EC-335004-I, TS-332, G-17, RJS-29-I, NIC-8174, ES-41, 78-505, SI-2073, NIC-17301, GRT-8368, S-0479, EC-132295, NIC-8590, 77-701, RJS-9613, RJS-4-79, EC-335000-A, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, IC-205206, Dharand, kolenyola, GRT-8342, G-20, NIC-8035, IS-475Chagata local IS-24-P S-0501 IS-39-B IC-131953 IS-299 SI-3097 IS-564A KMR-78 SI-2143 KIS-551 GRT-8385 TC-326 NIC-8020 78-831, NIC-8511, MOHUR-3, G-5, SI-7619-B, IS-101-2, IS-470, GRT-8368-I, RJS-8316, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, IS-431, EC-334968, SI-7178, IS-393-1-A, TKG-21, TKG-22, JTS-8, GT-10

Trait	Classes	Genotypes
Corolla colour	White (0)	None
	White with pink shading (136)	SI-1687-I, IC-14331, Oct-81, NIC-8033, SI-805, G-2, G-6, NIC-8282, IS-387, G-13, EC-334955, IS-205-I, NIC-8062, G-8, EC-35000, EC-334993-I, ES-110-A, GRT-8327, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, RJS-Bo, IC-152485, ES-120-1-84-B, ES-173, G-47, IS-99-A, SI-3275, IS-436-3-84, IS-449, IS-199-2-04, EC-334967, IS-156-3-84, IS-641-2-84, G-40, SI-3315-16, IC-2621694, G-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, EC-204704, EC-334995-I, ES-64, IS-564, S-0210, IS-350, ES-5503, IC-30884, NIC-8343, IS-90, GRT-8359, I-68, IS-686, 78-266-I, S-0281, TMV-12-52, IS-712, NIC-16218, IS-302, ES-560, Coredbose, ES-312955, IC-14142, GRT-8392, ES-370, NIC-6059, IS-607-2-04, SI-1873, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, S-0253, BS-10, IC-204997, IS-482-B, IS-109, KMS-4-238, G-9-1, IS-514, G-49, RJS-218, NIC-13006, IS-455, G-39, S-0126, IS-352, S-0650, NIC-13032, TS-332, G-17, NIC-8174, GRT-8609, GRT-8368, EC-335000-A, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, IC-205206, Dharand, kolenyola, GRT-8342, G-20, NIC-8035, IS-475, Chagata local, IS-24-P, IC-131953, IS-299, SI-3097, KIS-551, GRT-8385, TC-326, NIC-8020, SI-7619-B, RJS-8316, IS-431, EC-334968, IS-393-1-A, TKG-21, TKG-22, JTS-8, GT-10.
	White with deep pink shading (68)	EC-182832, G-18, RJS-185, NCR/82/No/Bo/NS, SI-1925, NIC-9835, IS-77, S-0627, WLR/92/No/217/Shal, EC-334987, SI-3114, EC-334969, GRT-83128, KJS-21, GAD-5, EC-335009, NIC-8210, 78-20, IS-261-2, NIC-16187, IC-204167, S-0486, Murg-1-7, G-44, ES-3196-I, NIC-3351, IS-101-213, G-1, IS-101-4, 54-1641, SI-2561, TC-171, S-0021, G-15, EC-310448, EC-335004-I, RJS-29-I, ES-41, NIC-17389, 78-505, SI-2073, NIC-17301, S-0479, EC-132295, NIC-8590, 77-701, RJS-9613, RJS-4-79, S-0501, IS-39-B, IS-564A, KMR-78, SI-2143, 78-831, NIC-8511, MOHUR-3, G-5, IS-101-2, IS-470, GRT-8368-I, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, SI-7178
	Pink (0)	None
	Light violet (0)	None
	Dark violet (0)	None
	Purple (0)	None
	Red (0)	None
	Light maroon (0)	None
Capsule Shape	Tapered at apex (0)	None
	Square (0)	None
	Broad Oblong (2)	G-13, NIC-8035

Trait	Classes	Genotypes
	Narrow oblong (202)	SI-1687-I, IC-14331, Oct-81, EC-182832, G-18, NIC-8033, SI-805, G-2, G-6, RJS-185, NIC-8282, IS-387, EC-334955, NCR/82/No/Bo/NS, IS-205-I, NIC-8062, G-8, SI-1925, EC-35000, NIC-9835, IS-77, EC-334993-I, ES-110-A, GRT-8327, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, RJS-Bo, S-0627, IC-152485, ES-120-1-84-B, ES-173, WLR/92/No/217/Shal, G-47, IS-99-A, SI-3275, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-156-3-84, IS-641-2-84, G-40, SI-3315-16, IC-2621694, G-16, IS-387-2, Guj Sel-12IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, SI-3114, EC-334969, EC-204704, EC-334995-I, ES-64, IS-564, S-0210, IS-350, ES-5503, IC-30884, NIC-8343, IS-90, GRT-8359, I-68, IS-686, 78-266-I, S-0281, TMV-12-52, IS-712, GRT-83128, NIC-16218, KJS-21, GAD-5, EC-335009, IS-302, NIC-8210, 78-20, ES-560, Coredbose, ES-312955, IC-14142, GRT-8392, ES-370, NIC-6059, IS-607-2-04, SI-1873, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, S-0253, BS-10, IC-204997, IS-482-B, IS-261-2, NIC-16187, IS-109, IC-204167, KMS-4-238, S-0486, G-9-1, IS-514, G-49, Murg-1-7, RJS-218, G-44, NIC-13006, IS-455, G-39, ES-3196-I, S-0126, NIC-3351, IS-101-213, G-1, IS-352, IS-101-4, 54-1641, S-0650, SI-2561, TC-171, NIC-13032, S-0021, G-15, EC-310448, EC-335004-I, TS-332, G-17, RJS-29-I, NIC-8174, ES-41, GRT-8609, NIC-17389, 78-505, SI-2073, NIC-17301, GRT-8368, S-0479, EC-132295, NIC-8590, 77-701, RJS-9613, RJS-4-79, EC-335000-A, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, IC-205206, Dharand, kolenyola, GRT-8342, G-20, IS-475, Chagata local, IS-24-P, S-0501, IS-39-B, IC-131953, IS-299, SI-3097, IS-564A, KMR-78, SI-2143, KIS-551, GRT-8385, TC-326, NIC-8020, 78-831, NIC-8511, MOHUR-3, G-5, SI-7619-B, IS-101-2, IS-470, GRT-8368-I, RJS-8316, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, IS-431, EC-334968, SI-7178, IS-393-1-A, TKG-21, TKG-22, JTS-8, GT-10
No. of locules per capsule	Four (203)	SI-1687-I, IC-14331, Oct-81, EC-182832, G-18, NIC-8033, SI-805, G-2, G-6, RJS-185, NIC-8282, IS-387, G-13, EC-334955, NCR/82/No/Bo/NS, IS-205-I, NIC-8062, G-8, SI-1925, EC-35000, NIC-9835, IS-77, EC-334993-I, ES-110-A, GRT-8327, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, RJS-Bo, S-0627, IC-152485, ES-120-1-84-B, ES-173, WLR/92/No/217/Shal, G-47, IS-99-A, SI-3275, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-156-3-84, IS-641-2-84, G-40, SI-3315-16, IC-2621694, G-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, SI-3114, EC-334969, EC-204704, EC-334995-I, ES-64, IS-564, S-0210, IS-350, ES-5503, IC-30884, NIC-8343, IS-90, GRT-8359, I-68, IS-686, 78-266-I, S-0281, TMV-12-52, IS-712, GRT-83128, NIC-16218, KJS-21, GAD-5, EC-335009, IS-302, NIC-8210, 78-20, ES-560, Coredbose, ES-312955, IC-14142, GRT-8392, ES-370, NIC-6059, IS-607-2-04, SI-1873, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, S-0253, BS-10, IC-204997, IS-482-B, IS-261-2, NIC-16187, IS-109, IC-204167, KMS-4-238, S-0486, G-9-1, IS-514, G-49, Murg-1-7, G-44, NIC-13006, IS-455, G-39, ES-3196-I, S-0126, NIC-3351, IS-101-213, G-1, IS-352, IS-101-4, 54-1641, S-0650, SI-2561, TC-171, NIC-13032, S-0021, G-15, EC-310448, EC-335004-I, TS-332, G-17, RJS-29-I, NIC-8174, ES-41, GRT-8609, NIC-17389, 78-505, SI-2073, NIC-17301, GRT-8368, S-0479, EC-132295, NIC-8590, 77-701, RJS-9613, RJS-4-79, EC-335000-A, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, IC-205206, Dharand, kolenyola, GRT-8342, G-20, NIC-8035, IS-475, Chagata local, IS-24-P, S-0501, IS-39-B, IC-131953, IS-299, SI-3097, IS-564A, KMR-78, SI-2143, KIS-551, GRT-8385, TC-326, NIC-8020, 78-831, NIC-8511, MOHUR-3, G-5, SI-7619-B, IS-101-2, IS-470, GRT-8368-I, RJS-8316, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, IS-431, EC-334968, SI-7178, IS-393-1-A, TKG-21, TKG-22, JTS-8, GT-10

Trait	Classes	Genotypes
	Six (0)	None
	Eight (1)	RJS-218
	Mixed (0)	None
Capsule arrangement	Monocapsular (204)	All
	Multicapsular (0)	None
Capsule hairiness	Absent (1)	WLR/92/No/217/Shal
	Sparse (110)	SI-1687-I, Oct-81, G-2, G-6, NIC-8282, IS-205-I, G-8, EC-35000, GRT-8327, ES-139-2-84, RJS-Bo, ES-120-1-84-B, ES-173, G-47, IS-99-A, IS-436-3-84, EC-334987, EC-334967, IS-156-3-84, G-40, IC-2621694, Guj Sel-12, NIC-7982, EC-310455, SI-3114, ES-64, IS-564, IS-350, ES-5503, 78-266-I, GRT-83128, KJS-21, EC-335009, IS-302, 78-20, ES-560, Coredbose, ES-312955, GRT-8392, S-0253, IC-204997, NIC-16187, IS-109, KMS-4-238, G-9-1, Murg-1-7, RJS-218, ES-3196-I, IS-101-213, IS-352, IS-101-4, 54-1641, TC-171, NIC-13032, S-0021, G-15, NIC-8174, GRT-8609, NIC-17301, S-0479, RJS-4-79, EC-335000-A, S-0501, IS-299, KIS-551, GRT-8385, NIC-8020, G-5, GRT-8368-I, RJS-8316, 18-Oct, SI-7178, IS-393-1-A, GT-10
	Medium (34)	IC-14331, G-18, NIC-8033, SI-805, NCR/82/No/Bo/NS, NIC-8062, NIC-8055-I, IS-132295, ES-131-1-84, IS-387-2, IS-446-1-84, EC-334992-I, EC-334969, EC-204704, IC-30884, NIC-8343, IS-90, GRT-8359, IS-686, S-0281, TMV-12-52, NIC-8210, IC-14142, ES-370, NIC-6059, SI-1873, RJS-61, IS-424, ES-334962, ES-303311, BS-10, IS-261-2, TKG-22, JTS-8
	Dense (95)	EC-182832, RJS-185, IS-387, G-13, EC-334955, SI-1925, NIC-9835, IS-77, EC-334993-I, ES-110-A, S-0619, S-0069, S-0627, IC-152485, SI-3275, IS-449, IS-199-2-04, IS-641-2-84, SI-3315-16, G-16, IS-289, G-19, EC-334995-I, S-0210, I-68, IS-712, NIC-16218, GAD-5, IS-607-2-04, NIC-8260, IS-562, IS-482-B, IC-204167, S-0486, IS-514, G-49, G-44, NIC-13006, IS-455, G-39, S-0126, NIC-3351, G-1, S-0650, SI-2561, EC-310448, EC-335004-I, TS-332, G-17, RJS-29-I, ES-41, NIC-17389, 78-505, SI-2073, GRT-8368, EC-132295, NIC-8590, 77-701, RJS-9613, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, IC-205206, Dharand, kolenyola, GRT-8342, G-20, NIC-8035, IS-475, Chagata local, IS-24-P, IS-39-B, IC-131953, SI-3097 IS-564A, KMR-78, SI-2143, TC-326, 78-831, NIC-8511, MOHUR-3, SI-7619-B, IS-101-2, IS-470, IS-733, B-223, EC-310425, NIC-8523, IS-445-I, RJS-738-2-84, IS-431, EC-334968, TKG-21
Colour of dry capsule	Green (0)	None
	Straw (38)	RJS-Bo, ES-120-1-84-B, NIC-16187, S-0126, NIC-3351, IS-101-213, IS-352, TC-171, NIC-13032, EC-310448, EC-335004-I, RJS-29-I, NIC-8174, SI-2073, GRT-8368, NIC-8590, RJS-9613, RJS-4-79, IC-204630, IC-204137, Local-1, kolenyola, GRT-8342, G-20, IS-475, IS-39-B, IC-131953, IS-299, KMR-78, KIS-551, NIC-8511, MOHUR-3, IS-101-2, RJS-8316, IS-733, B-223, NIC-8523, SI-7178

Trait	Classes	Genotypes
	Brown (166)	SI-1687-I, IC-14331, Oct-81, EC-182832, G-18, NIC-8033, SI-805, G-2, G-6, RJS-185, NIC-8282, IS-387, G-13, EC-334955, NCR/82/No/Bo/NS, IS-205-I, NIC-8062, G-8, SI-1925, EC-35000, NIC-9835, IS-77, EC-334993-I, ES-110-A, GRT-8327, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, S-0627, IC-152485, ES-173, WLR/92/No/217/Shal, G-47, IS-99-A, SI-3275, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-156-3-84, IS-641-2-84, G-40, SI-3315-16, IC-2621694, G-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, SI-3114, EC-334969, EC-204704, EC-334995-I, ES-64, IS-564, S-0210, IS-350, ES-5503, IC-30884, NIC-8343, IS-90, GRT-8359, I-68, IS-686, 78-266-I, S-0281, TMV-12-52, IS-712, GRT-83128, NIC-16218, KJS-21, GAD-5, EC-335009, IS-302, NIC-8210, 78-20, ES-560, Coredbose, ES-312955, IC-14142, GRT-8392, ES-370, NIC-6059, IS-607-2-04, SI-1873, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, S-0253, BS-10, IC-204997, IS-482-B, IS-261-2, IS-109, IC-204167, KMS-4-238, S-0486, G-9-1, IS-514, G-49, Murg-1-7, RJS-218, G-44, NIC-13006, IS-455, G-39, ES-3196-I, G-1, IS-101-4, 54-1641, S-0650, SI-2561, S-0021, G-15, TS-332, G-17, ES-41, GRT-8609, NIC-17389, 78-505, NIC-17301, S-0479, EC-132295, 77-701, EC-335000-A, NIC-16264, S-0248, IC-205206, Dharand, NIC-8035, Chagata local, IS-24-P, S-0501, SI-3097, IS-564A, SI-2143, GRT-8385, TC-326, NIC-8020, 78-831, G-5, SI-7619-B, IS-470, GRT-8368-I, EC-310425, 18-Oct, IS-445-I, RJS-738-2-84, IS-431, EC-334968, IS-393-1-A, TKG-21, TKG-22, JTS-8, GT-10
	Purple (0)	None
Type of capsule beak	Short (114)	SI-1687-I, Oct-81, EC-182832, G-18, NIC-8033, SI-805, RJS-185, G-13, EC-334955, NIC-8062, G-8, SI-1925, GRT-8327, NIC-8055-I, S-0619, IS-132295, WLR/92/No/217/Shal, IS-99-A, SI-3275, EC-334987, IS-156-3-84, G-40, SI-3315-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, S-0210, NIC-8343, S-0281, IS-712, NIC-16218, EC-335009, NIC-8210, ES-312955, NIC-6059, SI-1873, IS-562, IS-424, IS-482-B, IS-109, S-0486, G-9-1, G-49, RJS-218, NIC-13006, ES-3196-I, S-0126, NIC-3351, IS-101-213, IS-101-4, 54-1641, SI-2561, S-0021, EC-335004-I, G-17, RJS-29-I, ES-41, GRT-8609, SI-2073, NIC-17301, GRT-8368, S-0479, EC-132295, NIC-8590, RJS-9613, IC-204137, Local-1, IC-205206, G-20, IS-24-P, SI-2143, GRT-8385, EC-334968, SI-7178
	Long (64)	G-6, NIC-8282, IS-387, IS-77, EC-334993-I, S-0069, ES-139-2-84, RJS-Bo, S-0627, IC-152485, ES-120-1-84-B, ES-173, G-47, IS-436-3-84, IS-449, IS-641-2-84, IC-2621694, G-16, EC-310455, SI-3114, EC-334969, EC-204704, ES-64, IS-564, IS-350, ES-5503, IC-30884, IS-90, GRT-8359, I-68, IS-686, 78-266-I, TMV-12-52, ES-560, IC-14142, GRT-8392, ES-370, IS-607-2-04, RJS-61, NIC-8260, ES-334962, ES-303311, S-0253, BS-10, IC-204997, KMS-4-238, IS-514, Murg-1-7, IS-455, G-39, S-0650, TC-171, NIC-13032, TS-332, NIC-8174, 77-701, IC-204630, Dharand, kolenyola, NIC-8035, IS-564A, TKG-21, TKG-22, GT-10,
	Curved (62)	IC-14331, G-2, NCR/82/No/Bo/NS, IS-205-I, EC-35000, NIC-9835, ES-110-A, ES-131-1-84, IS-199-2-04, EC-334967, EC-334995-I, GRT-83128, KJS-21, GAD-5, IS-302, 78-20, Coredbose, IS-261-2, NIC-16187, IC-204167, G-44, G-1, IS-352, G-15, EC-310448, NIC-17389, 78-505, RJS-4-79, EC-335000-A, NIC-16264, S-0248, GRT-8342, IS-475, Chagata local, S-0501, IS-39-B, IC-131953, IS-299, SI-3097, KMR-78, KIS-551, TC-326, NIC-8020, 78-831, NIC-8511, MOHUR-3, G-5, SI-7619-B, IS-101-2, IS-470, GRT-8368-I, RJS-8316, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, IS-431, IS-393-1-A, JTS-8

Trait	Classes	Genotypes
	Cleft (0)	None
Seed coat colour	White (3)	TKG-21, TKG-22, JTS-8
	Dark brown (200)	SI-1687-I, IC-14331, Oct-81, EC-182832, G-18, NIC-8033, SI-805, G-2, G-6, RJS-185, NIC-8282, IS-387, G-13, EC-334955, NCR/82/No/Bo/NS, IS-205-I, NIC-8062, G-8, SI-1925, EC-35000, NIC-9835, IS-77, EC-334993-I, ES-110-A, GRT-8327, NIC-8055-I, S-0619, IS-132295, ES-131-1-84, S-0069, ES-139-2-84, RJS-Bo, S-0627, IC-152485, ES-120-1-84-B, ES-173, WLR/92/No/217/Shal, G-47, IS-99-A, SI-3275, IS-436-3-84, IS-449, EC-334987, IS-199-2-04, EC-334967, IS-156-3-84, IS-641-2-84, G-40, SI-3315-16, IC-2621694, G-16, IS-387-2, Guj Sel-12, IS-289, NIC-7982, IS-446-1-84, EC-334992-I, G-19, EC-310455, SI-3114, EC-334969, EC-204704, EC-334995-I, ES-64, IS-564, S-0210, IS-350, ES-5503, IC-30884, NIC-8343, IS-90, GRT-8359, I-68, IS-686, 78-266-I, S-0281, TMV-12-52, IS-712, GRT-83128, NIC-16218, KJS-21, GAD-5, EC-335009, IS-302, NIC-8210, 78-20, ES-560, Coredbose, ES-312955, IC-14142, GRT-8392, ES-370, NIC-6059, IS-607-2-04, SI-1873, RJS-61, NIC-8260, IS-562, IS-424, ES-334962, ES-303311, S-0253, BS-10, IC-204997, IS-482-B, IS-261-2, NIC-16187, IS-109, IC-204167, KMS-4-238, S-0486, G-9-1, IS-514, G-49, Murg-1-7, RJS-218, G-44, NIC-13006, IS-455, G-39, ES-3196-I, S-0126, NIC-3351, IS-101-213, G-1, IS-352, IS-101-4, 54-1641, S-0650, SI-2561, TC-171, NIC-13032, S-0021, G-15, EC-310448, EC-335004-I, TS-332, G-17, RJS-29-I, NIC-8174, ES-41, GRT-8609, NIC-17389, 78-505, SI-2073, NIC-17301, GRT-8368, S-0479, EC-132295, NIC-8590, 77-701, RJS-9613, RJS-4-79, EC-335000-A, IC-204630, NIC-16264, IC-204137, S-0248, Local-1, IC-205206, Dharand, kolenyola, GRT-8342, G-20, NIC-8035, IS-475, Chagata local, IS-24-P, S-0501, IS-39-B, IC-131953, IS-299, SI-3097, IS-564A, KMR-78, SI-2143, KIS-551, GRT-8385, TC-326, NIC-8020, 78-831, NIC-8511, MOHUR-3, G-5, SI-7619-B, IS-101-2, IS-470, GRT-8368-I, RJS-8316, IS-733, B-223, EC-310425, NIC-8523, 18-Oct, IS-445-I, RJS-738-2-84, IS-431, EC-334968, SI-7178, IS-393-1-A
	Black (1)	GT-10

4.2 Analysis of variance

The ANOVA revealed that the mean sum of square due to genotypes was highly significant for traits viz., days to flower initiation, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, capsule length (cm), number of seeds per capsule, days to maturity, thousand seed weight (g), seed yield per plant (g) and oil content (%). The analysis of variance for the characters under study has been given in Table 4.3.

4.3 Parameters of genetic variability

Table 4.4 shows the genetic variability parameters for each variable including mean, range, phenotypic and genotypic coefficients of variation (%), heritability in the broad sense (%), and genetic advance as a percentage of mean.

4.3.1 Mean and Range

Table 4.4 shows the mean and range estimates for all of the traits, which are explained trait by trait below.

4.3.1.1 Days to flower initiation

Days to flower initiation recorded minimum of 31.02 days (NIC-8343, IS-431) and maximum of 43 days (JTS-8) with a mean of 36.77 days.

4.3.1.2 Days to 50% flowering

Days to 50% flowering recorded minimum of 34.13 days (IS-431) and maximum of 48.38 days (I-68, Guj Sel-12, S-0281) with a mean of 41.69 days.

4.3.1.3 Days to maturity

Days to maturity recorded minimum of 82.25 days (IS-431) and maximum of 101.5 days (SI-2073) with a mean value of 92.75 days.

4.3.1.4 Plant height

The plant height ranged from 84.32 cm (TC-326) to 167.9 cm (IS-607-2-04) with a mean of 131.71 cm.

4.3.1.5 Number of primary branches per plant

Number of primary branches per plant recorded minimum of 0.84 (IS-562) and maximum of 8.1 (RJS-29-I) primary branches per plant with a mean of 3.65.

4.3.1.6 Number of secondary branches per plant

Number of secondary branches per plant recorded minimum of 0 (MOHUR-3, IS-455, EC-334968, IS-431) and maximum of 6 (NIC-17389) secondary branches per plant with a mean of 1.98 secondary branches per plant.

4.3.1.7 Number of capsules per plant

Number of capsules per plant varied from 13.34 (IC-205206) to 94.42 (IS-607-2-04) with a mean of 49.77 capsules per plant.

4.3.1.8 Capsule length

Capsule length recorded to be minimum i.e. 1.64 cm (GRT-8385) and maximum i.e. 3.9 cm (JTS-8) with a mean value of 2.53 cm.

4.3.1.9 Number of seed per capsule

Number of seeds per capsule recorded minimum of 31.65 (EC-310455) and maximum of 80.77 (G-6) seeds per capsule with a mean value of 60.65 seeds per capsule.

4.3.1.10 Thousand seed weight (g)

Thousand seed weight varied from 2.26g (IS-101-213) to 4.6g (GT-10) with a mean of 3.05 g.

4.3.1.11 Oil content (%)

Oil content ranged from 22.31% (GRT-8327) to 54.89% (NIC-13006) with a mean of 41.12%.

4.3.1.12 Seed yield/plant (g)

Seed yield per plant was recorded to be minimum i.e 1.62 g (NIC-8055-I) and maximum was recorded to be 20.71 g (B-223) with a mean of 10.28 g.

Table 4.3: Mean squares from analysis of variance of 12 quantitative traits in 204 sesame germplasm

Source of variation	Df	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC	SYP
Blocks	9	5.19 **	15.85 **	123.49 *	6.78 **	8.39 **	306.35 **	5.35 **	67.04 **	21.83 **	8.13 **	188.63 **	10.16 **
Entries	203	8.25 **	6.56	308.8 **	1.55 **	1.42 **	195.13 **	5.22 **	63.37 **	12.1 *	7.27 **	36.96 **	9.63 **
Variety	199	2.91**	5.77 **	261.08 **	1.52 **	1.17 **	178.1 **	4.03 **	59.73 **	10.17 **	5.09 **	17.77 **	9.28 **
Checks	3	21.23 **	16.43 **	397.24 **	5.11 **	8.66 **	158.13 *	4.95 **	171.01 **	35.67 **	4.71 **	6.45 **	6.27 **
Checks vs varieties	1	626.41 **	134.67 **	9539.21 **	1.79	30.19 **	3694.94 **	32.08 **	464.55 **	524.04 **	23.91 **	3947.99 **	107.98 **
Error	27	4.32	7.68	44.24	0.51	0.25	36.69	0.7	19.44	6.61	0.34	5.49	2

*Significant at probability level of 0.05 and **Significant at probability level

Where, DFI- Days to flower initiation, DFF- Days to 50% flowering, NPB- Number of primary branches, NSB- Number of secondary branches per plant, NCPP- Number of capsule per plant, PH- plant height, NSPC- Number of seeds per capsule, CL- capsule length, DM- Days to maturity, TSW- Thousand seed weight, OC- Oil content, SYP- Seed yield per plant.

Table 4.4: Genetic parameters of variability for yield and its component traits in sesame genotypes

Traits	Mean	Range		GCV (%)	PCV (%)	h ² b (%)	GA as % of mean 5%
		Minimum	Maximum				
Days to flower initiation	36.77	31.02	43	13.47	14.69	54.28	10.2
Days to 50% flowering	41.69	34.13	48.38	14.24	15.77	53.96	12.42
Plant height (cm)	167.9	84.32	167.9	11.18	12.27	83.05	21.02
No. of primary branches per plant	3.65	0.84	8.1	27.62	33.83	66.65	46.52
No. of secondary branches per plant	1.98	0	6	48.43	54.61	78.63	88.59
No. of capsules per plant	49.77	13.34	94.42	23.89	26.81	79.4	43.92
Capsule length (cm)	2.53	1.64	3.9	27.15	33.51	71.91	48.07
No. of seeds per capsule	60.65	31.61	80.77	10.47	12.74	67.45	17.73
Days to maturity	92.75	82.25	101.5	1.73	3.27	27.94	1.88
Thousand seed weight (g)	3.05	2.26	4.6	29.98	31.68	83.19	54.71
Oil content (%)	41.12	22.31	54.89	8.52	10.25	69.1	14.61
Seed yield/plant (g)	10.28	1.62	20.71	26.23	29.62	78.43	47.92

4.3.2 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variation for seed yield and its contributing traits is summarized in Table 4.4. The phenotypic coefficient of variation was significantly higher in magnitude than that of genotypic coefficient of variation for all the traits under study. Number of secondary branches per plant recorded highest GCV and PCV (48.43%, 54.61%) followed by thousand seed weight (29.98, 31.68%), number of primary branches per plant (27.62%, 33.83%), capsule length (27.15%, 33.51%), seed yield per plant (26.23%, 29.62%) and capsules per plant (23.89, 26.81%); while moderate GCV and PCV were recorded for days to 50% flowering (14.24%,15.77%) followed by days to flower initiation (13.47%, 14.69%), plant height (11.18%, 12.27%) and seeds per capsule (10.47%, 12.47%). Low GCV and PCV were recorded for oil content (8.52%, 10.25%) followed by days to maturity (1.73%, 3.27%).

4.3.3 Heritability (%) (bs)

Heritability was estimated for all the quantitative traits under study. (Table 4.4). Most of the characters expressed high estimates of broad sense heritability. The highest heritability was exhibited by thousand seed weight (83.19 %) followed by plant height (83.05%), capsules per plant (79.40%), secondary branches per plant (78.63%), seed yield per plant (78.43%) and capsule length (71.91%). Medium heritability was recorded for oil content (69.10%) followed by number of seeds per capsule (67.45%), primary branches per plant (66.65%), days to maturity (57.94%), days to flower initiation (54.28%) and days to 50% flowering (53.96%).

4.3.4 Genetic advance as percentage of mean

The highest genetic advance as percentage of mean (at 5% Selection intensity) was recorded for number of secondary branches per plant (88.59%) followed by thousand seed weight (54.71%), capsule length (48.07%), seed yield per plant (47.92%), primary branches per plant (46.52%), capsules per plant (43.92%) and plant height (21.02%). Moderate genetic advance as a percentage of mean was recorded for seeds per capsule (17.73%), days to maturity (14.88%), oil content (14.61%), days to 50% flowering (12.42%) and days to flower initiation (10.2%).

Heritability estimations combined with genetic advance provide insight into the type of gene action involved in character inheritance. High heritability coupled with high genetic advance was observed for number of secondary branches per plant, plant height, number of capsules per plant, capsule length, thousand seed weight and seed yield per plant. Moderate heritability with high genetic advance was observed for number of primary branches per plant. Moderate heritability with moderate genetic advance was observed for days to flower initiation, days to 50% flowering, days to maturity, number of seeds per capsule and oil content.

4.4.1 Correlation coefficient analysis

Correlation between seed yield per plant and various yield attributing traits viz., days to flower initiation, days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, days to maturity, number of seeds per capsule, thousand seed weight and oil content (%) are presented in Table 4.5.

Study revealed that seed yield per plant showed highly significant positive correlation with number of capsules per plant (0.675), number of seeds per capsule (0.506), number of primary branches per plant (0.459), plant height (0.385), oil content (0.364) and number of secondary branches per plant (0.209).

4.4.1.1 Days to flower initiation

Days to flower initiation expressed highly significant positive association with days to maturity (0.693) and days to 50% flowering (0.556), while negative significant association with oil content (-0.171) was recorded.

4.4.1.2 Days to 50% flowering

Days to 50% flowering expressed highly significant positive association with days to maturity (0.657), and negative association with number of seed per capsule (-0.257) and capsule length (-0.142).

4.4.1.3 Plant height (cm)

Plant height expressed positive and highly significant association with number of secondary branches per plant (0.503), number of primary branches per plant (0.394) and number of capsules per plant (0.179).

4.4.1.4 Number of primary branches per plant

Number of primary branches per plant expressed highly significant positive association with number of secondary branches per plant (0.571) and number of capsules per plant (0.486).

4.4.1.5 Number of secondary branches per plant

Number of secondary branches per plant expressed positive and highly significant association with number of capsules per plant (0.285) and capsule length (0.262).

4.4.1.6 Number of capsules per plant

Number of capsules per plant expressed significant positive association with oil content (0.399) and highly significant negative association with capsule length (-0.195).

4.4.1.7 Capsule length

Capsule length expressed positive and highly significant association with thousand seed weight (0.187), positive and significant association with number of seeds per capsule (0.168) and highly significant negative association with oil content (-0.192).

4.4.1.8 Number of seeds per capsule

None of the character showed significant positive and negative correlation with number of seeds per capsule.

4.4.1.9 Days to maturity

Days to maturity exhibited significant negative association with oil content (-0.144).

4.4.1.10 Thousand seed weight

Thousand seed weight showed significant positive correlation with oil content (0.148).

4.4.1.11 Oil content (%)

None of the character showed significant positive correlation with oil content.

Table 4.5: Correlation coefficient analysis for yield and its contributing trait in 204 sesame germplasm

Variables	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	OC	SYP
DFI	1	0.556**	0.018	0.125	0.071	-0.085	0.121	0.054	0.693**	-0.171*	0.083
DFF		1	-0.135	0.048	-0.007	0.087	-0.142*	-0.257**	0.657**	-0.043	-0.082
PH			1	0.394**	0.251**	0.503**	0.137	0.036	-0.028	0.179*	0.385**
NPB				1	0.571**	0.486**	0.128	0.095	0.055	-0.056	0.459**
NSB					1	0.285**	0.262**	0.033	0.007	-0.104	0.209**
NCPP						1	-0.195**	0.027	0.017	0.399**	0.675**
CL							1	0.168*	-0.036	-0.192**	0.024
NSPC								1	-0.109	0.012	0.506**
DM									1	-0.144*	-0.095
TSW										0.148*	0.096
OC										1	0.364**
SYP											1

*Significant at probability level of 0.05 and **significant at probability level 0.01

4.4.2 Path coefficient analysis

The contribution of numerous independent characters on the dependent characters is measured using path coefficient analysis. It displays whether these independent characters are associated with yield because of their direct effect on yield or because of their indirect effect through other component characters. Path coefficient analysis was used in this study with seed yield/plant as the dependent variable.

4.4.2.1 Direct effect

Results revealed that substantial high positive direct effect on seed yield was exerted by number of capsules per plant (0.6077), moderate positive direct effect was exhibited by number of seeds per capsule (0.4135), days to flower initiation (0.3063), number of primary branches per plant (0.1775) and oil content (0.1370). Low positive direct effect was exerted by thousand seed weight (0.0800) and capsule length (0.0379). Whereas, negative direct effect was exerted by days to maturity (-0.2315), days to 50% flowering (-0.0438), plant height (-0.0420) and number of secondary branches per plant (-0.0844) as shown in Table 4.6.

4.4.2.2 Indirect effect

4.4.2.2.1 Days to flower initiation

Days to flower initiation exhibited positive indirect effect on seed yield *via* number of seeds per capsule (0.0224) and number of primary branches per plant (0.0221). Days to flower initiation exhibited negative indirect effect on seed yield *via* days to 50% flowering (-0.0244), number of capsules per plant (-0.0516), days to maturity (-0.1604) and oil content (-0.0234). All other traits exhibited negligible indirect effect irrespective of the sign.

4.4.2.2.2 Days to 50% flowering

Days to 50% flowering exhibited positive indirect effect on seed yield *via* days to flower initiation (0.1702) and number of capsules per plant (0.0529). All other traits exhibited negligible indirect effect irrespective of the sign. Whereas, negative indirect effect was exerted *via* number of seeds per capsule (-0.1063) and days to maturity (-0.1522).

4.4.2.2.3 Plant height

Plant height exhibited indirect effect on seed yield *via* number of primary branches per plant (0.0698), number of capsules per plant (0.3056), oil content (0.0246) and number of seed per capsule (0.0149). Whereas, negative indirect effect was exerted *via* number of secondary branches (-0.0212). All other traits exhibited negligible indirect effect on seed yield per plant irrespective of the sign.

4.4.2.2.4 Number of primary branches per plant

Number of primary branches per plant exhibited positive indirect effect on seed yield per plant *via* number of capsules per plant (0.2954), number of seeds per capsule (0.0392) and days to flower initiation (0.0382). Whereas, negative indirect effect was exerted *via* days to maturity (-0.0127), plant height (-0.0165) and number of secondary branches per plant (-0.0482). All other traits exhibited negligible indirect effect irrespective of the sign.

4.4.2.2.5 Number of secondary branches per plant

Number of secondary branches per plant exhibited positive indirect effect on seed yield per plant *via* days to flower initiation (0.0218), number of capsules per plant (0.1729), number of primary branches per plant (0.1014) and number of seeds per capsule (0.0137). Whereas, negative indirect effect was exerted *via* plant height (-0.0106) and oil content (-0.0143).

4.4.2.2.6 Number of capsules per plant

Number of capsules per plant exhibited positive indirect effect on seed yield per plant *via* oil content (0.0547), number of primary branches per plant (0.0863) and number of seeds per capsule (0.0112). Whereas, negative indirect effect was exerted *via*, days to flower initiation (-0.0260), plant height (-0.0211) and number of secondary branches per plant (-0.0240).

4.4.2.2.7 Capsule length

Capsule length exhibited positive indirect effect on seed yield per plant *via* number of seeds per capsule (0.0693), days to flower initiation (0.0371), number of primary branches per plant (0.0228) and thousand seed weight (0.0149). Whereas, negative indirect effect was exerted *via* number of

secondary branches per plant (-0.0221) and oil content (-0.0263). All other traits exhibited negligible indirect effect irrespective of sign.

4.4.2.2.8 Number of seeds per capsule

Number of seeds per capsule exhibited positive indirect effect on seed yield *via* days to maturity (0.0253), days to flower initiation (0.0166), number of primary branches per plant (0.0168), number of capsules per plant (0.0164) and days to 50% flowering (0.0113).

4.4.2.2.9 Days to maturity

Days to maturity exhibited positive indirect effect on seed yield per plant *via* days to flower initiation (0.2122) and number of capsules per plant (0.0101). Days to maturity exhibited negative indirect effect on seed yield *via* days to 50% flowering (-0.0288), number of seeds per capsule (-0.0451) and oil content (-0.0198).

4.4.2.2.10 Thousand seed weight

Thousand seed weight exhibited positive indirect effect on seed yield per plant *via* oil content (0.0202), number of capsules per plant (0.0135) and number of seeds per capsule (0.0124) and negative indirect effect was exerted *via* days to flower initiation (-0.0208) and number of primary branches per plant (-0.0190). Whereas, all other traits exhibited negligible indirect effect irrespective of the sign.

4.4.2.2.11 Oil content

Oil content exhibited positive indirect effect on seed yield per plant *via* number of capsules per plant (0.2428), days to maturity (0.0334) and thousand seed weight (0.0118) and negative indirect effect was exerted *via* days to flower initiation (-0.0523). Whereas, all other traits exhibited negligible indirect effect on seed yield per plant irrespective of the sign.

Table 4.6: Path coefficient analysis for yield and its component traits in sesame

Traits	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC
DFI	0.3063	-0.0244	-0.0008	0.0221	-0.0060	-0.0516	0.0046	0.0224	-0.1604	-0.0054	-0.0234
DFF	0.1702	-0.0438	0.0057	0.0085	0.0006	0.0529	-0.0054	-0.1063	-0.1522	-0.0064	-0.0058
PH	0.0056	0.0059	-0.0420	0.0698	-0.0212	0.3056	0.0052	0.0149	0.0065	0.0197	0.0246
NPB	0.0382	-0.0021	-0.0165	0.1775	-0.0482	0.2954	0.0049	0.0392	-0.0127	-0.0086	-0.0076
NSB	0.0218	0.0003	-0.0106	0.1014	-0.0844	0.1729	0.0099	0.0137	-0.0016	0.0002	-0.0143
NCPP	-0.0260	-0.0038	-0.0211	0.0863	-0.0240	0.6077	-0.0074	0.0112	-0.0039	0.0018	0.0547
CL	0.0371	0.0062	-0.0058	0.0228	-0.0221	-0.1186	0.0379	0.0693	0.0084	0.0149	-0.0263
NSPC	0.0166	0.0113	-0.0015	0.0168	-0.0028	0.0164	0.0064	0.4135	0.0253	0.0024	0.0017
DM	0.2122	-0.0288	0.0012	0.0097	-0.0006	0.0101	-0.0014	-0.0451	-0.2315	-0.0013	-0.0198
TSW	-0.0208	0.0035	-0.0051	-0.0190	0.0002	0.0135	0.0071	0.0124	0.0037	0.0800	0.0202
OC	-0.0523	0.0019	-0.0075	-0.0099	0.0088	0.2428	-0.0073	0.0052	0.0334	0.0118	0.1370
SYP	-0.0234	-0.0821	0.3846	0.4594	0.2091	0.6754	0.0239	0.5060	-0.0952	0.0957	0.3638

Residual = 0.2230

4.5 Genetic divergence using Mahalanobis D² analysis

In the present study, genetic divergence of 204 sesame genotypes (200 germplasm + 4 checks) was determined by using ordinal variables of quantitative characters which were used as an input for UPGMA (unweighted pair group method with arithmetic mean) cluster analysis in which clustering was done using Ward's minimum variance method and Euclidean method of genetic distance was derived.

4.5.1 Grouping of germplasm into various clusters

In the present study, 204 genotypes were grouped into 9 clusters based on divergence analysis (Table 4.7). Clustering of genotypes was not associated with the geographical distribution and was mainly grouped due to their morphological differences. Cluster IX was the largest among all clusters comprising 34 genotypes followed by cluster VIII with 32 genotypes. Cluster IV had 28 genotypes followed by cluster V with 25 genotypes and cluster VI with 23 genotypes. Cluster I had 20 genotypes. Cluster II had 17 genotypes and cluster III had 13 genotypes. Cluster VII was the smallest and had 12 genotypes.

Table 4.7: Distribution of sesame genotypes in different clusters

Name of Cluster	No. of Genotypes	Genotypes
I	20	SI-1687-I, EC-182832, IS-132295, IC-2621694, GujSel-12, EC-310455, NIC-8210, IS-562, IS424, S0253, BS-10, IC-204167, G-15, EC310448, S-0479, RJS-9613, IC-204137, NIC8035, Chagata local
II	17	IC-14331, 29860, RJS-185, NIC-8282, EC-334955, SI-1925, EC-35000, S-0619, ES-139-2-84, RJS-Bo, IS-99-A, IS-564, NIC-16218, IC-14142, IC-204997 ES-3196-I, IS-24-P
III	13	G-18, SI-805, IS-387, EC-334993-I, GRT-8327, S-0627, IC-152485, G-16, IS-350, IS-109, NIC3351, NIC-13032, G-17
IV	28	NIC-8033, G-6, NIC-8062, NIC-9835, IS-90, GRT-8359, GRT-83128, KJS-21, GAD-5, EC-335009, IS302, ES-312955, IS-607-2-04, NIC-8260, IS-482B, G-39, TC-171 EC-335004-I, NIC-8174, GRT-8368, EC-132295, S 0501, IS-393-1-A, KMR-78, G-5, GRT-8368-I, RJS-738-2-84, SI-7178
V	25	G-2, G-13, IS-205-I, G-8, EC-204704, EC-334995-I, ES-

Name of Cluster	No. of Genotypes	Genotypes
		64,78-266-I,ES-370,RJS-61,ES-303311,IS-101-213, RJS-29-I,ES-41,NIC-17389,S-0248,IS-733,B-223, EC-310425,NIC-8523,TKG-21,TKG-22,JTS-8,GT-10, 10/18/2021
VI	23	NCR/82/No/Bo/NS,ES-110-A,ES-120-1-84-B,ES-173,WLR/92/No/217/Shal,G-47,SI-3275,IS-436-3-84,IS-449,EC-334987,IS-199-2-04,EC-334967,IS-156-3-84,SI-3315-16,IS-387-2,NIC-7982,IS-686, GRT-8392,G-9-1,SI-2561,Dharand,IS-299,GRT-8385
VII	12	IS-77,NIC-8055-I,IS-446-1-84,G-19,ES-5503,S-0281,IS-261-2,S-0650,IC-204630,IC-205206,TC-326,NIC-8020
VIII	32	ES-131-1-84,IC-30884,NIC-8343,TMV-12-52,IS-712, NIC-6059,SI-1873,ES-334962,IS-514,RJS-218,G-44, NIC-13006,IS-455,S-0126,G-1,IS-352,54-1641,GRT-8609,NIC-17301,77-701,G-20,IS-475,IC-131953,SI-3097,MOHUR-3,SI-7619-B,IS-470,RJS-8316,IS-445-I,IS-431,EC-334968,IS-39-B
IX	34	S-0069, IS-641-2-84, G-40,IS-289, EC-334992-I, SI-3114,EC-334969,S-0210,I-68,78-20,ES560, Coredbose,NIC-16187,KMS-4-238,S-0486,G-49, Murg-1-7,IS-101-4,S-0021,TS-332,78-505,SI-2073, NIC-8590,RJS-4-79,EC-335000-A,NIC-16264,Local-1, kolenyola,GRT-8342,IS-564A,SI-2143,KIS-551,78-831,NIC-8511

4.5.2 Contribution of individual character towards genetic divergence

The percentage of contribution towards genetic divergence by all the characters is presented in Table 4.8. The trait number of seeds per capsule (10.78%) contributed maximum towards genetic divergence by taking 2233 times first rank followed by oil content (10.61%) by 2197 times, days to 50% flowering (9.34%) by 1933 times, thousand seed weight (9.02%) by 1868 times, plant height (8.96%) by 1855 times, secondary branches per plant (8.73%) by 1807 times, number of primary branches per plant (8.71%) by 1804 times, days to maturity (8.09%) by 1675 times, days to flower initiation (7.22%) by 1494 times, number of capsules per plant (7.1%) by 1471 times, seed yield per plant (7.06%) by 1462 times and capsule length (4.38%) by 907 times 1st rank.

Table 4.8: Contribution of different traits toward clustering in sesame genotype

Source	Times ranked 1 st	Contribution %
Days to flower initiation	1494	7.22
Days to 50% flowering	1933	9.34
Number of primary branches per plant	1804	8.71
Number of secondary branches per plant	1807	8.73
Plant height	1855	8.96
Number of capsules per plant	1471	7.10
Capsule length	907	4.38
Number of seeds per capsule	2233	10.78
Days to maturity	1675	8.09
Thousand seed weight	1868	9.02
Oil content	2197	10.61
Seed yield per plant (g)	1462	7.06

4.5.3 Inter and intra cluster divergence (D^2)

The inter and intra cluster D^2 mean values are presented in Table 4.9. The highest intra cluster distance was recorded in cluster V (27.90) followed by cluster I (22.92), cluster IX (21.94), cluster IV (21.21), cluster VIII (19.67), cluster VII (19.57), cluster VI (18.46), cluster II (17.70) and cluster III (15.37). The inter cluster distance was highest between the clusters V and VII (70.42) followed by cluster V and VI (54.52), IV and VII (52.78) and II and VII (52.55) and the lowest inter cluster distance was observed between cluster IV and VI (36.55).

4.5.4 Cluster mean values of different characters

The cluster mean values of different characters are presented in Table 4.10. High cluster mean values were recorded for days to flower initiation (38.12) and days to maturity (94.18) in cluster II; number of primary branches

per plant (5.17), number of secondary branches per plant (3.27), plant height (156.75), number of capsules per plant (70.31), capsule length (2.81), thousand seed weight (3.16), oil content (44.43) and seed yield (14.16) in cluster V; Days to 50% flowering (43.25) in cluster VII and number of seeds/capsule (67.93) in cluster VIII.

The Lowest cluster mean values were recorded for traits capsule length (2.42) and number of seeds per capsule (50.65) in cluster I; days to 50% flowering (41.00) in cluster IV; number of primary branches per plant (2.58), number of secondary branches per plant (1.41) and oil content (37.96) in cluster VI; plant height (101.18), number of capsules per plant (28.33), thousand seed weight (2.99) and seed yield (6.42) in cluster VII; days to flower initiation (36.22) and days to maturity (92.06) in cluster VIII.

Table 4.9: Inter and intra cluster D² value for different clusters

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9
Cluster1	22.92	23.97	19.02	24.10	41.71	17.35	33.21	20.97	13.97
Cluster2		17.70	17.46	17.09	28.26	34.85	52.55	28.16	33.13
Cluster3			15.37	23.93	39.42	21.05	37.86	22.76	23.50
Cluster4				21.21	18.32	36.55	52.78	17.29	27.83
Cluster5					27.90	54.52	70.42	32.51	45.15
Cluster6						18.46	18.02	26.88	15.23
Cluster7							19.57	39.76	26.58
Cluster8								19.67	15.06
Cluster9									21.94

Table 4.10: Cluster mean for yield and yield contributing traits of sesame genotypes

Variable	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9
DFI	36.90	38.12	36.62	36.29	37.60	36.57	36.67	36.22	36.59
DFF	42.55	42.24	41.08	41.00	41.96	41.35	43.25	41.03	41.59
PH	126.87	150.28	137.87	143.38	156.75	117.80	101.17	128.20	117.87
NPB	3.28	3.80	3.28	4.28	5.17	2.58	2.64	3.72	3.12
NSB	1.65	2.14	1.70	2.01	3.27	1.41	1.65	1.85	1.84
NCPP	45.32	45.20	36.44	59.25	70.31	33.81	28.33	56.01	48.38
CL	2.42	2.43	2.49	2.50	2.81	2.48	2.46	2.60	2.54
NSPC	50.65	55.27	63.23	60.41	63.69	59.03	62.53	67.93	60.67
DM	93.15	94.18	92.08	92.11	93.00	92.09	93.08	92.06	92.65
TSW	3.00	3.04	3.12	3.04	3.16	3.07	2.99	3.05	3.01
OC	41.49	40.08	41.66	40.88	44.43	37.96	38.51	41.32	41.07
SYP	8.13	8.58	8.39	11.82	14.16	7.32	6.42	12.72	9.88

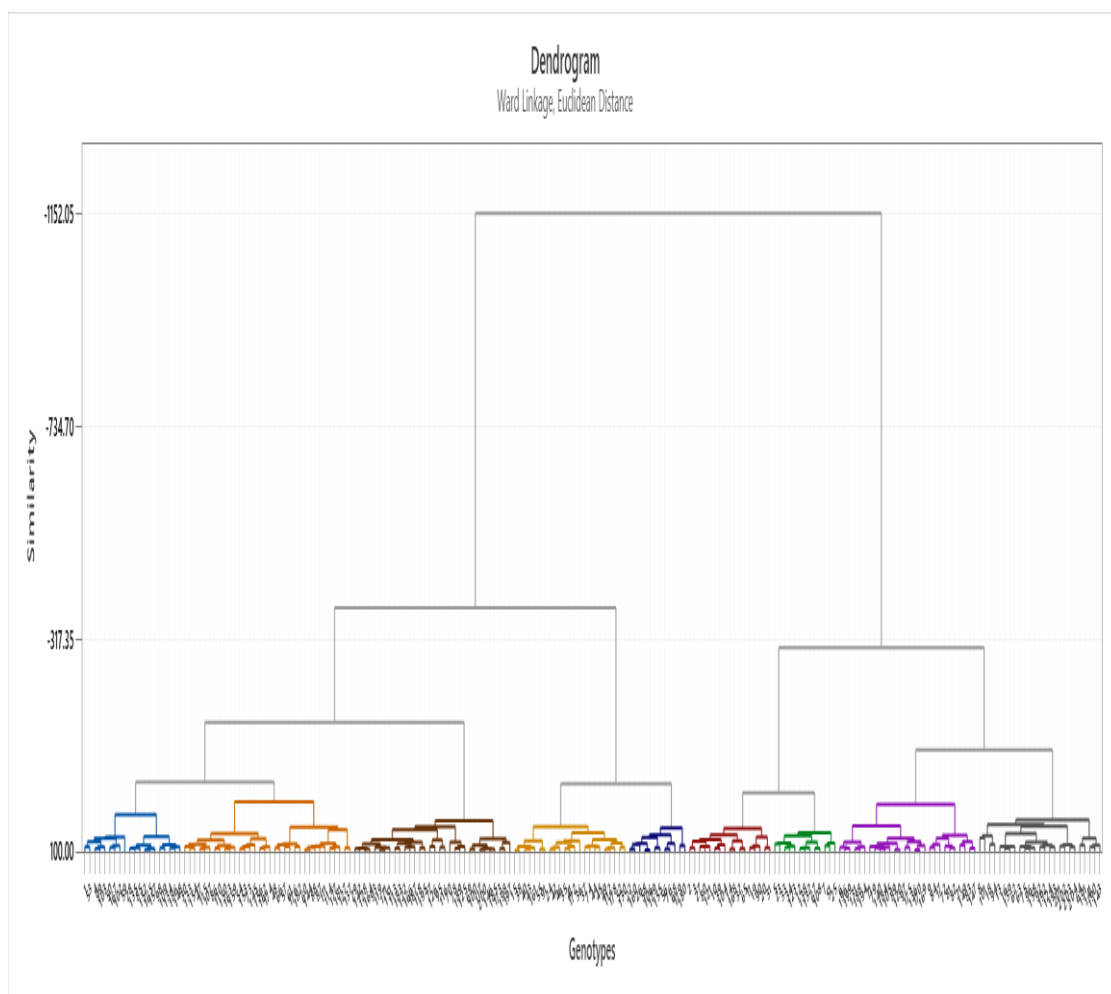


Fig. 1: Dendrogram

4.5.5 Principal Component Analysis

Principal Component Analysis is a mathematical process that converts a set of (potentially) correlated variables into a set of (smaller) uncorrelated variables known as principal components. The first principal component accounts for as much variability as feasible in the data, and each subsequent component accounts for as much variability as possible.

In the present study, eigen values, % variance and cumulative eigen values are mentioned in Table 4.11. Out of twelve, only 5 principal components (PCs) exhibited more than 1 Eigen value and showed about 77.235% variability among the traits studied. The PC1 had the highest variability (24.027 %) followed by PC2 (19.700%), PC3 (13.515 %), PC4 (10.604%) and PC5 (9.389) for all the traits under study.

Table 4.11: Eigen values, % variance and cumulative eigen values of different traits in sesame genotypes

Characters	Principal component (PC)	Eigen value	Variability (%)	Cumulative %
DFI	PC1	2.883	24.027	24.027
DFF	PC2	2.364	19.700	43.727
PH	PC3	1.622	13.515	57.241
NPB	PC4	1.272	10.604	67.846
NSB	PC5	1.127	9.389	77.235
NCPP	PC6	0.687	5.722	82.956
CL	PC7	0.609	5.077	88.033
NSPC	PC8	0.425	3.540	91.573
DM	PC9	0.342	2.850	94.422
TSW	PC10	0.287	2.388	96.811
OC	PC11	0.273	2.279	99.090
SYP	PC12	0.109	0.910	100.000

Scree plot explained the percentage of variance associated between eigen values and the principal components with each PC obtained by drawing a graph. First principal component recorded the highest variation PC1 (24.027%) followed by PC2 (19.700 %), PC3 (13.515 %), PC4 (10.604%) and PC5 (9.389%). Total variation of five PCs was recorded to be 77.235 %. Semi curve line obtained after fifth PC with little variation observed in each PC indicated that maximum variation was found in PC1; therefore selection of genotypes for traits under PC1 may be desirable.

Rotated component matrix revealed that first five PCs are representing maximum variability (77.235 %) hence, the traits falling in these PCs may be given due importance in sesame breeding programme. Results revealed that the first principal component (PC1) which accounted for the highest variation (24.027 %) was mostly related with yield and yield contributing traits such as number of primary branches per plant, number of secondary branches per plant and plant height. The second principal component (PC2) consisted of phenological traits such as days to flower initiation, days to 50% flowering and days to maturity. While the third principal component (PC3) was dominated by

traits viz., number of capsules per plant, oil content and seed yield per plant. Fourth principal component (PC4) was related to number of seeds per capsule. Fifth principal component (PC5) consisted of capsule length and thousand seed weight (Table 4.13). On the basis of PCA, most of the desirable yield attributing traits were present in PC1 and PC3.

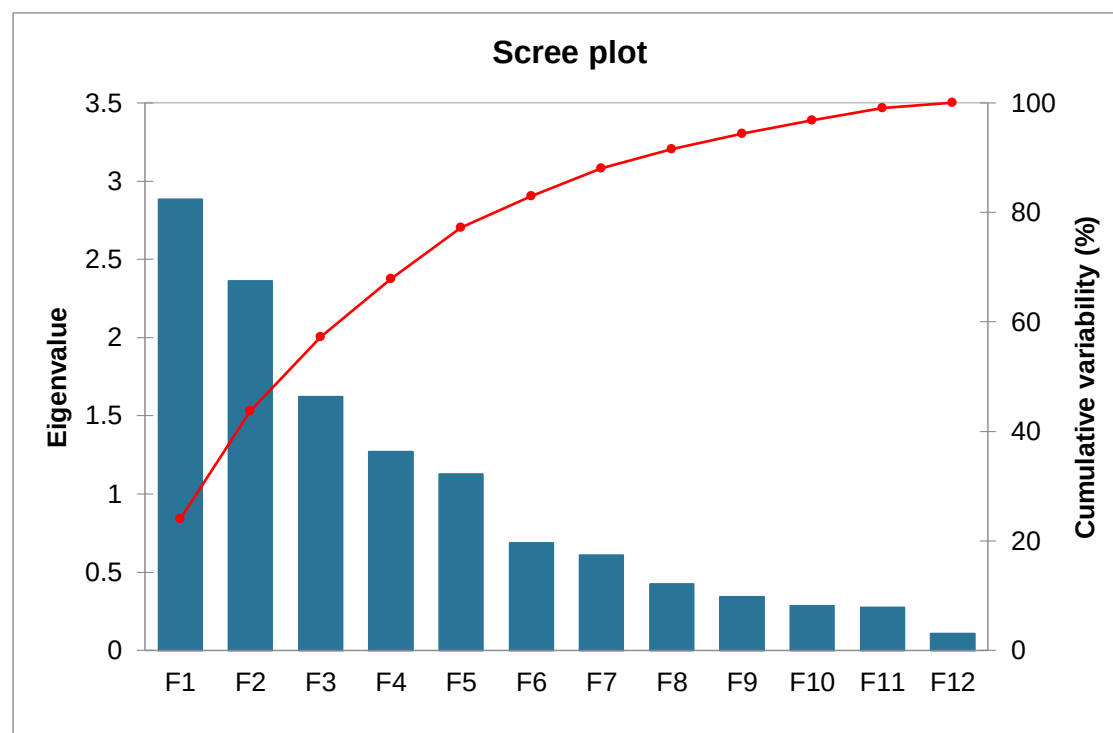


Fig. 2: Screen plot of sesame genotypes between Eigen values and Principal Components

Table 4.12: Rotated Component Matrix for different traits of sesame genotypes

Traits	PC1	PC2	PC3	PC4	PC5
DFI	0.099	0.869	-0.117	0.195	0.030
DFF	-0.044	0.831	0.095	-0.252	-0.117
NPB	0.504	-0.060	0.461	0.000	0.296
NSB	0.819	0.085	0.257	0.121	-0.145
PH	0.828	-0.001	-0.005	-0.021	0.037
NCPP	0.386	0.020	0.835	0.025	-0.059
CL	0.399	-0.019	-0.442	0.258	0.550
NSPC	-0.011	-0.072	0.011	0.946	0.007
DM	0.005	0.902	-0.026	-0.082	0.017
TSW	-0.117	-0.024	0.127	-0.027	0.874
OC	-0.273	-0.129	0.741	0.007	0.176
SYP	0.284	0.010	0.655	0.611	0.046

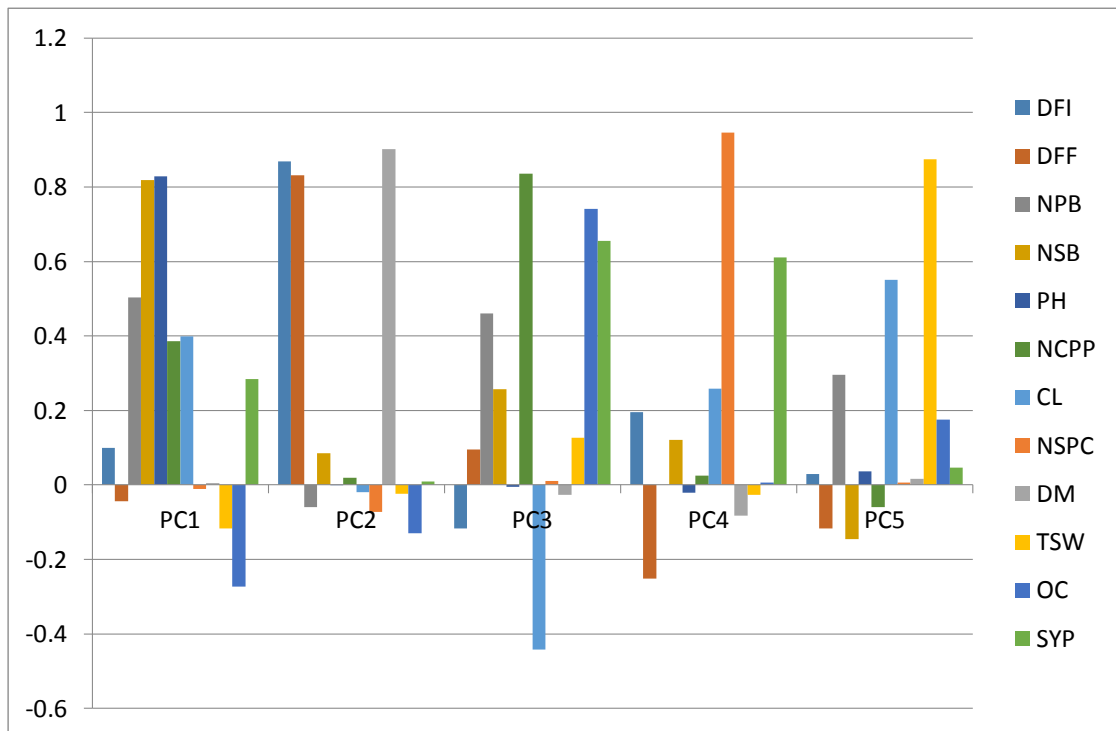


Fig. 3: Rotated Component Matrix

Table 4.13: Interpretation of rotated component matrix for the traits having maximum values in each PCs

	PC1	PC2	PC3	PC4	PC5
Traits	Number of primary branches per plant	Days to flower initiation	Number of capsules per plant	Seed per capsule	Capsule length
	Number of secondary branches per plant	Days to 50% flowering	Oil content	-	Thousand seed weight
	Plant height	Days to maturity	Seed yield per plant	-	-

PC scores of genotypes

The PC scores of each component (PC1, PC2, PC3, PC4 and PC5) had positive and negative values (Table 4.14). These scores can be used to develop exact selection indices, the intensity of which is determined by the variability described by each principal component. A high PC score for a certain genotype in a particular component indicates that the variables in that genotype have high values. In PC1, the positive scores ranged from 4.794 (B-223) to 0.017 (GRT-8342), while negative value ranged from -4.042 (NIC-8055-1) to -0.027 (IS-470). In PC2, the positive value of the component ranged from 3.096 (Guj Sel -12) to 0.01 (EC-35000) and negative value ranged from -5.486 (IS-431) to -0.003 (WLR/92/NO/27/Shal). In PC3, the positive value of the components ranged from 2.869 (IS-101-213) to 0.016 (IS-733) and negative from -3.719 (ES-303311) to -0.017 (EC-334987). In PC4, the positive value of the components ranged from 3.481 (JTS-8*) to 0.001 (IS-101-2), while negative value ranged from -2.997 (EC-310455) to -0.02 (S-0479). In PC5, the positive value of the components ranged from 4.058 (GT-10*) to 0.002 (IS-686 and ES-131-1-84), while negative value ranged from -2.68 (Kolenyola) to -0.028 (EC-204704).

In PC1, the higher value for traits viz., number of primary branches per plant, number of secondary branches per plant and plant height were obtained by genotypes B-223 (4.794) followed by IS-607-2-04 (4.3), NIC-17389 (4.1), ES-64 (3.841), G-2 (3.654), IS-733 (3.615), EC-334995-I (3.536), RJS-29-I

(3.413), 78-266-I (3.294), GT-10(2.959), G-8 (2.933), IS-101-213(2.845), EC-310425 (2.835), GAD-5 (2.805), ES-41 (2.802), S-0501 (2.561), SI-1873 (2.506), KJS-21 (2.46), RJS-61 (2.452), S-0248 (2.288), RJS-218 (2.267), EC-335009 (2.227), ES-370 (2.216) , EC-204704 (2.191), G-13 (2.07), IS-514 (2.068), JTS-8* (2.066), G-20 (2.051) ,IS-302 (2.018), EC-335004-I (1.998), GRT-8359 (1.96), KMR-78 (1.809), IS-39-B (1.8), G-6 (1.791), IS-712 (1.644), IS-205-I (1.643), IS-352 (1.642), SI-3097 (1.578), S-0126 (1.465), IC-131953 (1.44), NIC-13006 (1.43), KIS-551 (1.307), IS-455 (1.299), TS-332 (1.296), SI-805 (1.2730), Coredbose (1.25), GRT-8368-I (1.237), G-39 (1.225), GRT-83128 (1.177), NIC-6059 (1.166), TKG-22* (1.162), TKG-21* (1.149), G-44 (1.013)

Maximum negative values were recorded by S-0253 (-1.002), NIC-8590 (-1.037), S-0479 (-1.069), EC-334967 (-1.079), EC-35000 (-1.088), 78-505 (-1.110), NIC-16218 (-1.112), EC-334993-I (1.128), IS-446-1-84 (-1.173), G-18 (-1.182), NIC-17301 (-1.199), 78-831 (-1.213), SI-7619-B (-1.237), SI-3275 (-1.243), IC-204137 (-1.268), GRT-8385 (-1.280), IS-299 (-1.286), Dharand (1.345), EC-334987 (1.356), S-0069 (1.370), G-15 (1.374), ES-139-2-84 (1.411), G-47 (1.531), GRT-8327 (1.563), IS-101-2 (-1.566), EC-182832 (-1.571), SI-3315-16 (-1.585), S-0210 (-1.637), IS-445-I (-1.653), IS-199-2-04 (-1.672), NIC-3351 (-1.730), Local-1 (-1.764), SI-2073 (-1.769), RJS-4-79 (-1.807), NCR/82/No/Bo/NS (-1.811), IS-424 (-1.859), NIC-8511 (-1.883), EC-334992-I (-1.904), IS-261-2 (-1.910), EC-335000-A (-1.924), EC-334969 (-1.974), IC-2621694 (-2.016) followed by IS-449 (-2.062), S-0650 (-2.108), RJS-9613 (-2.111), ES-173 (-2.176), IS-686 (-2.181), S-0627 (-2.196), S-0281 (-2.273), G-19 (-2.373), ES-120-1-84-B (-2.385), IS-387-2 (-2.429), IS-156-3-84 (-2.53), IC-204630 (-2.586), EC-310455 (-2.598), ES-5503 (-2.614), IC-152485 (-2.615), NIC-8020 (-2.725), SI-2561 (-2.839), ES-110-A (-2.966), TC-326 (-3.043), IS-77 (-3.327), IC-205206 (-3.786) and NIC-8055-I (-4.042).

In PC2, higher value of traits viz., capsule length, number of seeds per capsule were present in genotypes Guj Sel-12 (3.096), RJS-29-I (3.034), JTS-8* (2.686), IS-387-2 (2.665), I-68 (2.652), S-0281 (2.554), SI-2073 (2.509), IC-2621694 (2.487), KMR-78 (2.353), S-0501 (2.346), ES-41 (2.308), IS-475 (2.251), IC-204137 (2.236), EC-334995-I (2.213), S-0210 (2.141), IC-14331

(2.080), ES-64 (2.048), GT-10 (2.000), TKG-22* (1.919), NIC-17389 (1.888) , IS-470 (1.885), Chagata local (1.845), NIC-16264 (1.775), IS-446-1-84 (1.744), RJS-4-79 (1.688), MOHUR-3 (1.654), SI-2143 (1.629), EC-335004-I (1.582), IS-289 (1.576), NIC-7982 (1.569), 01-10-81 (1.544), G-40 (1.536), G-19 (1.489), IS-607-2-04 (1.474), ES-5503 (1.464), G-5 (1.433), NIC-8174 (1.406), IS-564 (1.386), IC-14142 (1.381), IC-205206 (1.367), G-16 (1.347), SI-3275 (1.325), S-0021 (1.303), SI-1687-I (1.267), Dharand (1.260), NIC-17301 (1.209), G-15 (1.187), TMV-12-52 (1.179), TKG-21* (1.154), RJS-Bo (1.141), NIC-16218 (1.137), G-20 (1.135), S-0126 (1.127), EC-335000-A (1.098), GRT-8368-I (1.082), EC-334987 (1.065), GRT-8359 (1.059), IS-101-213 (1.054), S-0253 (1.033) .

Maximum negative values were recorded by EC-334967 (-1.026), NIC-8282 (-1.086), IS-101-4 (-1.121), IS-132295 (-1.125), RJS-8316 (-1.140), S-0619 (-1.163), G-9-1 (-1.210), IS-424 (-1.220), NIC-13006 (-1.233), RJS-185 (-1.239), 78-20 (-1.261), SI-1925 (-1.268), IS-77 (-1.283), IS-302 (-1.397), NCR/82/No/Bo/NS (-1.446), G-1 (-1.496), G-2 (-1.506), IS-261-2 (-1.563), NIC-6059 (-1.690), G-44 (-1.693), ES-131-1-84 (-1.708), S-0069 (-1.709), IS-199-2-04 (-1.753), IS-562 (-1.801), Murg-1-7 (-1.922), EC-334955 (-1.976), GAD-5 (-2.026), EC-334993-I (-2.027), RJS-218 (-2.056), ES-173 (-2.083), G-39 (-2.100), GRT-8368 (-2.221), ES-560 (-2.280), EC-182832 (-2.290), NIC-8055-I (-2.395), TS-332 (-2.519), KMS-4-238 (-2.525), G-18 (-2.529), ES-120-1-84-B (-2.839), IS-455 (-2.896), IS-387 (-2.944), NIC-16187 (-2.992), NIC-8062 (-3.014), EC-335009 (-3.151), IC-204167 (-3.505), G-6 (-3.552), NIC-8343 (-3.593), IS-109 (-4.765) and IS-431 (-5.486) .

In PC3, highest PC scores were obtained by genotypes IS-101-213 (2.869), NIC-9835 (2.827), GRT-8327 (2.611), S-0069 (2.605), RJS-29-I (2.483), EC-334993-I (2.369), NIC-8282 (2.271), GT-10 (2.218), TS-332 (2.029), G-1 (1.991), S-0126 (1.984), IS-77 (1.977), NIC-17389 (1.929), 77-701 (1.898), JTS-8* (1.880), EC-335004-I (1.819), ES-3196-I (1.803), NIC-3351 (1.763), SI-1925 (1.734), G-6 (1.702), EC-132295 (1.683), S-0619 (1.677), IS-352 (1.663), ES-131-1-84 (1.653), 54-1641 (1.590), S-0650 (1.566), NIC-8055-I (1.577), G-18 (1.476), ES-110-A (1.472), IS-132295 (1.467), IC-205206 (1.447), WLR/92/No/217/Shal (1.352), EC-35000 (1.335),

RJS-185 (1.293), NIC-8343 (1.286), EC-310425 (1.281), IS-199-2-04 (1.264) , IC-14331 (1.250), S-0248 (1.248), SI-805 (1.238), ES-41 (1.222), EC-310448 (1.217), NIC-8174 (1.167), GRT-8368 (1.154), 78-266-I (1.153), ES-139-2-84 (1.141), ES-120-1-84-B (1.133), IC-204630 (1.119), IC-152485 (1.118), IS-101-4 (1.108), SI-2561 (1.087) and IS-641-2-84 (1.007) .

Maximum negative values were recorded in KIS-551 (-1.003), SI-7178 (-1.028), ES-64 (-1.034), NIC-8020 (-1.049), 78-20 (-1.068), G-9-1 (-1.071), MOHUR-3 (-1.090), Dharand (-1.096), SI-2143 (-1.112) ,Guj Sel-12 (-1.135), GRT-8392 (-1.143), KJS-21 (-1.187), IS-564A (-1.198), S-0501 (-1.249), 78-831 (-1.266), G-39 (-1.269), IS-261-2 (-1.290), G-5 (-1.323), GRT-8385 (-1.328), IS-289 (-1.337), NIC-8511 (-1.396), IS-607-2-04 (-1.417), G-44 (-1.419), SI-1873 (-1.456), ES-312955 (-1.461), NIC-8035 (-1.487), IS-109 (-1.503), G-49 (-1.504), NIC-8523 (-1.509), 10/18/2021 (-1.512), NIC-8210 (-1.528), IS-24-P (-1.557), IS-455 (-1.570), GRT-8368-I (-1.616), RJS-218 (-1.622), IS-482-B (-1.637), IC-14142 (-1.657), S-0253 (-1.664), IS-445-I (-1.696), RJS-738-2-84 (-1.739), EC-334992-I (-1.809), NIC-6059 (-1.832), IS-101-2 (-1.851), RJS-61(-1.901), BS-10 (-1.947), NIC-13006 (-2.068), IC-204997 (-2.135), IS-562 (-2.207), NIC-8260 (-2.715), IS-424 (-2.727), ES-370 (-2.942) and ES-303311 (-3.719).

In PC4, highest PC scores were obtained by genotypes JTS-8* (3.481) followed by GT-10* (3.027), SI-805 (2.527), EC-335000-A (2.25), NIC-8062 (2.199), S-0021 (2.164), NIC-6059 (2.145), NIC-17301 (1.962), TKG-21* (1.887), EC-334968 (1.850), G-44 (1.742), S-0069 (1.711), G-13 (1.700), NCR/82/No/Bo/NS (1.651) , IC-204137 (1.580) , IS-564A (1.580) , IS-302 (1.564), 78-20(1.507), NIC-13006 (1.482), NIC-16187 (1.472), G-16 (1.456), Murg-1-7 (1.443) , SI-2073 (1.429) , IS-475 (1.428) , SI-7619-B (1.427) , S-0650 (1.427), SI-3315-16 (1.407), RJS-61 (1.375), EC-35000 (1.371), SI-1925 (1.363), SI-1873 (1.359), ES-64 (1.322), G-6 (1.319), TKG-22* (1.282), IC-204630 (1.245), ES-370 (1.200), MOHUR-3 (1.149), SI-2143 (1.105), S-0627 (1.076), kolenyola (1.019) and RJS-8316 (1.007)

Maximum negative values were recorded in IC-30884 (-1.021) followed by IS-641-2-84 (-1.026), GRT-8342 (-1.039), IS-199-2-04 (-1.041), EC-334992-I (1.094), WLR/92/No/217/Shal (1.102), EC-310425 (1.135), ES-5503

(1.152), EC-334967 (1.171), ES-560 (1.266), IS-156-3-84 (1.274), G-40 (1.306), Coredbose (1.314), S-0210 (1.318), ES-3196-I (1.325), EC-204704 (1.333), Chagata local (1.413), KMR-78 (1.414), EC-334993-I (1.432), GRT-8359 (1.439), RJS-29-I (1.461), IS-607-2-04 (1.478), NIC-8260 (1.564), ES-303311 (1.574), IC-204167 (1.730), IS-436-3-84 (1.791), ES-173 (1.867), EC-335009 (1.873), IS-99-A (1.926), IS-424 (1.930), NIC-9835 (2.052), Guj Sel-12 (2.062), 78-266-I (2.077), IS-101-213 (2.114), BS-10 (2.301), IS-101-4 (2.665), TS-332 (2.943) and EC-310455 (2.997) for the traits days to flower initiation and days to maturity.

In PC5, the highest value for thousand seed weight and capsule length were obtained by GT-10 (4.058), JTS-8* (3.649), ES-303311 (3.125), BS-10 (2.045), Murg-1-7 (2.009), S-0253 (1.853), TKG-21*(1.846), SI-3315-16 (1.836), S-0619(1.833), IS-564 (1.772), G-40 (1.619), EC-310455(1.613), EC-334955 (1.610), IS-261-2 (1.541), EC-182832 (1.538), IS-99-A (1.415), NIC-16187 (1.336), IS-132295 (1.309), IC-204167(1.299), G-44(1.289), G-13 (1.279), IS-289 (1.270), NIC-7982 (1.268), IS-109 (1.266), Guj Sel-12 (1.188), IC-204997 (1.114), RJS-Bo (1.107), IC-2621694 (1.084), G-18 (1.080), IS-156-3-84 (1.032), SI-3275 (1.031) and RJS-185 (1.019).

Maximum negative values were recorded in IS-39-B (-1.040) followed by S-0650 (-1.056), NIC-8590 (-1.058), IC-204630 (-1.089), GAD-5 (-1.108), NIC-8343 (-1.165), 54-1641 (-1.660), S-0126 (-1.174), RJS-8316 (-1.182), Local-1 (-1.184), IC-14142 (-1.186), SI-3097 (-1.192), S-0248 (-1.225), NIC-16264 (-1.293), G-20 (-1.359), ES-560 (-1.366), KJS-21 (-1.381), Chagata local (-1.406), IS-564A (-1.434), NIC-8055-I (-1.468), GRT-8609 (1.471), EC-334968 (1.483), B-223 (1.484), 78-831 (1.505), G-5 (1.595), TC-326 (1.621), IS-445-I (1.744), G-1 (1.849), IS-431 (1.885), MOHUR-3 (2.022), IC-131953 (2.024), GRT-8342 (2.044), IS-475 (2.373), GRT-8385 (2.472), kolenyola (2.680).

Checks are signified by * sign.

**Table 4.14: PC scores of sesame germplasm having positive values >1
in each PCs**

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
1	SI-1687-I	-0.415	1.267	0.465	-0.246	0.936
2	IC-14331	0.4	2.08	1.25	-0.158	0.298
3	01-10-1981	-0.603	1.544	0.407	-0.595	0.736
4	EC-182832	-1.571	-2.29	0.105	0.448	1.538
5	G-18	-1.182	-2.529	1.476	0.246	1.08
6	NIC-8033	0.784	-0.733	0.52	0.856	0.909
7	SI-805	1.273	-0.211	1.238	2.527	0.016
8	G-2	3.654	-1.506	0.976	-0.521	0.605
9	G-6	1.791	-3.552	1.702	1.319	-0.268
10	RJS-185	-0.047	-1.239	1.293	-0.342	1.019
11	NIC-8282	0.318	-1.086	2.271	0.752	0.753
12	IS-387	0.252	-2.944	0.954	0.605	0.457
13	G-13	2.07	-0.94	0.869	1.7	1.279
14	EC-334955	0.985	-1.976	0.767	0.735	1.61
15	NCR/82/No/Bo/NS	-1.811	-1.446	0.877	1.651	-0.382
16	IS-205-I	1.643	-0.924	0.677	0.65	-0.24
17	NIC-8062	0.532	-3.014	0.44	2.199	-0.142
18	G-8	2.933	0.045	0.876	-0.845	0.536
19	SI-1925	-0.139	-1.268	1.734	1.363	0.353
20	EC-35000	-1.088	0.01	1.335	1.371	0.449
21	NIC-9835	0.747	-0.612	2.827	-2.052	-0.663
22	IS-77	-3.327	-1.283	1.977	-0.244	-0.516
23	EC-334993-I	-1.128	-2.027	2.369	-1.432	0.696
24	ES-110-A	-2.966	-0.716	1.472	0.02	0.542
25	GRT-8327	-1.563	0.181	2.611	0.116	-0.736
26	NIC-8055-I	-4.042	-2.395	1.517	-0.104	-1.468
27	S-0619	0.853	-1.163	1.677	-0.935	1.833

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
28	IS-132295	-0.408	-1.125	1.467	-0.706	1.309
29	ES-131-1-84	0.621	-1.708	1.653	-0.555	0.002
30	S-0069	-1.37	-1.709	2.605	1.711	0.203
31	ES-139-2-84	-1.411	-0.75	1.141	-0.785	0.945
32	RJS-Bo	-0.09	1.141	0.764	0.284	1.107
33	S-0627	-2.196	-0.242	0.507	1.076	0.888
34	IC-152485	-2.615	0.599	1.118	0.271	0.982
35	ES-120-1-84-B	-2.385	-2.839	1.133	0.599	0.882
36	ES-173	-2.176	-2.083	-0.259	-1.867	0.857
37	WLR/92/No/217/Shal	-0.337	-0.003	1.352	-1.102	0.854
38	G-47	-1.531	0.237	-0.434	-0.143	0.564
39	IS-99-A	-0.301	0.959	-0.512	-1.926	1.415
40	SI-3275	-1.243	1.325	0.037	-0.586	1.031
41	IS-436-3-84	-0.789	-0.888	0.361	-1.791	0.57
42	IS-449	-2.062	0.347	0.118	-0.628	0.738
43	EC-334987	-1.356	1.065	-0.017	-0.705	0.736
44	IS-199-2-04	-1.672	-1.753	1.264	-1.041	-0.396
45	EC-334967	-1.079	-1.026	0.529	-1.171	-0.092
46	IS-156-3-84	-2.53	0.094	-0.106	-1.274	1.032
47	IS-641-2-84	-0.441	0.789	1.007	-1.026	-0.153
48	G-40	-0.532	1.536	0.469	-1.306	1.619
49	SI-3315-16	-1.585	0.541	-0.325	1.407	1.836
50	IC-2621694	-2.016	2.487	-0.136	-0.792	1.084
51	G-16	0.135	1.347	0.74	1.456	0.942
52	IS-387-2	-2.429	2.665	-0.155	-0.448	0.014
53	Guj Sel-12	-0.582	3.096	-1.135	-2.062	1.188
54	IS-289	-0.649	1.576	-1.337	0.173	1.27
55	NIC-7982	-0.597	1.569	-0.301	-0.48	1.268
56	IS-446-1-84	-1.173	1.744	0.212	-0.779	-0.234

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
57	EC-334992-I	-1.904	0.216	-1.809	-1.094	0.698
58	G-19	-2.373	1.489	-0.245	-0.643	0.67
59	EC-310455	-2.598	-0.112	-0.937	-2.997	1.613
60	SI-3114	0.25	-0.186	-0.574	-0.799	0.009
61	EC-334969	-1.974	0.688	-0.071	-0.342	0.521
62	EC-204704	2.191	0.068	0.651	-1.333	-0.028
63	EC-334995-I	3.536	2.213	0.615	-0.073	0.723
64	ES-64	3.841	2.048	-1.034	1.322	-0.042
65	IS-564	0.728	1.386	-0.369	0.795	1.772
66	S-0210	-1.637	2.141	-0.905	-1.318	0.959
67	IS-350	-0.535	-0.712	-0.035	-0.375	0.282
68	ES-5503	-2.614	1.464	0.041	-1.152	-0.638
69	IC-30884	-0.105	0.174	-0.678	-1.021	-0.187
70	NIC-8343	-0.11	-3.593	1.286	-0.788	-1.165
71	IS-90	0.295	0.882	-0.675	-0.232	0.927
72	GRT-8359	1.96	1.059	0.421	-1.439	-0.414
73	I-68	-0.706	2.652	-0.287	-0.954	0.282
74	IS-686	-2.181	0.469	0.641	0.08	0.002
75	78-266-I	3.294	0.812	1.153	-2.077	-0.393
76	S-0281	-2.273	2.554	0.294	0.379	-0.276
77	TMV-12-52	0.2	1.179	-0.715	0.182	0.136
78	IS-712	1.644	0.749	0.982	0.215	-0.626
79	GRT-83128	1.177	0.946	-0.085	-0.323	0.656
80	NIC-16218	-1.112	1.137	-0.807	-0.63	0.797
81	KJS-21	2.46	-0.8	-1.187	0.085	-1.381
82	GAD-5	2.805	-2.026	-0.674	-0.377	-1.108
83	EC-335009	2.227	-3.151	-0.534	-1.873	-0.825
84	IS-302	2.018	-1.397	-0.68	1.564	0.266
85	NIC-8210	-0.306	-0.981	-1.528	0.284	0.279

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
86	78-20	-0.063	-1.261	-1.068	1.507	-0.864
87	ES-560	-0.435	-2.28	-0.832	-1.266	-1.366
88	Coredbose	1.25	-0.865	-0.474	-1.314	-0.767
89	ES-312955	0.472	-0.889	-1.461	-0.091	0.083
90	IC-14142	0.383	1.381	-1.657	0.071	-1.186
91	GRT-8392	-0.461	-0.617	-1.143	0.141	-0.069
92	ES-370	2.216	-0.189	-2.942	1.2	0.234
93	NIC-6059	1.166	-1.69	-1.832	2.145	-0.68
94	IS-607-2-04	4.3	1.474	-1.417	-1.478	-0.384
95	SI-1873	2.506	0.025	-1.456	1.359	-0.223
96	RJS-61	2.452	-0.914	-1.901	1.375	-0.117
97	NIC-8260	0.935	-0.759	-2.715	-1.564	-0.665
98	IS-562	-0.93	-1.801	-2.207	0.353	0.448
99	IS-424	-1.859	-1.22	-2.727	-1.93	-0.221
100	ES-334962	0.67	-0.34	-0.885	0.268	-0.459
101	ES-303311	0.924	-0.8	-3.719	-1.574	3.125
102	S-0253	-1.002	1.033	-1.664	-0.788	1.853
103	BS-10	0.652	0.15	-1.947	-2.301	2.045
104	IC-204997	-0.275	0.775	-2.135	-0.685	1.114
105	IS-482-B	0.831	-0.655	-1.637	-0.889	0.474
106	IS-261-2	-1.91	-1.563	-1.29	0.894	1.541
107	NIC-16187	0.867	-2.992	-0.446	1.472	1.336
108	IS-109	0.135	-4.765	-1.503	-0.027	1.266
109	IC-204167	0.672	-3.505	-0.606	-1.73	1.299
110	KMS-4-238	0.545	-2.525	-0.983	0.508	0.863
111	S-0486	-0.029	-0.555	-0.763	-0.352	-0.608
112	G-9-1	-0.976	-1.21	-1.071	0.243	0.327
113	IS-514	2.068	0.225	-0.409	0.154	-0.729
114	G-49	0.199	-0.729	-1.504	0.157	0.112

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
115	Murg-1-7	0.264	-1.922	-0.57	1.443	2.009
116	RJS-218	2.267	-2.056	-1.622	0.228	0.331
117	G-44	1.013	-1.693	-1.419	1.742	1.289
118	NIC-13006	1.43	-1.233	-2.068	1.482	0.684
119	IS-455	1.299	-2.896	-1.57	0.922	0.014
120	G-39	1.225	-2.1	-1.269	-0.645	0.937
121	ES-3196-I	0.427	-0.665	1.803	-1.325	0.43
122	S-0126	1.465	1.127	1.984	-0.088	-1.174
123	NIC-3351	-1.735	-0.292	1.763	0.66	-0.454
124	IS-101-213	2.845	1.054	2.869	-2.114	-0.849
125	G-1	0.378	-1.496	1.991	0.579	-1.849
126	IS-352	1.642	-0.42	1.663	-0.661	-0.811
127	IS-101-4	0.35	-1.121	1.108	-2.665	0.434
128	54-1641	0.357	0.264	1.59	0.087	-1.166
129	S-0650	-2.108	0.032	1.566	1.427	-1.056
130	SI-2561	-2.839	0.779	1.087	0.569	-0.341
131	TC-171	0.843	0.458	-0.477	0.274	0.684
132	NIC-13032	-0.51	-0.03	0.369	-0.235	-0.466
133	S-0021	-0.973	1.303	0.801	2.164	-0.355
134	G-15	-1.374	1.187	0.44	-0.22	0.302
135	EC-310448	-0.443	0.697	1.217	-0.586	0.165
136	EC-335004-I	1.998	1.582	1.819	-0.109	0.621
137	TS-332	1.296	-2.519	2.029	-2.943	-0.19
138	G-17	-0.685	0.591	0.68	0.209	-0.106
139	RJS-29-I	3.413	3.034	2.483	-1.461	-0.18
140	NIC-8174	0.825	1.406	1.167	-0.152	-0.186
141	ES-41	2.802	2.308	1.222	-0.804	-0.643
142	GRT-8609	0.264	0.477	0.873	-0.467	-1.471
143	NIC-17389	4.1	1.888	1.929	-0.828	-0.732

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
144	78-505	-1.11	0.129	0.766	0.016	-0.113
145	SI-2073	-1.769	2.509	-0.555	1.429	-0.68
146	NIC-17301	-1.199	1.209	0.111	1.962	-0.402
147	GRT-8368	-0.617	-2.221	1.154	-0.793	-0.831
148	S-0479	-1.069	0.708	0.327	-0.02	0.08
149	EC-132295	0.767	0.068	1.683	0.83	-0.551
150	NIC-8590	-1.037	0.495	0.966	-0.023	-1.058
151	77-701	0.471	0.156	1.898	-0.215	-0.557
152	RJS-9613	-2.111	0.942	-0.063	-0.062	-0.8
153	RJS-4-79	-1.807	1.688	-0.225	0.452	-0.388
154	EC-335000-A	-1.924	1.098	0.361	2.25	-0.436
155	IC-204630	-2.586	0.604	1.119	1.245	-1.089
156	NIC-16264	-0.926	1.775	0.803	-0.199	-1.293
157	IC-204137	-1.268	2.236	-0.071	1.58	0.442
158	S-0248	2.288	0.099	1.248	-0.753	-1.225
159	Local-1	-1.764	-0.049	0.925	0.546	-1.184
160	IC-205206	-3.786	1.367	1.447	0.955	-0.816
161	Dharand	-1.345	1.26	-1.096	0.644	-0.755
162	Kolenyola	-0.837	0.676	-0.68	1.019	-2.68
163	GRT-8342	0.017	-0.353	0.116	-1.039	-2.044
164	G-20	2.051	1.135	-0.123	0.168	-1.359
165	NIC-8035	0.214	0.729	-1.487	0.663	-0.583
166	IS-475	0.899	2.251	-0.809	1.428	-2.373
167	Chagata local	-0.663	1.845	-0.705	-1.413	-1.406
168	IS-24-P	0.261	0.795	-1.557	0.078	0.567
169	S-0501	2.561	2.346	-1.249	0.321	-0.574
170	IS-393-1-A	-0.339	-0.775	-0.322	0.99	-0.409
171	IC-131953	1.44	-0.299	-0.841	0.254	-2.024
172	IS-299	-1.286	-0.892	-0.662	-0.055	-0.313
173	SI-3097	1.578	0.121	-0.293	0.981	-1.192
174	IS-564A	-0.898	0.448	-1.198	1.58	-1.434
175	KMR-78	1.809	2.353	-0.938	-1.414	-0.085

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
176	SI-2143	-0.193	1.629	-1.112	1.105	-0.478
177	KIS-551	1.307	0.528	-1.003	0.402	-0.604
178	GRT-8385	-1.28	-0.858	-1.328	-0.2	-2.472
179	TC-326	-3.043	-0.242	-0.322	-0.158	-1.621
180	NIC-8020	-2.725	0.243	-1.049	-0.425	-0.703
181	78-831	-1.213	0.016	-1.266	0.792	-1.505
182	NIC-8511	-1.883	0.877	-1.396	-0.429	-0.276
183	MOHUR-3	-0.67	1.654	-1.09	1.149	-2.022
184	G-5	-0.334	1.433	-1.323	-0.975	-1.595
185	SI-7619-B	-1.237	-0.064	-0.943	1.427	-0.675
186	IS-101-2	-1.566	0.016	-1.851	0.001	-0.612
187	IS-470	-0.027	1.885	-0.113	0.621	-0.748
188	GRT-8368-I	1.237	1.082	-1.616	-0.134	0.257
189	RJS-8316	0.939	-1.14	0.597	1.007	-1.182
190	IS-733	3.615	-0.04	0.016	0.4	-0.338
191	B-223	4.794	0.405	0.467	-0.346	-1.484
192	EC-310425	2.835	-0.496	1.281	-1.135	-0.661
193	NIC-8523	0.624	0.127	-1.509	-0.146	-0.966
194	18 Oct	0.044	0.911	-1.512	-0.122	0.101
195	IS-445-I	-1.653	0.634	-1.696	-0.164	-1.744
196	RJS-738-2-84	-0.556	0.619	-1.739	0.002	0.333
197	IS-431	-0.865	-5.486	-0.955	0.142	-1.885
198	EC-334968	-0.215	-0.231	-0.828	1.85	-1.483
199	SI-7178	0.025	-0.578	-1.028	-0.334	-0.213
200	IS-39-B	1.8	0.547	-0.966	0.3	-1.04
201	TKG-21	1.149	1.154	0.537	1.887	1.846
202	TKG-22	1.162	1.919	-0.17	1.282	0.774
203	JTS-8	2.066	2.686	1.88	3.481	3.649
204	GT-10	2.959	2	2.218	3.027	4.058

Table 4.15: List of selected genotypes in each principal component having positive values

PC1	PC2	PC3	PC4	PC5
SI-805	SI-1687-I	IC-14331	SI-805	EC-182832
G-2	IC-14331	G-18	G-6	G-18
G-6	DATE	SI-805	G-13	RJS-185
G-13	RJS-Bo	G-6	NCR/82/No/Bo/NS	G-13
IS-205-I	SI-3275	RJS-185	NIC-8062	EC-334955
G-8	EC-334987	NIC-8282	SI-1925	S-0619
EC-204704	G-40	SI-1925	EC-35000	IS-132295
EC-334995-I	IC-2621694	EC-35000	S-0069	RJS-Bo
ES-64	G-16	NIC-9835	S-0627	IS-99-A
GRT-8359	IS-387-2	IS-77	SI-3315-16	SI-3275
78-266-I	Guj Sel-12	EC-334993-I	G-16	IS-156-3-84
IS-712	IS-289	ES-110-A	ES-64	G-40
GRT-83128	NIC-7982	GRT-8327	IS-302	SI-3315-16
KJS-21	IS-446-1-84	NIC-8055-I	78-20	IC-2621694
GAD-5	G-19	S-0619	ES-370	Guj Sel-12
EC-335009	EC-334995-I	IS-132295	NIC-6059	IS-289
IS-302	ES-64	ES-131-1-84	SI-1873	NIC-7982
Coredbose	IS-564	S-0069	RJS-61	EC-310455
ES-370	S-0210	ES-139-2-84	NIC-16187	IS-564
NIC-6059	ES-5503	IC-152485	Murg-1-7	ES-303311
IS-607-2-04	GRT-8359	ES-120-1-84-B	G-44	S-0253
SI-1873	I-68	WLR/92/No/217/Shal	NIC-13006	BS-10
RJS-61	S-0281	IS-199-2-04	S-0650	IC-204997
IS-514	TMV-12-52	IS-641-2-84	S-0021	IS-261-2
RJS-218	NIC-16218	NIC-8343	SI-2073	NIC-16187
G-44	IC-14142	78-266-I	NIC-17301	IS-109
NIC-13006	IS-607-2-04	ES-3196-I	EC-335000-A	IC-204167
IS-455	S-0253	S-0126	IC-204630	Murg-1-7
G-39	S-0126	NIC-3351	IC-204137	G-44

PC1	PC2	PC3	PC4	PC5
S-0126	IS-101-213	IS-101-213	kolenyola	TKG-21
IS-101-213	S-0021	G-1	IS-475	JTS-8
IS-352	G-15	IS-352	IS-564A	GT-10
EC-335004-I	EC-335004-I	IS-101-4	SI-2143	
TS-332	RJS-29-I	54-1641	MOHUR-3	
RJS-29-I	NIC-8174	S-0650	SI-7619-B	
ES-41	ES-41	SI-2561	RJS-8316	
NIC-17389	NIC-17389	EC-310448	EC-334968	
S-0248	SI-2073	EC-335004-I	TKG-21	
G-20	NIC-17301	TS-332	TKG-22	
S-0501	RJS-4-79	RJS-29-I	JTS-8	
IC-131953	EC-335000-A	NIC-8174	GT-10	
SI-3097	NIC-16264	ES-41		
KMR-78	IC-204137	NIC-17389		
KIS-551	IC-205206	GRT-8368		
GRT-8368-I	Dharand	EC-132295		
IS-733	G-20	77-701		
B-223	IS-475	IC-204630		
EC-310425	Chagata local	S-0248		
IS-39-B	S-0501	IC-205206		
TKG-21	KMR-78	EC-310425		
TKG-22	SI-2143	JTS-8		
JTS-8	MOHUR-3	GT-10		
GT-10	G-5			
	IS-470			
	GRT-8368-I			
	TKG-21			
	TKG-22			
	JTS-8			
	GT-10			

**Table 4.16: PC scores of sesame germplasm having negative values >1
in each PCs**

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
1	SI-1687-I	-0.415	1.267	0.465	-0.246	0.936
2	IC-14331	0.4	2.08	1.25	-0.158	0.298
3	1/10/1981	-0.603	1.544	0.407	-0.595	0.736
4	EC-182832	-1.571	-2.29	0.105	0.448	1.538
5	G-18	-1.182	-2.529	1.476	0.246	1.08
6	NIC-8033	0.784	-0.733	0.52	0.856	0.909
7	SI-805	1.273	-0.211	1.238	2.527	0.016
8	G-2	3.654	-1.506	0.976	-0.521	0.605
9	G-6	1.791	-3.552	1.702	1.319	-0.268
10	RJS-185	-0.047	-1.239	1.293	-0.342	1.019
11	NIC-8282	0.318	-1.086	2.271	0.752	0.753
12	IS-387	0.252	-2.944	0.954	0.605	0.457
13	G-13	2.07	-0.94	0.869	1.7	1.279
14	EC-334955	0.985	-1.976	0.767	0.735	1.61
15	NCR/82/No/Bo/NS	-1.811	-1.446	0.877	1.651	-0.382
16	IS-205-I	1.643	-0.924	0.677	0.65	-0.24
17	NIC-8062	0.532	-3.014	0.44	2.199	-0.142
18	G-8	2.933	0.045	0.876	-0.845	0.536
19	SI-1925	-0.139	-1.268	1.734	1.363	0.353
20	EC-35000	-1.088	0.01	1.335	1.371	0.449
21	NIC-9835	0.747	-0.612	2.827	-2.052	-0.663
22	IS-77	-3.327	-1.283	1.977	-0.244	-0.516
23	EC-334993-I	-1.128	-2.027	2.369	-1.432	0.696
24	ES-110-A	-2.966	-0.716	1.472	0.02	0.542
25	GRT-8327	-1.563	0.181	2.611	0.116	-0.736
26	NIC-8055-I	-4.042	-2.395	1.517	-0.104	-1.468
27	S-0619	0.853	-1.163	1.677	-0.935	1.833
28	IS-132295	-0.408	-1.125	1.467	-0.706	1.309
29	ES-131-1-84	0.621	-1.708	1.653	-0.555	0.002
30	S-0069	-1.37	-1.709	2.605	1.711	0.203
31	ES-139-2-84	-1.411	-0.75	1.141	-0.785	0.945
32	RJS-Bo	-0.09	1.141	0.764	0.284	1.107
33	S-0627	-2.196	-0.242	0.507	1.076	0.888
34	IC-152485	-2.615	0.599	1.118	0.271	0.982
35	ES-120-1-84-B	-2.385	-2.839	1.133	0.599	0.882
36	ES-173	-2.176	-2.083	-0.259	-1.867	0.857
37	WLR/92/No/217/Shal	-0.337	-0.003	1.352	-1.102	0.854
38	G-47	-1.531	0.237	-0.434	-0.143	0.564

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
39	IS-99-A	-0.301	0.959	-0.512	-1.926	1.415
40	SI-3275	-1.243	1.325	0.037	-0.586	1.031
41	IS-436-3-84	-0.789	-0.888	0.361	-1.791	0.57
42	IS-449	-2.062	0.347	0.118	-0.628	0.738
43	EC-334987	-1.356	1.065	-0.017	-0.705	0.736
44	IS-199-2-04	-1.672	-1.753	1.264	-1.041	-0.396
45	EC-334967	-1.079	-1.026	0.529	-1.171	-0.092
46	IS-156-3-84	-2.53	0.094	-0.106	-1.274	1.032
47	IS-641-2-84	-0.441	0.789	1.007	-1.026	-0.153
48	G-40	-0.532	1.536	0.469	-1.306	1.619
49	SI-3315-16	-1.585	0.541	-0.325	1.407	1.836
50	IC-2621694	-2.016	2.487	-0.136	-0.792	1.084
51	G-16	0.135	1.347	0.74	1.456	0.942
52	IS-387-2	-2.429	2.665	-0.155	-0.448	0.014
53	Guj Sel-12	-0.582	3.096	-1.135	-2.062	1.188
54	IS-289	-0.649	1.576	-1.337	0.173	1.27
55	NIC-7982	-0.597	1.569	-0.301	-0.48	1.268
56	IS-446-1-84	-1.173	1.744	0.212	-0.779	-0.234
57	EC-334992-I	-1.904	0.216	-1.809	-1.094	0.698
58	G-19	-2.373	1.489	-0.245	-0.643	0.67
59	EC-310455	-2.598	-0.112	-0.937	-2.997	1.613
60	SI-3114	0.25	-0.186	-0.574	-0.799	0.009
61	EC-334969	-1.974	0.688	-0.071	-0.342	0.521
62	EC-204704	2.191	0.068	0.651	-1.333	-0.028
63	EC-334995-I	3.536	2.213	0.615	-0.073	0.723
64	ES-64	3.841	2.048	-1.034	1.322	-0.042
65	IS-564	0.728	1.386	-0.369	0.795	1.772
66	S-0210	-1.637	2.141	-0.905	-1.318	0.959
67	IS-350	-0.535	-0.712	-0.035	-0.375	0.282
68	ES-5503	-2.614	1.464	0.041	-1.152	-0.638
69	IC-30884	-0.105	0.174	-0.678	-1.021	-0.187
70	NIC-8343	-0.11	-3.593	1.286	-0.788	-1.165
71	IS-90	0.295	0.882	-0.675	-0.232	0.927
72	GRT-8359	1.96	1.059	0.421	-1.439	-0.414
73	I-68	-0.706	2.652	-0.287	-0.954	0.282
74	IS-686	-2.181	0.469	0.641	0.08	0.002
75	78-266-I	3.294	0.812	1.153	-2.077	-0.393
76	S-0281	-2.273	2.554	0.294	0.379	-0.276
77	TMV-12-52	0.2	1.179	-0.715	0.182	0.136
78	IS-712	1.644	0.749	0.982	0.215	-0.626

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
79	GRT-83128	1.177	0.946	-0.085	-0.323	0.656
80	NIC-16218	-1.112	1.137	-0.807	-0.63	0.797
81	KJS-21	2.46	-0.8	-1.187	0.085	-1.381
82	GAD-5	2.805	-2.026	-0.674	-0.377	-1.108
83	EC-335009	2.227	-3.151	-0.534	-1.873	-0.825
84	IS-302	2.018	-1.397	-0.68	1.564	0.266
85	NIC-8210	-0.306	-0.981	-1.528	0.284	0.279
86	78-20	-0.063	-1.261	-1.068	1.507	-0.864
87	ES-560	-0.435	-2.28	-0.832	-1.266	-1.366
88	Coredbose	1.25	-0.865	-0.474	-1.314	-0.767
89	ES-312955	0.472	-0.889	-1.461	-0.091	0.083
90	IC-14142	0.383	1.381	-1.657	0.071	-1.186
91	GRT-8392	-0.461	-0.617	-1.143	0.141	-0.069
92	ES-370	2.216	-0.189	-2.942	1.2	0.234
93	NIC-6059	1.166	-1.69	-1.832	2.145	-0.68
94	IS-607-2-04	4.3	1.474	-1.417	-1.478	-0.384
95	SI-1873	2.506	0.025	-1.456	1.359	-0.223
96	RJS-61	2.452	-0.914	-1.901	1.375	-0.117
97	NIC-8260	0.935	-0.759	-2.715	-1.564	-0.665
98	IS-562	-0.93	-1.801	-2.207	0.353	0.448
99	IS-424	-1.859	-1.22	-2.727	-1.93	-0.221
100	ES-334962	0.67	-0.34	-0.885	0.268	-0.459
101	ES-303311	0.924	-0.8	-3.719	-1.574	3.125
102	S-0253	-1.002	1.033	-1.664	-0.788	1.853
103	BS-10	0.652	0.15	-1.947	-2.301	2.045
104	IC-204997	-0.275	0.775	-2.135	-0.685	1.114
105	IS-482-B	0.831	-0.655	-1.637	-0.889	0.474
106	IS-261-2	-1.91	-1.563	-1.29	0.894	1.541
107	NIC-16187	0.867	-2.992	-0.446	1.472	1.336
108	IS-109	0.135	-4.765	-1.503	-0.027	1.266
109	IC-204167	0.672	-3.505	-0.606	-1.73	1.299
110	KMS-4-238	0.545	-2.525	-0.983	0.508	0.863
111	S-0486	-0.029	-0.555	-0.763	-0.352	-0.608
112	G-9-1	-0.976	-1.21	-1.071	0.243	0.327
113	IS-514	2.068	0.225	-0.409	0.154	-0.729
114	G-49	0.199	-0.729	-1.504	0.157	0.112
115	Murg-1-7	0.264	-1.922	-0.57	1.443	2.009
116	RJS-218	2.267	-2.056	-1.622	0.228	0.331
117	G-44	1.013	-1.693	-1.419	1.742	1.289
118	NIC-13006	1.43	-1.233	-2.068	1.482	0.684

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
119	IS-455	1.299	-2.896	-1.57	0.922	0.014
120	G-39	1.225	-2.1	-1.269	-0.645	0.937
121	ES-3196-I	0.427	-0.665	1.803	-1.325	0.43
122	S-0126	1.465	1.127	1.984	-0.088	-1.174
123	NIC-3351	-1.735	-0.292	1.763	0.66	-0.454
124	IS-101-213	2.845	1.054	2.869	-2.114	-0.849
125	G-1	0.378	-1.496	1.991	0.579	-1.849
126	IS-352	1.642	-0.42	1.663	-0.661	-0.811
127	IS-101-4	0.35	-1.121	1.108	-2.665	0.434
128	54-1641	0.357	0.264	1.59	0.087	-1.166
129	S-0650	-2.108	0.032	1.566	1.427	-1.056
130	SI-2561	-2.839	0.779	1.087	0.569	-0.341
131	TC-171	0.843	0.458	-0.477	0.274	0.684
132	NIC-13032	-0.51	-0.03	0.369	-0.235	-0.466
133	S-0021	-0.973	1.303	0.801	2.164	-0.355
134	G-15	-1.374	1.187	0.44	-0.22	0.302
135	EC-310448	-0.443	0.697	1.217	-0.586	0.165
136	EC-335004-I	1.998	1.582	1.819	-0.109	0.621
137	TS-332	1.296	-2.519	2.029	-2.943	-0.19
138	G-17	-0.685	0.591	0.68	0.209	-0.106
139	RJS-29-I	3.413	3.034	2.483	-1.461	-0.18
140	NIC-8174	0.825	1.406	1.167	-0.152	-0.186
141	ES-41	2.802	2.308	1.222	-0.804	-0.643
142	GRT-8609	0.264	0.477	0.873	-0.467	-1.471
143	NIC-17389	4.1	1.888	1.929	-0.828	-0.732
144	78-505	-1.11	0.129	0.766	0.016	-0.113
145	SI-2073	-1.769	2.509	-0.555	1.429	-0.68
146	NIC-17301	-1.199	1.209	0.111	1.962	-0.402
147	GRT-8368	-0.617	-2.221	1.154	-0.793	-0.831
148	S-0479	-1.069	0.708	0.327	-0.02	0.08
149	EC-132295	0.767	0.068	1.683	0.83	-0.551
150	NIC-8590	-1.037	0.495	0.966	-0.023	-1.058
151	77-701	0.471	0.156	1.898	-0.215	-0.557
152	RJS-9613	-2.111	0.942	-0.063	-0.062	-0.8
153	RJS-4-79	-1.807	1.688	-0.225	0.452	-0.388
154	EC-335000-A	-1.924	1.098	0.361	2.25	-0.436
155	IC-204630	-2.586	0.604	1.119	1.245	-1.089
156	NIC-16264	-0.926	1.775	0.803	-0.199	-1.293
157	IC-204137	-1.268	2.236	-0.071	1.58	0.442
158	S-0248	2.288	0.099	1.248	-0.753	-1.225
159	Local-1	-1.764	-0.049	0.925	0.546	-1.184
160	IC-205206	-3.786	1.367	1.447	0.955	-0.816
161	Dharand	-1.345	1.26	-1.096	0.644	-0.755

S.No.	Genotypes	PC1 Score	PC2 Score	PC3 Score	PC4 Score	PC5 Score
162	Kolenyola	-0.837	0.676	-0.68	1.019	-2.68
163	GRT-8342	0.017	-0.353	0.116	-1.039	-2.044
164	G-20	2.051	1.135	-0.123	0.168	-1.359
165	NIC-8035	0.214	0.729	-1.487	0.663	-0.583
166	IS-475	0.899	2.251	-0.809	1.428	-2.373
167	Chagata local	-0.663	1.845	-0.705	-1.413	-1.406
168	IS-24-P	0.261	0.795	-1.557	0.078	0.567
169	S-0501	2.561	2.346	-1.249	0.321	-0.574
170	IS-393-1-A	-0.339	-0.775	-0.322	0.99	-0.409
171	IC-131953	1.44	-0.299	-0.841	0.254	-2.024
172	IS-299	-1.286	-0.892	-0.662	-0.055	-0.313
173	SI-3097	1.578	0.121	-0.293	0.981	-1.192
174	IS-564A	-0.898	0.448	-1.198	1.58	-1.434
175	KMR-78	1.809	2.353	-0.938	-1.414	-0.085
176	SI-2143	-0.193	1.629	-1.112	1.105	-0.478
177	KIS-551	1.307	0.528	-1.003	0.402	-0.604
178	GRT-8385	-1.28	-0.858	-1.328	-0.2	-2.472
179	TC-326	-3.043	-0.242	-0.322	-0.158	-1.621
180	NIC-8020	-2.725	0.243	-1.049	-0.425	-0.703
181	78-831	-1.213	0.016	-1.266	0.792	-1.505
182	NIC-8511	-1.883	0.877	-1.396	-0.429	-0.276
183	MOHUR-3	-0.67	1.654	-1.09	1.149	-2.022
184	G-5	-0.334	1.433	-1.323	-0.975	-1.595
185	SI-7619-B	-1.237	-0.064	-0.943	1.427	-0.675
186	IS-101-2	-1.566	0.016	-1.851	0.001	-0.612
187	IS-470	-0.027	1.885	-0.113	0.621	-0.748
188	GRT-8368-I	1.237	1.082	-1.616	-0.134	0.257
189	RJS-8316	0.939	-1.14	0.597	1.007	-1.182
190	IS-733	3.615	-0.04	0.016	0.4	-0.338
191	B-223	4.794	0.405	0.467	-0.346	-1.484
192	EC-310425	2.835	-0.496	1.281	-1.135	-0.661
193	NIC-8523	0.624	0.127	-1.509	-0.146	-0.966
194	18 Oct	0.044	0.911	-1.512	-0.122	0.101
195	IS-445-I	-1.653	0.634	-1.696	-0.164	-1.744
196	RJS-738-2-84	-0.556	0.619	-1.739	0.002	0.333
197	IS-431	-0.865	-5.486	-0.955	0.142	-1.885
198	EC-334968	-0.215	-0.231	-0.828	1.85	-1.483
199	SI-7178	0.025	-0.578	-1.028	-0.334	-0.213
200	IS-39-B	1.8	0.547	-0.966	0.3	-1.04
201	TKG-21	1.149	1.154	0.537	1.887	1.846
202	TKG-22	1.162	1.919	-0.17	1.282	0.774
203	JTS-8	2.066	2.686	1.88	3.481	3.649
204	GT-10	2.959	2	2.218	3.027	4.058

4.5.5 Germplasm having common PC scores

On the basis of yield and yield attributing traits, out of top five principal components, the value of PC1 was higher than PC2, PC3, PC4 and PC5. Germplasm lines showing maximum PC scores and common in PC1 and PC3 for number of primary branches per plant, number of secondary branches per plant, plant height, number of capsules per plant, seed yield per plant and oil content are SI-805, G-6, S-0126, IS-101-213, IS-352, EC-335004-I, RJS-29-1, ES-41, NIC-17389, SI-0248, EC-310425, JTS-8* and GT-10*. Genotypes showing high PC scores in PC3 for seed yield per plant and oil content and low PC scores in PC2 for phenological traits days to flower initiation, days to 50% flowering and days to maturity are EC-35000, GRT-8327, IC-152485, IS-641-2-84, 54-1641, S-0650, SI-2561, EC-310448, EC-132295, 77-701, IC-204630, 78-266-I and S-0248. Thus, selection of these lines can help in further development of new high yielding, early maturing varieties.

4.5.6 Sesame lines with low oxalic acid and high oil content

Titration of 200 sesame genotypes for oxalic acid was done. The results revealed that highest oxalic acid content of 1.89 % was present in genotypes NIC-8033, G-8, NIC-8055-I, ES-131-1-84, IS-99-A, EC-334992-I, IC-30884, 77-701, RJS-4-79, SI-7178 whereas genotypes G-13, NIC-9835, IS-156-3-84, Guj Sel-12, IS-446-1-84, IS-302, NIC-8260, IS-514, EC-310448, NIC-17389, EC-132295, IC-205206, GRT-8385, NIC-8020 had the lowest oxalic acid content of 0.25%. Genotypes having oxalic acid content less than 1% and oil content higher than 45% were IS-302, IS-514, NIC-8260, G-13, S-0253, EC-335009, RJS-61, KJS-21, G-2, SI-2073, IS-482-B, IS-24-P, SI-3097, Coredbose, BS-10, G-9-1, Murg-1-7, ES-370, RJS-21878-20, IC-204997, NIC-6059, ES-334962, NIC-16187, G-49, G-39, NIC-8210, ES-312955, EC-334955, NIC-13006, IS-109, G-44, KMS-4-238, SI-1873, IS-424, ES-560, IC-14142, EC-334968, ES-303311, IC-204167, IS-562, IS-455, IS-607-2-04, GRT-8368-I, GRT-8392, I-68, GAD-5, IS-261-2, S-0486 and NIC-8062. Out of these genotypes SI-1873, RJS-61, ES-370, RJS-218, NIC-6059 recorded seed yield ≥ 15 g.

Table 4.17: List of putative lines with low oxalic acid and high oil content

Oxalic acid (%)	Genotypes having high oil content
0.25	IS-302, IS-514, NIC-8260, G-13
0.37	S-0253, EC-335009, RJS-61, KJS-21, G-2, SI-2073, IS-482-B, IS-24-P, SI-3097, Coredbose
0.5	BS-10, G-9-1, Murg-1-7, ES-370, RJS-21878-20, IC-204997, NIC-6059, ES-334962, NIC-16187, G-49, G-39, NIC-8210, ES-312955, EC-334955
0.63	NIC-13006, IS-109, G-44, KMS-4-238, SI-1873, IS-424, ES-560, IC-14142, EC-334968
0.75	ES-303311, IC-204167, I S-562, IS-455, IS-607-2-04, GRT-8368-I, GRT-8392, I-68
0.88	GAD-5, IS-261-2, S-0486, NIC-8062

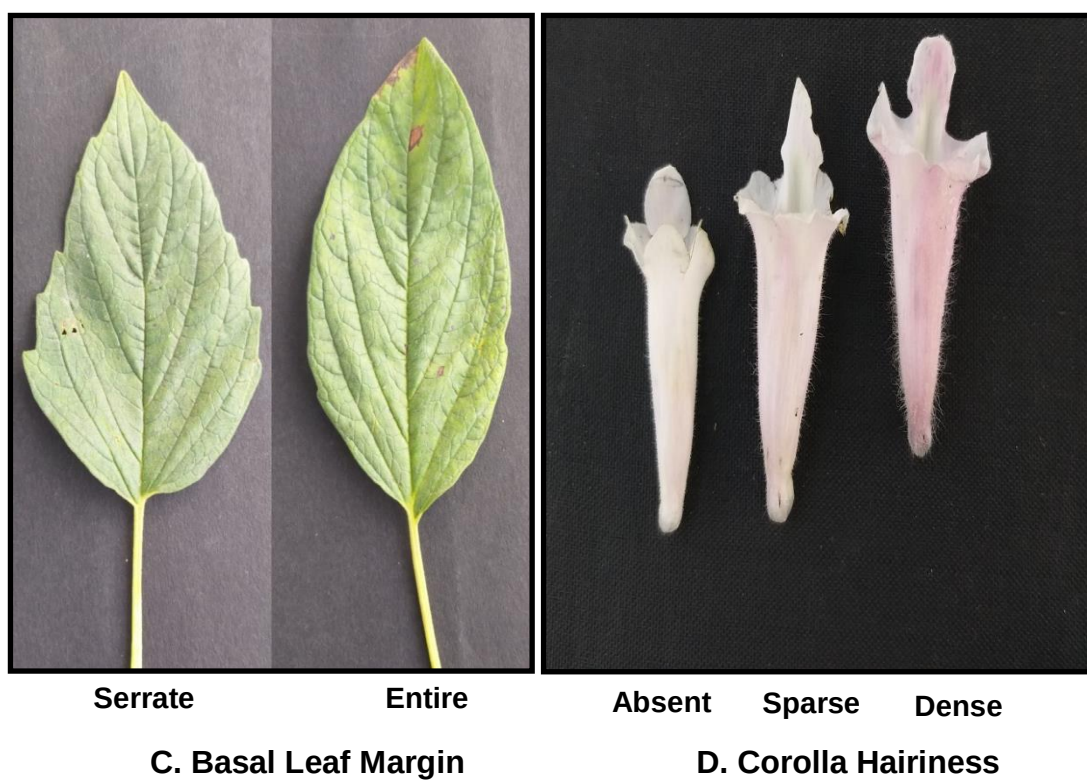
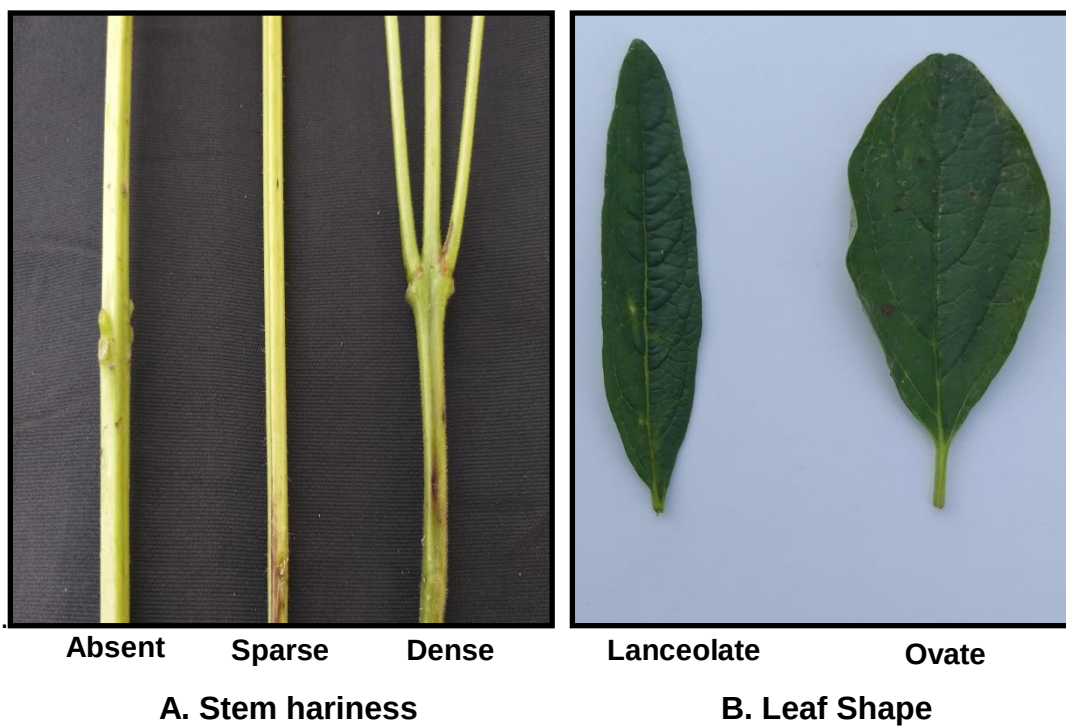


Plate 1: Morphological Characterization



White with
pink shading

White with
deep pink
shading

E. Corolla Colour



Broad oblong

Narrow oblong

F.Capsule shape



Four locules

Eight locules

G. Number of locules



Absent

Medium

Dense

H. Capsule hairiness

Plate 2: Morphological Characterization

Chapter – V

DISCUSSION

DISCUSSION

Sesame (*Sesamum indicum* L.), also known as "benni seed," "gingelly," "simsim" and "til" is one of the most important and ancient oil seed crops known to man. Despite the fact that sesame is widely utilised for a variety of reasons, output in the Indian subcontinent has been woefully poor. Selection of high-yielding, adaptable varieties will aid in boosting production both locally and globally.

In light of the foregoing, the current study underwent several genetic researches, including morphological characterisation, genetic variability, heritability, genetic advance, association analysis, path coefficient analysis, genetic divergence and principal component analysis. These studies can be used to rank germplasm and superior germplasm can be identified in future breeding programmes for the development of new varieties. The results of the experiment are discussed under the following headings:

- 5.1 Morphological Characterization
- 5.2 Parameters of genetic variability
 - 5.2.1 Analysis of variance
 - 5.2.2 Genotypic and phenotypic coefficient of variation
 - 5.2.3 Heritability and Genetic advance
- 5.3 Association analysis
 - 5.3.1 Correlation coefficient analysis
 - 5.3.2 Path coefficient analysis
- 5.4 Genetic divergence using Mahalanobis D² analysis
- 5.5 Principal component analysis
- 5.6 Screening of sesame germplasm against charcoal rot

5.1 Morphological Characterization

Germplasm is the starting point for any crop improvement project. Qualitative characters are considered morphological markers in the identification of landraces to estimate relationships between genotypes

because they are generally highly heritable, can be easily seen by the eye, and are equally expressed in all environments. Germplasm characterization and evaluation studies reveal a wide range of qualitative characters for optimal germplasm exploitation and the identification of viable gene sources.

Plant growth type, plant growth habit, main stem colour, stem hairiness, plant branching and branching pattern, leaf hairiness, leaf shape, basal leaf margin, lobe incision of basal leaf, petiole colour, number of flowers per leaf axil, corolla hairiness, corolla colour, number of locules per capsule, capsule arrangement were the traits used for characterization of 204 sesame genotypes. From the study, the traits plant growth habit, branching habit, branching pattern, stem hairiness, corolla colour, corolla hairiness, capsule hairiness, type of capsule beak and seed coat colour were observed to be important criterion for differentiation among the genotypes and easy identification for different sesame genotypes. However, no one trait was able to distinguish the genotypes individually, therefore they were utilised in combination. Similar characterization pattern was adopted by Kiranmayi *et al.* (2014), Singh *et al.* (2017), Bhoot *et al.* (2019) and Pavani *et al.* (2020).

5.2.1 Analysis of variance

Results of analysis of variance revealed that the mean sum of squares due to genotype were highly significant for most of the yield contributing traits viz., days to flower initiation, plant height, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, capsule length, number of seeds per capsule, days to maturity, thousand seed weight, seed yield per plant and oil content (%). This indicates that sufficient variability is present for most of the important characters among different sesame genotypes.

Similar results have been reported by Parameshwarappa *et al.* (2009) for number of branches per plant, plant height, number of capsules per plant, capsule length, number of seeds per capsule, thousand seed weight, seed yield per plant and oil content; Gangadhara *et al.* (2012) for days to maturity, number of branches per plant, number of capsules per plant and seed yield per plant, Shekhawat *et al.* (2013) and Singh *et al.* (2017) for days to flower initiation.

5.2.2 Genotypic and phenotypic coefficient of variation

The most logical method to begin any breeding programme is to examine the availability of current genetic variability, as this is the foundation of every crop improvement effort. If there is significant genetic diversity within the population, it is required to examine variability in terms of quantitative features with reference to genetic parameters such as genotypic and phenotypic coefficients of variation to enable the isolation of superior genotypes via selection.

In the present study, the phenotypic coefficient of variation was significantly higher in magnitude than that of genotypic coefficient of variation for most of the traits under study. Number of secondary branches per plant recorded highest PCV and GCV followed by thousand seed weight, number of primary branches per plant capsule length, seed yield per plant and number of capsules per plant, while moderate PCV and GCV were recorded for days to 50% flowering followed by days to flower initiation, plant height and seeds per capsule. Low PCV and GCV were recorded for oil content followed by days to maturity. Results indicated that selection of these traits for further breeding work will be effective.

Similar results have been reported by Tripathi *et al.* (2013) and Teklu *et al.* (2021) for seed yield per plant, number of secondary branches, 1000 seed weight and number of primary branches; Desawi *et al.* (2014), Saxena and Bisen (2016), Bamrotiya *et al.* (2016) and Patil and lokesha (2018) for seed yield per plant and number of capsules per plant; Parveen *et al.* (2017), Gokulakrishnan *et al.* (2018), Singh *et al.* (2018) and Kalaiyarasi *et al.* (2019) for seed yield, number of branches per plant and number of capsules per; Saxena and Bisen (2017) for seed yield per plant, number of primary branches per plant; Umamaheswari *et al.* (2019) for number of secondary branches, number of primary branches; Takele *et al.* (2019) for number of capsules per plant; Tripathi *et al.* (2013) recorded moderate PCV and GCV for days to 50 per cent flowering and plant height; Patil and lokesha (2018) for plant height and number of seeds/capsule and Shanmugam *et al.* (2018) for days to 50 per cent flowering and plant height number of seeds/capsule.

5.2.3 Heritability (%) (bs) and Genetic Advance

Heritability (in the broad sense) is defined as the ratio of genotypic variance to phenotypic variance, which provides an estimate of which individuals are more likely to be closely related than others and which traits are passed down from parents to offspring. Genetic advance estimates are useful for determining the degree of genetic gain of a trait under selection. The optimal selection of traits for high yield is achieved by combining high heritability with high genetic progress. It also displays the degree of additive nature of a gene for breeding programme selection.

An attempt was made to estimate the broad sense heritability broadly classified into low (below 50%), medium (50-70%) and high (above 70%). Genetic advance estimates have been classified into low (below 10%), medium (10-20%) and high (above 20%) in order to draw some valid conclusions about the possibilities of the improvement in the various traits. The highest heritability was exhibited by thousand seed weight followed plant height, capsules per plant, secondary branches per plant, seed yield per plant and capsule length. High heritability values for these traits indicated that variation observed was mainly due to genetic and less influenced by environment. These results are in confirmation with those of Bhagasara *et al.* (2017) and Saxena and Bisen (2017) for thousand seed weight; Shanmugam *et al.* (2018) and Teklu *et al.* (2021) for number of secondary branches, number of capsules per plant, capsule length, 1000 seed weight and Kalaiyarasi *et al.* (2019) and Umamaheswari *et al.* (2019) for number of capsules per plant, seed yield per plant, plant height, thousand and Kehie *et al.* (2020) for number of capsules per plant and thousand seed weight.

Medium heritability was recorded by oil content followed by number of seeds per capsule, primary branches per plant, days to maturity, days to flower initiation and days to 50% flowering. On the contrary, Singh *et al.* (2018) for oil content and days to 50% flowering, Shanmugam *et al.* (2018) for days to 50 per cent flowering, days to maturity, number of primary branches, number of seeds per capsule and oil content and Patidar *et al.* (2020) for oil content and number of seeds per capsule recorded high heritability. Low heritability was not recorded for any trait.

The highest genetic advance as percentage of mean (at 5% Selection intensity) was recorded for number number of secondary branches per plant followed by thousand seed weight, capsule length, seed yield/plant, primary branches per plant, capsules per plant, plant height. Similar findings were reported by Vanishree *et al.* (2013) and Saxena and Bisen (2017) for number of primary branches per plant and number of secondary branches per plant; Shanmugam *et al.* (2018) and Teklu *et al.* (2021) for number of secondary branches, number of capsules per plant, capsule length, thousand seed weight and Kalaiyarasi *et al.* (2019) and Umamaheswari *et al.* (2019) for number of capsules per plant, seed yield per plant, plant height, 1000 seed weight. Takeleet *et al.* (2019) for seed yield per plant and number of branches per plant; moderate genetic advance as a percentage of mean was recorded for number of seeds per capsule, days to maturity, oil content, days to 50% flowering and days to flower initiation. Low genetic advance was not recorded for any trait. On the contrary, low genetic advance was recorded by Soury *et al.* (2016) for days to maturity.

High heritability coupled with high genetic advance was observed for number of secondary branches per plant, plant height, capsules per plant, capsule length, thousand seed weight and seed yield per plant. These results indicated the preponderance of additive gene action in the expression of this trait and simple selection would be effective. Similar results for high heritability with high genetic advance were reported by Shanmugam *et al.* (2018) and Teklu *et al.* (2021) for number of secondary branches, number of capsules per plant, capsule length, thousand seed weight; Kalaiyarasi *et al.* (2019) and Umamaheswari *et al.* (2019) for number of capsules per plant, seed yield per plant, plant height, thousand seed weight and Kehie *et al.* (2020) for number of capsules per plant and 1000 seed weight.

Moderate heritability with high genetic advance was reported for number of primary branches per plant. Moderate heritability with moderate genetic advance was observed for days to flower initiation, days to 50% flowering, days to maturity, number of seeds per capsule and oil content. In contradiction, Saxena and Bisen (2017) reported that oil content, days to 50% flowering, days to maturity per plant exhibited high heritability coupled with high genetic advance.

5.3 Association analysis

5.3.1 Correlation coefficient analysis

Correlation analysis is a statistical technique for determining the strength of a linear relationship between two traits as well as the relationship's direction. Because yield is a polygenic property that is strongly affected by the environment, selection for yield may not be fulfilling without taking into account yield component traits. Estimating the relationship between yield component qualities and their impacts on yield is helpful in defining selection criteria for a successful breeding programme. It is useful to understand how one character's improvement causes changes in other characters.

Study revealed that seed yield per plant showed highly significant positive correlation with number of capsules per plant followed by number of seeds per capsule, number of primary branches per plant, plant height, oil content and number of secondary branches per plant. Similar results were reported by Bharathi *et al.* (2015), Fazal *et al.* (2015), Abate (2018), Navaneetha *et al.* (2019) for number of capsules per plant, number of seeds per capsule and plant height; Saxena and Bisen (2016), Agrawal *et al.* (2017), Patil and Lokesha (2018), Sasipriya *et al.* (2018), Manjeet *et al.* (2019) and Umamaheswari *et al.* (2019) for number of primary branches, number of secondary branches, number of capsules per plant and seeds per capsule; Lalpantluangi and Shah (2018), Iqbal *et al.* (2018) and Vinoth *et al.* (2018) for number of capsules per plant; Saxena and Bisen (2016) and Singh *et al.* (2018) for oil content; Aye *et al.* (2018) and Singh *et al.* (2018) for plant height, number of secondary branches per plant; Bamrotiya *et al.* (2016) and Kalaiyarasi *et al.* (2019) number of seeds/capsule and plant height; Navaneetha *et al.* (2019) for number of primary branches per plant and Sabiel *et al.* (2015) plant height.

In contradiction, Saxena and Bisen (2016), Manjeet *et al.* (2019) and Singh *et al.* (2018) recorded that plant height had significant negative correlation with seed yield per plant.

5.3.2 Path coefficient analysis

Path coefficient analysis has been widely used in crop breeding program to determine the nature of relationships between grain yield and its contributing components and to identify the components with significant effects on yield to be used as selection criteria. Path analysis shows the direct and indirect effects of cause variables on effect variables. According to this method, the correlation coefficient between two traits is separated into the components that measure the direct and indirect effects.

The present study revealed that high positive direct effect on seed yield was exerted by number of capsules per plant followed by number of seeds per capsule, days to flower initiation, number of primary branches per plant and oil content. Thus, selection based on these traits may lead to increase in yield. Low positive direct effect was exerted by thousand seed weight and capsule length. These results are in agreement with the findings of Bharathi *et al.* (2015), Bamrotiya *et al.* (2016), Soundharya *et al.* (2017), Agrawal *et al.* (2017), Tidke *et al.* (2018), Patil and Lokesha (2018), Sasipriya *et al.* (2018) and Umamaheswari *et al.* (2019) for number of seeds per capsule and number of capsules per plant; Rehab *et al.* (2019) and Navaneetha *et al.* (2019) for number of seeds per capsule; Saxena and Bisen (2016), Abate (2018) for number of capsules per plant; Singh *et al.* (2018), Rehab *et al.* (2019), Teklu *et al.* (2021), Kehie *et al.* (2020) and Patidar *et al.* (2020) for number of seeds/capsule and oil content and Agrawal *et al.* (2017) and Tidke *et al.* (2018) for number of primary branches per plant.

Low positive direct effect was exerted by thousand seed weight and capsule length. These results are in agreement with the findings Bharathi *et al.* (2015), Agrawal *et al.* (2017) and Navaneetha *et al.* (2019) for capsule length.

Whereas, negative direct effect was exerted by days to maturity, days to 50% flowering, plant height and number of secondary branches per plant. These results are in agreement with the findings of Bharathi *et al.* (2015) for days to 50% flowering; Patil and Lokesha (2018) for days to maturity and in contradiction, Rehab *et al.* (2019) and Kalaiyarasi *et al.* (2019) reported

positive direct effect of plant height on seed yield per plant; Saxena and Bisen (2016) and Agrawal *et al.* (2017) reported positive direct effect of number of secondary branches per plant.

On the basis of above study, the traits *viz.*, number of capsules per plant, number of seeds per capsule and thousand seed weight have positive direct association along with significant positive correlation with seed yield. Thus, these characters can be considered as a criterion for improving seed yield in breeding programs of sesame.

5.4 Genetic divergence using Mahalanobis D² analysis

The genetic diversity of parents is critical for a successful breeding programme, because crossings between parents with the greatest genetic divergence are more likely to produce desirable recombinants in the progenies. Multivariate analysis using Mahalanobis D² statistics has been utilised in numerous crops to find such varied parents for crossing. It is a useful tool for determining the degree of genetic diversity between genotypes and determining the relationship between clustering patterns and geographic origin.

The present study revealed that grouping of 204 genotypes into clusters using Wards's method resulted in the formation of nine clusters. Clustering of genotypes was not associated with the geographical distribution and mainly grouped due to their morphological differences. Thus, showing evidence that geographical isolation is not the only factor causing genetic diversity in sesame. Clustering pattern was random and independent. Cluster IX was the largest among all clusters comprising 34 genotypes followed by cluster VIII with 32 genotypes. Cluster IV had 28 genotypes followed by cluster V with 25 genotypes and cluster VI with 23 genotypes. Cluster I had 20 genotypes. Cluster II had 17 genotypes and cluster III had 13 genotypes. Cluster VII was the smallest and had 12 genotypes. Similar results have been given by Baraki *et al.* (2015), Iqbal *et al.* (2018), Soundharya *et al.* (2017) and Mohanty *et al.* (2020) for cluster I. In contradiction, Iqbal *et al.* (2018) and Soundharya *et al.* (2017) reported maximum genotypes for cluster I.

The results also revealed that the trait number of seeds per capsule contributed maximum towards genetic divergence followed by oil content, days to 50% flowering, thousand seed weight, plant height, secondary branches per plant, number of primary branches per plant, days to maturity, days to flower initiation, number of capsules per plant, seed yield per plant and capsule length. The results were supported by Tripathi *et al.* (2013) for days to 50% flowering; Dash *et al.* (2018) for thousand seed weight and number of seeds per capsule and Singh *et al.* (2018) and Mohanty *et al.* (2020) for oil content.

In the present study, the highest inter cluster distance was observed between the clusters V and VII followed by cluster V and VI, IV and VII and II and VII suggesting the presence of variability in genetic make-up of genotypes included in these clusters. High heterotic combinations will be obtained when genotypes of these distinctly placed clusters would be crossed. The lowest inter cluster distance was observed between cluster IV and VI indicating existence of closer proximity between these clusters. The results were in contradiction with the findings of Tripathi *et al.* (2013) for cluster VI and XI and lowest inter cluster distance for cluster IV and V; Chandramohan *et al.* (2014) for cluster VI and XII; Baraki *et al.* (2015) for cluster II and III. Soundharya *et al.* (2017) for cluster IV and VI; Singh *et al.* (2018) for cluster XII and IV; Dash *et al.* (2018) for cluster II and IV and Iqbal *et al.* (2018) for cluster V and III and Sirisha *et al.* (2020) for cluster V and XI.

Highest cluster mean values were recorded for days to flower initiation and days to maturity in cluster II; number of primary branches per plant, number of secondary branches per plant, plant height, number of capsules per plant, capsule length, thousand seed weight, oil content and seed yield in cluster V; Days to 50% flowering in cluster VII and number of seeds/capsule in cluster VIII. Similar reports have been given by Tripathi *et al.* (2013) for Cluster VI which exhibited highest means for plant height, number of primary and secondary branches per plant; Parameshwarappa *et al.* (2012) for Cluster VII exhibiting highest means for seed yield and number of capsules per plant.

The lowest cluster mean values were recorded for traits capsule length and number of seeds per capsule in cluster I; days to 50% flowering in cluster IV; number of primary branches, number of secondary branches and oil content in cluster VI; plant height, number of capsules, thousand seed weight and seed yield in cluster VII; days to 50% flowering and days to maturity in cluster VIII. Similar reports have been given by Tripathi *et al.* (2013) for cluster XI which exhibited lowest means for days to 50% flowering and days to maturity. On the basis of these traits, superior genotypes can be selected and used in hybridization programme.

5.5 Principal Component Analysis

Principal Component Analysis was used to convert interdependent traits into a set of independent traits and to minimise the data structure's dimensionality. It's a data reduction technique for elucidating the associations between two or more characters and dividing the total variance of the original characters into a small number of uncorrelated new variables. Principal Component Analysis (PCA) can be used to uncover similarities between variables.

The first principal component i.e. PC1 accounted for maximum proportion of total variability in the set of all variables and remaining components accounted for progressively lesser amount of variation. The first Principal Component accounted for maximum variability i.e., 24.027% which reduced gradually to 9.389% in fifth principal component. The first five principal components having eigen values greater than 1 and altogether explained 77.235% of the total variation. Rotated component matrix revealed that each principal component was separately loaded with various yield and quality attributing traits under study.

The PC1 was composed of traits *viz.*, number of primary branches per plant, number of secondary branches per plant and plant height. The second principal component (PC2) consisted of phenological traits such as days to flower initiation, days to 50% flowering and days to maturity. While the third principal component (PC3) was dominated by traits *viz.*, number of capsules per plant, oil content and seed yield per plant. Fourth principal component

(PC4) was related to number of seeds per capsule. Fifth principal component (PC5) consisted of capsule length and thousand seed weight. Similar results were reported by Saha *et al.* (2012) for plant height, number of primary branches per plant, number of secondary branches per plant, days to 50% flowering and days to maturity; Ismaila and Usman (2014) for plant height; Tanwar and Bisen (2017) for oil content; and Baraki and Berhe (2019) for branches per plant and plant height. In contradiction, Singh *et al.* (2018) reported that PC1 was mostly related with phenological traits *viz.*, days to flower initiation, days to 50% flowering and days to maturity.

On the basis of yield and yield attributing traits, out of top five principal components, the value of PC1 was highest than PC2, PC3, PC4 and PC5. Germplasm lines showing maximum positive PC scores and common in PC1 and PC3 for traits *viz.*, number of primary branches per plant, number of secondary branches per plant, plant height, number of capsules per plant, seed yield per plant and oil content are SI-805, G-6, S-0126, IS-101-213, IS-352, EC-335004-I, RJS-29-1, ES-41, NIC-17389, SI-0248, EC-310425, JTS-8* and GT-10*. Selection of these lines for utilization in the crossing program can help in development of high yielding, good quality cultivars. Genotypes showing high PC scores in PC3 for seed yield per plant and oil content and low PC scores in PC2 for phenological traits days to flower initiation, days to 50% flowering and days to maturity are EC-35000, GRT-8327, IC-152485, IS-641-2-84, 54-1641, S-0650, SI-2561, EC-310448, EC-132295, 77-701, IC-204630, 78-266-I, S-0248. Thus, selection of these lines can help in further lead to the development of new high yielding, early maturing varieties through involvement in hybridization program.

5.6 Identification of Putative lines with low oxalic acid and high oil content

Titration of 200 sesame germplasm for oxalic acid revealed that germplasm G-13, NIC-9835, IS-156-3-84, Guj Sel-12, IS-446-1-84, IS-302, NIC-8260, IS-514, EC-310448, NIC-17389, EC-132295, IC-205206, GRT-8385, NIC-8020 had the lowest oxalic acid content of 0.25%. Genotypes having oxalic acid content less than 1% and oil content higher than 45%

were IS-302, IS-514, NIC-8260, G-13,S-0253, EC-335009, RJS-61, KJS-21, G-2,SI-2073, IS-482-B, IS-24-P, SI-3097, Coredbose, BS-10, G-9-1, Murg-1-7, ES-370, RJS-21878-20, IC-204997, NIC-6059, ES-334962, NIC-16187, G-49, G-39, NIC-8210, ES-312955, EC-334955, NIC-13006, IS-109, G-44, KMS-4-238, SI-1873, IS-424, ES-560, IC-14142, EC-334968, ES-303311, IC-204167, IS-562, IS-455, IS-607-2-04, GRT-8368-I, GRT-8392, I-68, GAD-5, IS-261-2, S-0486 and NIC-8062. The results are similar to findings of Sahu *et al.* (2016) and Thakur *et al.* (2017). Out of these genotypes SI-1873, RJS-61, ES-370, RJS-218, NIC-6059 recorded seed yield ≥ 15 g.

Chapter – VI

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER WORK

SUMMARY, CONCLUSIONS AND SUGGESTIONS

FOR FURTHER WORK

6.1 Summary

The present investigation entitled “**Genetic Assessment for Seed Yield and Quality Traits in Sesame (*Sesamum indicum* L.)**” was conducted under BSP (Groundnut), Research Farm, JNKVV, Jabalpur (M.P.) during *kharif* 2020. Experimental material consisted of 204 genotypes including 4 checks of sesame grown in Augmented Block Design. Observations were recorded on five randomly selected plants from each replication. Data were recorded on traits *viz.*, days to flower initiation, days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, capsule length, number of seeds per capsule, days to maturity, thousand seed weight, oil content (%) and seed yield per plant. The objectives of this study were to characterize the sesame genotypes and estimate the genetic variability, heritability, genetic advance, association analysis, path coefficient analysis and to identify promising genotypes based on genetic divergence and principal component analysis for higher yield and quality related traits in sesame and identifying of putative sesame lines for low oxalic acid and high oil content.

Sesame germplasm were characterized in different categories on the basis of twenty morphological traits *viz.*, plant growth type, plant growth habit, main stem colour, stem hairiness, plant branching and branching pattern, leaf hairiness, leaf shape, basal leaf margin, lobe incision of basal leaf, petiole colour, number of flowers per leaf axil, corolla hairiness, corolla colour, number of locules per capsule, capsule arrangement, capsule hairiness, colour of dry capsule, type of capsule beak and seed coat colour. Analysis of variance showed sufficient amount of variability for most of the characters which indicates that there is enough scope for selection considering these characters.

Highest GCV and PCV were recorded by number of secondary branches per plant followed by thousand seed weight, number of primary branches per plant capsule length, seed yield per plant and number of capsules per plant while moderate GCV and PCV were recorded for days to 50% flowering followed by days to flower initiation plant height and seeds per capsule. Low GCV and PCV were recorded for oil content followed by days to maturity.

Heritability was estimated for all the characters under study. The highest heritability was exhibited by thousand seed weight followed plant height, capsules per plant, secondary branches per plant, seed yield per plant and capsule length. Medium heritability was recorded for oil content followed by number of seeds per capsule, primary branches per plant, days to maturity, days to flower initiation and days to 50% flowering. Low heritability was not recorded for any trait.

The highest genetic advance as percentage of mean (at 5% Selection intensity) was recorded for number of secondary branches per plant followed by thousand seed weight, capsule length, seed yield/plant, number of primary branches per plant, number of capsules per plant and plant height. Moderate genetic advance as a percentage of mean was recorded for number of seeds per capsule, days to maturity, oil content, days to 50% flowering and days to flower initiation. Low genetic advance was not recorded for any trait.

The study revealed that high heritability coupled with high genetic advance was observed for number of secondary branches per plant, plant height, number of capsules per plant, capsule length, thousand seed weight and seed yield per plant. Moderate heritability with high genetic advance was observed for number of primary branches per plant. Moderate heritability with moderate genetic advance was observed for days to flower initiation, days to 50% flowering, days to maturity, number of seeds per capsule and oil content.

Seed yield per plant showed highly significant positive correlation with number of capsules per plant followed by number of seeds per capsule, number of primary branches per plant, plant height, oil content and number of secondary branches per plant.

Path analysis revealed that high positive direct effect on seed yield was exhibited by number of capsules per plant. Moderate positive direct effect on seed yield was exhibited by number of seeds per capsule, days to flower initiation, number of primary branches per plant and oil content. Whereas, negative direct effect was exerted by days to maturity, days to 50% flowering, plant height and number of secondary branches per plant.

On the basis of D2 values, 204 genotypes were grouped into nine clusters using Ward's method. Clustering pattern was random and independent. Cluster IX was the largest among all clusters comprising 34 genotypes followed by cluster VIII with 32 genotypes. Cluster IV had 28 genotypes followed by cluster V with 25 genotypes and cluster VI with 23 genotypes. Cluster I had 20 genotypes. Cluster II had 17 genotypes and cluster III had 13 genotypes. Cluster VII was the smallest and had 12 genotypes.

The trait number of seeds per capsule contributed maximum towards genetic divergence followed by oil content, days to 50% flowering, thousand seed weight, plant height, number of secondary branches per plant, number of primary branches per plant, days to maturity, days to flower initiation, number of capsules per plant, seed yield per plant and capsule length.

The highest intra cluster distance was recorded in cluster V followed by cluster I and cluster IX. The inter cluster distance was highest between clusters V and VII followed by cluster V and VI and the lowest inter cluster distance was observed between cluster IV and VI.

Highest cluster mean values were recorded for days to flower initiation and days to maturity in cluster II; number of primary branches, number of secondary branches, plant height, number of capsules per plant, capsule length, thousand seed weight, oil content and seed yield in cluster V; days to 50% flowering in cluster VII and number of seeds/capsule in cluster VIII.

The lowest cluster mean values were recorded for traits capsule length and number seeds per capsule in cluster I; days to 50% flowering in cluster IV; number of primary branches, number of secondary branches and oil content in cluster VI; plant height, number of capsules, thousand seed weight and seed yield in cluster VII; days to 50% flowering and days to maturity in cluster VIII.

Principal components analysis was performed using the yield and quality components in sesame genotypes. Out of twelve, only 5 principal components (PCs) exhibited more than 1 Eigen value and showed about 77.235% variability among the traits studied. The PC1 had the highest variability followed by PC2, PC3, PC4 and PC5 for traits under study. The first principal component (PC1) accounted for the highest variation comprised of traits viz; number of primary branches per plant, number of secondary branches per plant and plant height. The second principal component (PC2) consisted of phenological traits such as days to flower initiation, days to 50% flowering and days to maturity. While the third principal component (PC3) was dominated by traits viz; number of capsules per plant, oil content and seed yield per plant. Fourth principal component (PC4) was related to number of seeds per capsule. Fifth principal component (PC5) consisted of capsule length and thousand seed weight

Putative sesame germplasm for low oxalic acid and high oil content were IS 302, IS-514, NIC-8260, G-13, S-0253, EC-335009, RJS-61, KJS-21, G-2, SI 2073, IS-482-B, IS-24-P, SI-3097, Coredbose, BS-10, G-9-1, Murg-1-7, ES-370, RJS-21878-20, IC-204997, NIC-6059, ES-334962, NIC-16187, G-49, G-39, NIC-8210, ES-312955, EC-334955, NIC-13006, IS-109, G-44, KMS-4-238, SI-1873, IS-424, ES-560, IC-14142, EC-334968, ES-303311, IC-204167, IS-562, IS-455, IS-607-2-04, GRT-8368-I, GRT-8392, I-68, GAD-5, IS-261-2, S-0486 and NIC-8062 and out of which SI-1873, RJS-61, ES-370, RJS-218, NIC-6059 were high seed yielding lines.

6.2 Conclusions

1. Analysis of variance suggested that the mean sum of squares due to genotypes were highly significant for most of the traits under consideration, indicating the presence of variation among the genotypes for these characters. Hence, further selection for these characters may be effective.
2. High genotypic and phenotypic coefficient of variation and heritability coupled with genetic advance as percentage of mean was observed for primary branches per plant, secondary branches per plant, number of capsules per plant, capsule length, thousand seed weight and seed

- yield per plant, which showed that these traits were influenced by additive gene action. Hence, selection for such traits can be rewarding.
3. Correlation analysis and path coefficient analysis revealed positive association and positive direct effect for number of capsules per plant, number of primary branches per plant, oil content (%) and number of seeds per capsule. Selection based on these traits can be beneficial in improving yield.
 4. The percentage contribution towards genetic divergence was found highest for number of seed per capsule followed by oil content, days to 50% flowering and thousand seed weight, indicating that selection based on these traits would be effective.
 5. The maximum inter cluster distance was reported between cluster V and cluster VII followed by cluster V and cluster VI, indicating that superior recombinations can be realized by crossing between the lines of these clusters.
 6. On the basis of Principal component analysis, genotypes common in PC1 and PC3 primarily for yield and quality traits viz., SI-805, G-6, S-0126, IS-101-213, IS-352, EC-335004-I, RJS-29-1, ES-41, NIC-17389, SI-0248 and EC-31042 have been identified as potential genotypes and may be further utilized in breeding programme.
 7. The genotypes RJS-61, ES-370, NIC-6059, RJS-218, SI-1873 have been identified as promising ones for low oxalic acid, high oil content and yield.

6.3 Suggestions for furtherwork

The following suggestions have been made for further study:

1. The potential genotypes viz., SI-805, G-6, S-0126, IS-101-213, IS-352, EC-335004I, RJS-29-1, ES-41, NIC-17389, SI-0248 and EC-310425 should be put to test in multilocal trials to determine their adaptability and superiority in different seasons and locations.
2. To isolate potential genotypes, characters viz., primary branches per plant, secondary branches per plant, number of capsules per plant and thousand seed weight with high heritability and high genetic advance

should be used. These traits may be considered in the future for the development of high yielding and quality cultivars.

3. Promising genotypes from distant clusters could be used in hybridization to take advantage of the heterotic effect and desired genes, resulting in potential segregants.
4. The identified lines for low oxalic acid with high oil content and yield viz., RJS-61, ES-370, NIC-6059, RJS-218, SI-1873 can be utilized in the hybridization programme.

Chapter- VII

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APPENDICES

APPENDICES

Appendix-I

Categorization of sesame genotypes based on morphological characters

S. No.	Entry name	PGT	PGH	MSC	SH	BH	BP	LH	LS	BLM	LIBL	PC	NFPLA	CoH	CC	CS	NLPC	CA	CaH	CDC	TCB	SCC
1	SI-1687-I	ID	E	G	A	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	SH	DBR
2	IC-14331	ID	E	G	A	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	C	DBR
3	Oct-81	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	SH	DBR
4	EC-182832	ID	E	G	A	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	SH	DBR
5	G-18	ID	E	G	A	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	M	BR	SH	DBR
6	NIC-8033	ID	E	G	A	P	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	SH	DBR
7	SI-805	ID	E	G	A	M	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	M	BR	SH	DBR
8	G-2	ID	E	G	S	P	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	S	BR	C	DBR
9	G-6	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
10	RJS-185	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	SH	DBR
11	NIC-8282	ID	E	G	S	M	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
12	IS-387	ID	SE	G	S	M	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
13	G-13	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	BO	4	MONO	D	BR	SH	DBR
14	EC-334955	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
15	NCR/82/No/Bo/NS	ID	SE	G	A	F	T	S	O/L	SE	S	GP	1	D	WDPS	NO	4	MONO	M	BR	C	DBR
16	IS-205-I	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	C	DBR
17	NIC-8062	ID	E	G	D	F	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	M	BR	SH	DBR
18	G-8	ID	E	G	A	P	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	SH	DBR
19	SI-1925	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	SH	DBR
20	EC-35000	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	C	DBR
21	NIC-9835	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR

S. No.	Entry name	PGT	PGH	MSC	SH	BH	BP	LH	LS	BLM	LIBL	PC	NFPLA	CoH	CC	CS	NLPC	CA	CaH	CDC	TCB	SCC
22	IS-77	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	LO	DBR
23	EC-334993-I	ID	E	G	A	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
24	ES-110-A	ID	E	G	A	F	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
25	GRT-8327	ID	E	G	A	M	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	S	BR	SH	DBR
26	NIC-8055-I	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	SH	DBR
27	S-0619	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
28	IS-132295	ID	E	G	A	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	SH	DBR
29	ES-131-1-84	ID	E	G	A	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	C	DBR
30	S-0069	ID	E	G	A	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
31	ES-139-2-84	ID	E	G	A	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
32	RJS-Bo	ID	E	G	A	M	T	S	O/L	E	W	GP	1	D	WPS	NO	4	MONO	S	ST	LO	DBR
33	S-0627	ID	E	G	S	F	T	S	O/L	SE	W	GP	1	D	WDPS	NO	4	MONO	D	BR	LO	DBR
34	IC-152485	ID	E	G	S	F	T	S	O/L	E	W	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
35	ES-120-1-84-B	ID	E	G	S	F	T	S	O/L	E	W	GP	1	D	WPS	NO	4	MONO	S	ST	LO	DBR
36	ES-173	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
37	WLR/92/No/217/Shal	ID	E	G	A	M	T	S	O/L	SE	W	GP	1	D	WDPS	NO	4	MONO	A	BR	SH	DBR
38	G-47	ID	E	G	A	F	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
39	IS-99-A	ID	E	G	S	M	T	S	O/L	E	W	GP	1	D	WPS	NO	4	MONO	S	BR	SH	DBR
40	SI-3275	ID	E	G	S	M	T	S	O/L	E	W	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
41	IS-436-3-84	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
42	IS-449	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
43	EC-334987	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	S	WDPS	NO	4	MONO	S	BR	SH	DBR
44	IS-199-2-04	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
45	EC-334967	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	C	DBR
46	IS-156-3-84	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	S	WPS	NO	4	MONO	S	BR	SH	DBR
47	IS-641-2-84	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
48	G-40	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	S	BR	SH	DBR
49	SI-3315-16	ID	E	G	S	F	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	D	BR	SH	DBR

S. No.	Entry name	PGT	PGH	MSC	SH	BH	BP	LH	LS	BLM	LIBL	PC	NFPLA	CoH	CC	CS	NLPC	CA	CaH	CDC	TCB	SCC
50	IC-2621694	ID	E	G	A	M	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
51	G-16	ID	E	G	S	M	T	S	O/L	E	W	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
52	IS-387-2	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	S	WPS	NO	4	MONO	M	BR	SH	DBR
53	Guj Sel-12	ID	SE	G	S	M	T	S	O/L	SE	M	GP	1	S	WPS	NO	4	MONO	S	BR	SH	DBR
54	IS-289	ID	SE	G	S	M	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	D	BR	SH	DBR
55	NIC-7982	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	S	WPS	NO	4	MONO	S	BR	SH	DBR
56	IS-446-1-84	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	M	BR	SH	DBR
57	EC-334992-I	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	S	WPS	NO	4	MONO	M	BR	SH	DBR
58	G-19	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
59	EC-310455	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
60	SI-3114	ID	SE	G	S	M	T	S	O/L	E	A	GP	1	D	WDPS	NO	4	MONO	S	BR	LO	DBR
61	EC-334969	ID	SE	G	S	F	T	S	O/L	SE	W	GP	1	D	WDPS	NO	4	MONO	M	BR	LO	DBR
62	EC-204704	ID	E	G	S	M	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	M	BR	LO	DBR
63	EC-334995-I	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
64	ES-64	ID	E	G	A	P	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
65	IS-564	ID	E	G	S	M	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
66	S-0210	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	D	BR	SH	DBR
67	IS-350	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
68	ES-5503	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
69	IC-30884	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	M	BR	LO	DBR
70	NIC-8343	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	M	BR	SH	DBR
71	IS-90	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	M	BR	LO	DBR
72	GRT-8359	ID	E	G	S	P	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	M	BR	LO	DBR
73	I-68	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
74	IS-686	ID	E	G	S	F	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	M	BR	LO	DBR
75	78-266-I	ID	E	G	S	P	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
76	S-0281	ID	E	G	S	F	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	M	BR	SH	DBR
77	TMV-12-52	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	S	WPS	NO	4	MONO	M	BR	LO	DBR

S. No.	Entry name	PGT	PGH	MSC	SH	BH	BP	LH	LS	BLM	LIBL	PC	NFPLA	CoH	CC	CS	NLPC	CA	CaH	CDC	TCB	SCC
78	IS-712	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
79	GRT-83128	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	C	DBR
80	NIC-16218	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
81	KJS-21	ID	E	G	S	P	T	S	O/L	SE	W	GP	1	D	WDPS	NO	4	MONO	S	BR	C	DBR
82	GAD-5	ID	E	G	S	P	T	S	O/L	SE	W	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
83	EC-335009	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WDPS	NO	4	MONO	S	BR	SH	DBR
84	IS-302	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	S	BR	C	DBR
85	NIC-8210	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	M	BR	SH	DBR
86	78-20	ID	E	G	S	F	T	G	O/L	E	M	GP	1	D	WDPS	NO	4	MONO	S	BR	C	DBR
87	ES-560	ID	E	G	S	F	T	S	O/L	E	M	GP	1	S	WPS	NO	4	MONO	S	BR	LO	DBR
88	Coredbose	ID	SE	G	S	M	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	S	BR	C	DBR
89	ES-312955	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	S	BR	SH	DBR
90	IC-14142	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	LO	DBR
91	GRT-8392	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
92	ES-370	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	LO	DBR
93	NIC-6059	ID	E	G	S	F	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	M	BR	SH	DBR
94	IS-607-2-04	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
95	SI-1873	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	M	BR	SH	DBR
96	RJS-61	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	S	WPS	NO	4	MONO	M	BR	LO	DBR
97	NIC-8260	ID	E	G	S	F	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
98	IS-562	ID	E	G	S	F	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	D	BR	SH	DBR
99	IS-424	ID	E	G	S	F	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	M	BR	SH	DBR
100	ES-334962	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	LO	DBR
101	ES-303311	ID	E	G	S	F	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	M	BR	LO	DBR
102	S-0253	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
103	BS-10	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	LO	DBR
104	IC-204997	ID	E	G	S	F	T	S	O/L	SE	S	GP	1	S	WPS	NO	4	MONO	S	BR	LO	DBR
105	IS-482-B	ID	SE	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR

S. No.	Entry name	PGT	PGH	MSC	SH	BH	BP	LH	LS	BLM	LIBL	PC	NFPLA	CoH	CC	CS	NLPC	CA	CaH	CDC	TCB	SCC
106	IS-261-2	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	S	WDPS	NO	4	MONO	M	BR	C	DBR
107	NIC-16187	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	ST	C	DBR
108	IS-109	ID	E	G	S	F	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	S	BR	SH	DBR
109	IC-204167	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
110	KMS-4-238	ID	E	G	S	M	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	S	BR	LO	DBR
111	S-0486	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WDPS	NO	4	MONO	D	BR	SH	DBR
112	G-9-1	ID	E	G	A	F	T	S	O/L	E	M	GP	1	S	WPS	NO	4	MONO	S	BR	SH	DBR
113	IS-514	ID	E	G	S	P	T	G	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
114	G-49	ID	E	G	A	F	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
115	Murg-1-7	ID	E	G	A	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	LO	DBR
116	RJS-218	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WPS	NO	8	MONO	S	BR	SH	DBR
117	G-44	ID	E	G	S	F	T	S	O/L	E	M	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
118	NIC-13006	ID	E	G	A	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
119	IS-455	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
120	G-39	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
121	ES-3196-I	ID	E	G	A	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	SH	DBR
122	S-0126	ID	E	G	S	M	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	D	ST	SH	DBR
123	NIC-3351	ID	E	G	S	F	T	S	O/L	E	A	GP	1	D	WDPS	NO	4	MONO	D	ST	SH	DBR
124	IS-101-213	ID	E	G	A	P	T	S	O/L	SE	S	GP	1	D	WDPS	NO	4	MONO	S	ST	SH	DBR
125	G-1	ID	E	G	A	M	T	S	O/L	E	W	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
126	IS-352	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	ST	C	DBR
127	IS-101-4	ID	E	G	S	M	T	S	O/L	SE	S	GP	1	D	WDPS	NO	4	MONO	S	BR	SH	DBR
128	54-1641	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	SH	DBR
129	S-0650	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
130	SI-2561	ID	E	G	A	F	T	S	O/L	E	W	GP	1	D	WDPS	NO	4	MONO	D	BR	SH	DBR
131	TC-171	ID	E	G	A	M	T	S	O/L	E	W	GP	1	D	WDPS	NO	4	MONO	S	ST	LO	DBR
132	NIC-13032	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	ST	LO	DBR
133	S-0021	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	SH	DBR

S. No.	Entry name	PGT	PGH	MSC	SH	BH	BP	LH	LS	BLM	LIBL	PC	NFPLA	CoH	CC	CS	NLPC	CA	CaH	CDC	TCB	SCC
134	G-15	ID	E	G	A	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	C	DBR
135	EC-310448	ID	E	G	S	P	T	G	O/L	E	M	GP	1	D	WDPS	NO	4	MONO	D	ST	C	DBR
136	EC-335004-I	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	ST	SH	DBR
137	TS-332	ID	E	G	D	P	T	S	O/L	SE	A	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR
138	G-17	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
139	RJS-29-I	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	ST	SH	DBR
140	NIC-8174	ID	E	G	A	P	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	S	ST	LO	DBR
141	ES-41	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	SH	DBR
142	GRT-8609	ID	E	G	A	M	T	S	O/L	SE	W	GP	1	S	WPS	NO	4	MONO	S	BR	SH	DBR
143	NIC-17389	ID	E	G	S	P	T	S	O/L	E	A	GP	1	S	WDPS	NO	4	MONO	D	BR	C	DBR
144	78-505	ID	E	G	S	M	T	S	O/L	SE	A	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
145	SI-2073	ID	E	G	A	F	T	S	O/L	SE	A	GP	1	D	WDPS	NO	4	MONO	D	ST	SH	DBR
146	NIC-17301	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	SH	DBR
147	GRT-8368	ID	E	G	S	M	T	S	O/L	SE	A	GP	1	D	WPS	NO	4	MONO	D	ST	SH	DBR
148	S-0479	ID	E	G	S	M	T	S	O/L	SE	W	GP	1	D	WDPS	NO	4	MONO	S	BR	SH	DBR
149	EC-132295	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	SH	DBR
150	NIC-8590	ID	E	G	A	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	ST	SH	DBR
151	77-701	ID	E	G	S	M	T	S	O/L	E	A	GP	1	D	WDPS	NO	4	MONO	D	BR	LO	DBR
152	RJS-9613	ID	E	G	S	F	T	G	O/L	SE	S	GP	1	D	WDPS	NO	4	MONO	D	ST	SH	DBR
153	RJS-4-79	ID	E	G	A	F	T	S	O/L	SE	S	GP	1	D	WDPS	NO	4	MONO	S	ST	C	DBR
154	EC-335000-A	ID	E	G	S	F	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	S	BR	C	DBR
155	IC-204630	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	ST	LO	DBR
156	NIC-16264	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
157	IC-204137	ID	E	G	S	M	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	D	ST	SH	DBR
158	S-0248	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
159	Local-1	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	ST	SH	DBR
160	IC-205206	ID	E	G	A	F	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
161	Dharand	ID	E	G	S	F	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	D	BR	LO	DBR

S. No.	Entry name	PGT	PGH	MSC	SH	BH	BP	LH	LS	BLM	LIBL	PC	NFPLA	CoH	CC	CS	NLPC	CA	CaH	CDC	TCB	SCC
162	kolenyola	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	ST	LO	DBR
163	GRT-8342	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	ST	C	DBR
164	G-20	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	ST	SH	DBR
165	NIC-8035	ID	E	G	A	M	T	S	O/L	SE	M	GP	1	D	WPS	BO	4	MONO	D	BR	LO	DBR
166	IS-475	ID	E	G	A	M	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	D	ST	C	DBR
167	Chagata local	ID	E	G	S	M	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
168	IS-24-P	ID	E	G	S	M	T	G	O/L	E	A	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
169	S-0501	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	C	DBR
170	IS-39-B	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	ST	C	DBR
171	IC-131953	ID	E	G	S	P	T	S	O/L	E	M	GP	1	D	WPS	NO	4	MONO	D	ST	C	DBR
172	IS-299	ID	E	G	S	M	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	S	ST	C	DBR
173	SI-3097	ID	E	G	S	M	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
174	IS-564A	ID	E	G	S	F	T	S	O/L	E	A	GP	1	D	WDPS	NO	4	MONO	D	BR	LO	DBR
175	KMR-78	ID	E	G	S	P	T	S	O/L	E	W	GP	1	D	WDPS	NO	4	MONO	D	ST	C	DBR
176	SI-2143	ID	E	G	S	M	T	S	O/L	SE	A	GP	1	D	WDPS	NO	4	MONO	D	BR	SH	DBR
177	KIS-551	ID	E	G	S	P	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	S	ST	C	DBR
178	GRT-8385	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	SH	DBR
179	TC-326	ID	E	G	S	F	T	S	O/L	SE	W	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
180	NIC-8020	ID	E	G	S	F	T	S	O/L	E	W	GP	1	D	WPS	NO	4	MONO	S	BR	C	DBR
181	78-831	ID	E	G	A	F	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
182	NIC-8511	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	ST	C	DBR
183	MOHUR-3	ID	E	G	A	M	T	S	O/L	SE	W	GP	1	D	WDPS	NO	4	MONO	D	ST	C	DBR
184	G-5	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	C	DBR
185	SI-7619-B	ID	E	G	S	F	T	S	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
186	IS-101-2	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	ST	C	DBR
187	IS-470	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
188	GRT-8368-I	ID	E	G	A	P	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	C	DBR
189	RJS-8316	ID	E	G	A	M	T	S	O/L	SE	S	GP	1	D	WPS	NO	4	MONO	S	ST	C	DBR

S. No.	Entry name	PGT	PGH	MSC	SH	BH	BP	LH	LS	BLM	LIBL	PC	NFPLA	CoH	CC	CS	NLPC	CA	CaH	CDC	TCB	SCC
190	IS-733	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	ST	C	DBR
191	B-223	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	ST	C	DBR
192	EC-310425	ID	E	G	S	P	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
193	NIC-8523	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	ST	C	DBR
194	18-Oct	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	S	BR	C	DBR
195	IS-445-I	ID	E	G	S	F	T	S	O/L	E	M	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
196	RJS-738-2-84	ID	E	G	S	M	T	S	O/L	SE	M	GP	1	D	WDPS	NO	4	MONO	D	BR	C	DBR
197	IS-431	ID	E	G	S	F	T	S	O/L	E	A	GP	1	D	WPS	NO	4	MONO	D	BR	C	DBR
198	EC-334968	ID	E	G	S	M	T	S	O/L	E	W	GP	1	D	WPS	NO	4	MONO	D	BR	SH	DBR
199	SI-7178	ID	E	G	S	M	T	S	O/L	SE	W	GP	1	D	WDPS	NO	4	MONO	S	ST	SH	DBR
200	IS-393-1-A	ID	E	G	S	M	T	S	O/L	E	W	GP	1	D	WPS	NO	4	MONO	S	BR	C	DBR
C1	TKG-21	ID	E	G	S	M	T	G	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	D	BR	LO	W
C2	TKG-22	ID	E	G	S	M	T	G	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	LO	W
C3	JTS-8	ID	E	G	S	M	T	G	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	M	BR	C	W
C4	GT-10	ID	E	G	S	M	T	G	O/L	SE	M	GP	1	D	WPS	NO	4	MONO	S	BR	LO	B

Noted: PGT= Plant growth type, ID= Indeterminate, D= Determinate, PGH= Plant growth habit, E= Erect, SE= Semi-erect, MSC= Main stem colour, G= Green, SH= Stem hairiness, A= Absent, S= Sparse, D= Dense, BH= Branching habit, F= Few, M= Medium, P= Profuse, BP= Branching pattern, B= Basal, T= Top, LH= Leaf hairiness, Gb= Glabrous, LS=Leaf shape, O/L= ovate and lanceolate, BLM=Basal leaf margin, En= Entire, Se= Serrate, LIBL= Lobe incision of basal leaf A= absent, W= Weak, M= Medium, S= Strong, PC= Petiole colour, GP= Greenish purple, NFPLA= No. of flowers per leaf axil, 1= one, >1= more than one, CoH= Corolla hairiness, A= Absent, S= Sparse, D= Dense, CC= Corolla colour, WPS= White with pink shading, WDPS= White with deep pink shading, NLPC= No. of locules per capsule, 4= four, CA= Capsule arrangement, MONO= monocapsular, multi= multicapsular, CaH= Capsule hairiness, A= absent, S= sparse, D= dense, CDC= Colour of dry capsule, St= Straw, Br= Brown, TCB= Type of capsule beak, L= Long, C= Curved, Cl= Cleft, S0=Short, SCC= Seed coat colour, DBR= dark brown, W= White, B= Black

APPENDIX – II

Mean value of quantitative, qualitative and phenological traits of sesame genotypes

S. No.	Treatment	DFI	DFF	PH	NPB	NSB	NCP	CL	NSP	DM	TSW	OC	SYP	OA
1	SI-1687-I	39.27	41.63	118.07	4.51	2.57	46.93	2.60	50.44	95.00	3.38	39.58	9.50	0.630
2	IC-14331	40.27	42.63	137.40	4.84	2.90	47.93	2.84	58.10	96.00	2.98	37.71	9.77	1.130
3	1/10/1981	40.28	41.62	139.07	3.51	2.57	49.26	2.47	51.77	95.00	3.08	35.86	7.30	0.630
4	EC-182832	35.27	37.62	113.40	2.18	1.23	38.26	2.67	50.44	89.00	3.68	42.70	8.94	1.130
5	G-18	34.27	37.62	123.40	2.84	2.23	26.59	2.74	59.77	88.00	3.60	38.41	8.13	1.130
6	NIC-8033	36.27	39.62	131.40	5.18	1.23	50.26	2.77	63.44	92.00	3.65	43.69	10.80	1.890
7	SI-805	37.27	40.62	130.07	4.18	2.57	37.93	2.80	79.10	94.00	3.68	45.13	14.92	0.750
8	G-2	35.27	37.63	164.40	6.18	3.23	60.93	2.80	65.77	88.00	3.20	49.22	13.62	0.370
9	G-6	32.27	36.63	138.74	3.51	2.57	45.93	2.87	80.77	86.00	3.48	41.23	14.35	1.630
10	RJS-185	35.27	38.63	140.07	3.84	2.57	35.93	2.80	57.77	91.00	3.28	40.62	8.78	1.760
11	NIC-8282	35.27	38.63	135.07	4.18	2.90	33.59	2.80	69.10	92.00	3.71	32.98	10.71	1.760
12	IS-387	33.28	37.63	126.40	3.51	2.23	37.93	2.60	67.77	87.00	3.62	41.88	11.18	1.630
13	G-13	35.27	39.63	152.07	4.84	1.57	49.93	3.00	69.77	93.00	3.77	45.67	14.37	0.250
14	EC-334955	35.28	37.63	147.74	4.84	1.23	40.59	2.80	60.77	89.00	3.78	45.46	11.05	0.504
15	NCR/82/No/Bo/NS	36.27	39.63	113.07	1.84	0.90	32.59	2.80	69.10	91.00	3.22	37.84	9.38	0.630
16	IS-205-I	35.27	39.62	149.07	4.18	1.90	55.26	2.80	71.10	92.00	3.05	42.15	13.03	0.630
17	NIC-8062	34.27	37.63	146.07	2.18	0.57	42.59	2.87	77.77	88.00	3.28	46.73	12.49	0.880
18	G-8	36.27	39.62	148.07	5.84	3.23	72.59	2.80	59.10	92.00	3.18	39.56	14.00	1.890
19	SI-1925	36.27	38.63	140.07	2.51	1.90	39.26	2.84	70.10	91.00	3.48	31.82	11.38	1.130
20	EC-35000	38.27	40.63	145.74	2.18	1.57	29.59	2.87	66.77	94.00	3.18	36.71	8.55	1.510
21	NIC-9835	35.52	39.13	137.07	5.10	4.48	49.01	2.58	65.28	88.50	2.88	23.40	7.78	0.250

S. No.	Treatment	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC	SYP	OA
22	IS-77	35.52	40.13	105.07	3.10	1.14	22.34	2.58	63.61	89.50	3.17	23.47	3.20	1.510
23	EC-334993-I	34.52	38.13	144.74	3.43	2.81	30.34	2.55	59.28	86.50	3.28	24.53	4.56	1.130
24	ES-110-A	37.52	40.13	119.74	2.10	1.48	26.68	2.68	57.28	90.50	3.24	29.80	3.61	0.630
25	GRT-8327	37.52	41.13	133.40	3.10	2.48	31.34	2.71	72.28	92.50	2.97	22.31	5.39	1.130
26	NIC-8055-I	35.52	38.13	105.07	1.43	0.81	17.34	2.61	66.94	87.50	2.57	31.63	1.62	1.890
27	S-0619	35.52	39.13	152.07	4.10	3.48	48.34	2.75	55.94	88.50	3.60	34.86	8.38	1.510
28	IS-132295	35.52	39.13	132.74	3.43	2.81	47.01	2.58	55.28	89.50	3.64	28.46	8.11	1.510
29	ES-131-1-84	35.52	38.13	127.40	3.76	3.14	56.01	2.58	63.94	86.50	3.37	29.19	10.68	1.890
30	S-0069	36.52	39.13	120.07	2.10	1.48	35.68	3.41	72.94	88.50	3.30	34.46	7.29	1.130
31	ES-139-2-84	36.52	40.13	158.74	2.76	2.14	28.34	2.35	58.61	90.50	3.21	30.75	3.99	0.630
32	RJS-Bo	39.52	42.13	154.07	3.10	2.81	44.34	2.51	60.94	94.50	3.37	36.39	7.75	1.008
33	S-0627	38.52	41.13	138.07	1.76	1.14	29.01	2.51	62.61	92.50	3.42	37.05	4.91	1.008
34	IC-152485	38.52	42.13	136.07	2.10	1.48	30.01	2.65	57.94	94.50	3.27	30.43	3.34	0.504
35	ES-120-1-84-B	34.52	38.13	121.40	1.76	0.48	33.01	2.75	60.28	86.50	3.57	31.40	5.80	1.510
36	ES-173	33.52	38.38	121.99	3.00	1.90	32.76	2.29	46.61	90.00	3.00	43.59	3.13	1.008
37	WLR/92/No/217/Shal	35.52	40.38	125.99	5.00	3.56	39.76	2.42	58.61	94.00	3.47	34.91	6.05	1.510
38	G-47	36.52	41.38	131.99	2.67	0.90	49.09	2.39	54.61	96.00	3.15	35.01	6.87	1.510
39	IS-99-A	36.52	41.38	152.99	4.34	1.90	54.09	2.39	43.28	97.00	2.95	39.21	5.90	1.890
40	SI-3275	37.52	42.38	129.32	4.00	1.90	45.09	2.39	51.61	98.00	3.31	35.57	6.12	0.504
41	IS-436-3-84	34.52	39.38	129.65	4.00	2.23	48.43	2.49	50.28	92.00	2.96	37.07	5.86	1.760
42	IS-449	36.52	41.38	131.65	3.00	1.23	39.43	2.42	52.28	96.00	3.12	33.30	4.82	1.008
43	EC-334987	36.52	42.38	129.65	3.34	1.56	47.43	2.49	49.61	98.00	3.10	32.39	7.92	0.504
44	IS-199-2-04	33.52	38.38	119.32	3.00	1.56	45.09	2.79	60.28	91.00	2.75	31.67	4.84	0.504
45	EC-334967	34.52	39.38	127.32	3.34	1.90	48.09	2.42	57.28	92.00	2.95	32.02	6.53	1.760

S. No.	Treatment	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC	SYP	OA
46	IS-156-3-84	35.52	41.38	128.32	2.67	1.23	38.43	2.52	45.28	96.00	2.95	35.61	3.83	0.250
47	IS-641-2-84	36.52	41.38	130.99	4.00	2.56	53.09	2.72	58.61	96.00	2.75	33.12	7.07	0.504
48	G-40	37.52	42.38	125.65	4.34	2.56	60.76	2.69	44.28	97.00	3.35	32.60	7.11	0.504
49	SI-3315-16	37.52	42.38	120.99	2.67	0.56	47.09	2.69	54.95	97.00	3.85	39.39	8.03	0.504
50	IC-2621694	38.52	44.38	127.99	3.34	1.23	49.09	2.79	44.28	101.00	2.85	36.12	5.12	1.510
51	G-16	37.52	43.38	140.65	3.34	2.23	49.09	2.89	68.95	99.00	3.45	40.53	9.37	1.760
52	IS-387-2	39.52	44.38	120.65	3.67	1.23	40.09	2.46	52.28	101.00	2.77	35.71	4.36	1.510
53	Guj Sel-12	37.52	48.38	136.65	4.34	2.90	59.43	2.19	42.95	99.00	3.00	36.77	6.73	0.250
54	IS-289	36.52	47.38	130.65	3.00	1.56	57.76	2.49	53.95	97.00	3.35	43.12	8.95	1.386
55	NIC-7982	36.52	46.38	134.32	3.34	2.23	56.43	2.42	52.95	96.00	3.45	31.97	8.80	1.760
56	IS-446-1-84	35.52	47.38	112.99	4.34	2.56	47.43	2.49	60.95	97.00	2.98	34.23	6.86	0.250
57	EC-334992-I	34.52	45.38	124.99	3.00	0.23	54.09	2.19	46.61	94.00	3.07	37.29	6.58	1.890
58	G-19	37.52	46.38	112.65	3.67	1.90	36.43	2.32	52.28	95.00	3.25	36.74	4.47	1.008
59	EC-310455	34.52	44.38	140.65	3.00	0.90	41.09	2.39	31.61	91.00	2.75	35.17	2.85	1.760
60	SI-3114	35.52	40.38	125.99	4.00	1.90	65.43	2.32	56.28	94.00	3.07	38.40	9.94	1.008
61	EC-334969	37.02	42.38	108.99	2.76	1.76	47.18	2.52	50.86	96.00	3.17	35.24	7.26	0.504
62	EC-204704	36.02	40.38	160.32	5.76	3.09	59.84	2.42	62.86	92.00	2.93	38.30	10.67	1.386
63	EC-334995-I	38.02	43.38	158.32	5.42	4.76	71.51	2.52	65.86	98.00	3.41	39.62	15.75	1.008
64	ES-64	39.02	43.38	166.32	5.42	1.76	81.84	2.42	70.19	98.00	3.28	44.12	18.59	1.760
65	IS-564	38.02	42.38	150.99	3.76	2.42	51.51	2.46	58.52	99.00	3.68	44.53	10.66	1.008
66	S-0210	37.02	47.38	114.65	3.42	2.42	52.84	2.26	44.52	97.00	3.19	34.77	7.28	0.504
67	IS-350	36.02	40.38	145.99	3.76	1.53	38.18	2.39	60.86	92.00	3.00	43.57	6.45	1.760
68	ES-5503	36.02	47.38	98.99	3.09	2.09	43.51	2.49	54.19	95.00	2.70	30.98	5.99	1.008
69	IC-30884	34.02	45.38	130.65	4.09	2.09	53.51	2.39	59.86	93.00	2.84	41.70	8.73	1.890

S. No.	Treatment	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC	SYP	OA
70	NIC-8343	31.02	36.38	119.65	3.42	1.76	51.84	2.62	68.86	86.00	2.90	30.74	9.88	0.880
71	IS-90	35.02	46.38	137.32	3.09	2.09	63.84	2.69	56.19	95.00	3.16	39.98	11.08	1.386
72	GRT-8359	35.02	45.38	151.99	5.76	2.76	67.51	2.59	63.52	93.00	2.75	34.00	11.51	0.370
73	I-68	37.02	48.38	119.32	4.09	3.76	45.84	2.52	56.52	99.00	2.83	45.42	6.94	0.750
74	IS-686	35.02	46.38	114.65	2.09	2.42	35.84	2.62	64.19	94.00	3.10	32.53	6.55	0.880
75	78-266-I	36.02	40.38	155.99	6.76	4.76	68.18	2.52	63.86	94.00	2.70	40.30	11.47	0.880
76	S-0281	38.02	48.38	106.32	2.76	2.42	38.51	2.69	62.52	99.00	2.90	36.81	6.46	0.880
77	TMV-12-52	36.02	46.38	120.32	3.09	2.09	68.84	2.52	59.52	95.00	3.23	35.45	12.98	0.370
78	IS-712	37.02	41.38	120.99	4.76	3.76	63.18	2.69	69.86	95.00	3.10	39.64	13.27	0.880
79	GRT-83128	37.02	41.38	137.99	5.42	1.42	67.51	2.59	54.86	96.00	3.31	36.28	12.05	0.880
80	NIC-16218	38.02	42.38	151.32	2.42	1.09	52.51	2.39	49.19	97.00	2.86	36.67	7.12	1.386
81	KJS-21	35.02	39.12	149.24	5.18	1.39	68.76	2.21	72.77	93.50	2.70	50.03	13.56	0.370
82	GAD-5	34.02	37.13	153.90	5.84	1.39	65.09	2.34	71.44	89.50	2.73	51.86	12.75	0.880
83	EC-335009	32.02	36.13	140.57	4.18	3.73	64.09	2.27	64.11	86.50	2.54	52.67	10.74	0.370
84	IS-302	36.02	38.13	144.57	3.18	2.73	56.09	2.31	73.77	92.50	3.51	52.52	13.99	0.250
85	NIC-8210	34.02	40.13	129.57	2.84	0.39	59.42	2.44	57.44	95.50	3.07	46.52	10.58	0.504
86	78-20	36.02	39.13	119.57	1.51	1.60	55.76	2.47	70.44	93.50	2.91	51.59	12.38	0.504
87	ES-560	34.02	37.13	120.24	2.51	2.06	56.09	2.31	59.77	89.50	2.30	48.29	8.24	0.630
88	Coredbose	35.02	38.13	121.24	4.51	3.73	62.42	2.04	61.11	92.50	2.91	45.28	11.22	0.370
89	ES-312955	36.02	40.13	139.57	3.18	1.06	62.76	2.24	57.77	91.50	3.04	45.96	11.13	0.504
90	IC-14142	38.02	45.13	149.57	4.51	0.39	56.42	2.24	66.11	95.50	2.45	47.76	9.48	0.630
91	GRT-8392	36.02	43.13	128.57	2.18	1.82	53.09	2.31	61.11	90.50	3.01	45.86	9.84	0.750
92	ES-370	36.02	44.13	158.24	2.51	0.39	83.76	2.31	63.77	92.50	3.11	52.37	16.51	0.504
93	NIC-6059	35.02	41.13	134.57	2.51	0.39	63.09	2.27	75.77	90.50	3.31	51.00	15.37	0.504

S. No.	Treatment	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC	SYP	OA
94	IS-607-2-04	38.02	43.13	167.90	4.84	4.39	94.42	2.24	61.44	93.50	2.52	51.13	14.95	0.750
95	SI-1873	38.02	39.13	135.90	3.18	2.73	75.76	2.37	68.44	95.50	3.16	54.19	16.17	0.630
96	RJS-61	36.02	41.13	153.57	2.84	1.39	74.42	2.31	70.11	91.50	3.19	52.63	16.38	0.370
97	NIC-8260	35.02	41.13	145.24	2.84	1.73	76.42	1.94	54.11	91.50	2.40	51.03	10.45	0.250
98	IS-562	35.02	39.13	131.90	0.84	1.71	47.76	2.01	58.11	92.50	3.10	53.37	8.70	0.750
99	IS-424	35.02	42.13	125.24	1.51	1.38	50.42	1.94	44.11	89.50	2.36	52.37	5.98	0.630
100	ES-334962	36.02	43.13	131.24	2.84	2.73	57.09	2.41	67.44	91.50	2.88	50.76	11.12	0.504
101	ES-303311	34.52	44.63	162.40	2.92	1.57	69.26	1.89	35.10	89.00	3.62	54.10	9.96	0.750
102	S-0253	37.52	46.63	128.07	3.25	1.90	46.93	2.66	41.44	93.00	3.05	54.00	6.87	0.370
103	BS-10	35.52	44.63	126.74	5.25	3.57	55.59	1.99	38.77	90.00	3.49	52.38	8.50	0.504
104	IC-204997	36.52	46.63	143.40	2.92	1.90	52.93	2.19	49.77	93.00	3.06	51.04	8.83	0.504
105	IS-482-B	35.52	40.63	144.40	2.92	1.90	69.26	2.26	52.10	92.00	2.92	46.96	11.18	0.370
106	IS-261-2	34.52	44.63	106.40	2.59	0.90	34.26	2.39	56.10	88.00	3.87	50.83	7.61	0.880
107	NIC-16187	33.52	38.63	127.07	3.25	1.57	49.59	2.49	66.10	87.00	4.06	49.91	13.04	0.504
108	IS-109	31.52	36.63	147.07	1.92	0.90	44.93	2.39	57.77	83.00	3.33	54.76	8.97	0.630
109	IC-204167	31.52	37.63	135.40	3.59	2.57	52.26	2.62	49.10	85.00	3.07	54.56	8.57	0.750
110	KMS-4-238	33.52	39.63	120.74	3.25	1.57	54.59	2.69	59.77	88.00	3.39	53.12	11.30	0.630
111	S-0486	35.52	41.63	118.40	3.25	1.90	59.59	2.59	60.10	92.00	2.67	48.27	10.02	0.880
112	G-9-1	36.52	40.63	119.74	2.59	1.23	45.59	2.52	56.10	90.00	3.02	53.21	8.21	0.504
113	IS-514	35.52	42.63	126.74	5.59	2.57	64.26	2.62	69.77	94.00	2.91	52.02	13.10	0.250
114	G-49	35.52	41.63	121.40	2.92	1.23	65.59	2.52	56.77	92.00	3.01	49.74	11.67	0.504
115	Murg-1-7	34.52	40.63	124.40	1.92	2.44	49.93	2.69	60.44	90.00	3.97	52.97	11.98	0.504
116	RJS-218	33.52	39.63	138.07	3.25	1.57	79.59	2.52	60.77	89.00	3.20	51.74	15.73	0.504
117	G-44	35.52	40.63	131.40	2.59	1.23	57.59	2.69	61.77	90.00	3.64	53.51	14.03	0.630

S. No.	Treatment	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC	SYP	OA
118	NIC-13006	35.52	41.63	132.74	2.92	0.90	67.59	2.59	62.44	91.00	3.37	54.89	14.78	0.630
119	IS-455	33.52	38.63	134.40	3.92	0.00	63.59	2.39	66.44	87.00	3.37	52.41	13.24	0.750
120	G-39	33.52	39.63	139.40	3.92	1.33	66.26	2.46	53.44	88.00	3.27	49.31	11.78	0.504
121	ES-3196-I	36.52	40.38	148.32	3.76	2.67	45.93	3.09	51.52	87.50	2.72	33.05	10.98	0.370
122	S-0126	38.52	42.38	133.32	4.76	3.67	50.59	3.02	68.19	92.50	2.59	36.08	14.05	1.760
123	NIC-3351	37.52	41.38	133.65	2.43	1.34	22.93	3.06	64.19	91.50	2.70	34.68	8.53	0.880
124	IS-101-213	37.52	41.38	156.32	6.43	4.67	58.26	3.19	61.52	90.50	2.26	32.82	12.91	0.880
125	G-1	35.52	39.38	115.32	4.76	1.01	45.26	3.22	71.86	87.50	2.61	34.88	13.65	0.880
126	IS-352	36.52	40.38	120.65	4.43	3.67	60.93	3.06	61.19	88.50	2.72	37.00	15.28	0.370
127	IS-101-4	35.52	39.38	118.99	3.76	4.67	51.26	2.79	43.19	86.50	2.68	41.54	10.24	1.386
128	54-1641	37.52	41.38	128.65	4.10	2.01	48.59	2.99	64.86	91.50	2.63	32.06	13.28	1.630
129	S-0650	37.52	42.38	109.32	2.43	1.68	20.93	2.99	70.86	93.50	2.80	38.48	8.94	1.386
130	SI-2561	38.52	43.38	108.99	2.43	1.34	20.26	3.06	56.86	94.50	2.65	40.03	7.32	0.750
131	TC-171	37.52	42.38	150.32	3.43	1.34	55.26	2.76	53.86	93.50	3.00	43.89	13.87	0.750
132	NIC-13032	36.52	45.38	139.32	4.10	1.01	34.26	2.89	60.19	88.50	2.57	42.67	9.85	1.386
133	S-0021	39.52	44.38	119.99	2.76	1.34	33.93	2.99	68.52	95.50	3.10	40.52	12.37	1.386
134	G-15	39.52	43.38	127.32	2.76	2.10	35.59	2.89	49.86	93.50	2.68	42.32	9.06	0.370
135	EC-310448	37.52	42.38	128.65	5.76	0.67	39.26	3.12	50.86	92.50	2.82	36.13	10.10	0.250
136	EC-335004-I	38.52	43.38	144.32	4.76	3.67	57.93	3.19	57.86	93.50	3.09	34.78	15.56	1.386
137	TS-332	33.52	36.38	120.99	5.43	4.01	53.59	3.09	48.19	83.50	2.51	40.66	10.91	0.750
138	G-17	38.52	42.38	137.65	4.43	0.34	36.26	3.02	55.86	92.50	2.70	40.27	9.99	1.386
139	RJS-29-I	39.52	44.38	154.32	8.10	5.01	53.93	3.12	61.52	95.50	2.64	39.74	13.74	1.386
140	NIC-8174	38.52	43.38	139.99	5.10	1.80	51.26	3.02	57.86	93.50	2.80	34.61	13.21	1.760
141	ES-41	40.77	44.38	150.48	6.09	4.00	65.01	2.80	63.19	91.50	2.65	39.22	13.97	0.370

S. No.	Treatment	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC	SYP	OA
142	GRT-8609	37.77	40.38	130.82	4.76	2.00	48.34	2.63	64.86	93.50	2.47	36.97	10.54	0.370
143	NIC-17389	37.77	41.38	144.15	6.76	6.00	65.34	2.80	70.19	96.50	2.81	42.22	16.47	0.250
144	78-505	37.77	40.38	119.82	3.09	2.00	40.34	2.70	56.86	93.50	2.95	36.82	9.52	1.630
145	SI-2073	40.77	44.38	125.82	2.09	1.79	32.01	2.50	65.19	101.50	2.64	48.16	8.28	0.370
146	NIC-17301	39.77	42.38	130.82	2.42	1.00	34.67	2.57	68.19	97.50	3.09	40.04	10.68	0.370
147	GRT-8368	34.77	36.38	139.48	3.09	1.33	40.01	2.70	60.86	88.50	2.55	34.48	8.81	1.260
148	S-0479	38.77	42.38	128.48	3.09	2.33	35.01	2.63	56.86	93.50	2.85	43.60	8.29	1.260
149	EC-132295	37.77	40.38	143.48	2.76	3.33	45.01	2.67	71.86	92.50	3.09	31.35	13.68	0.250
150	NIC-8590	38.77	41.38	125.48	4.09	1.33	36.01	2.80	62.19	92.50	2.52	38.87	8.23	0.750
151	77-701	37.77	40.38	135.15	4.76	3.00	38.67	2.83	65.86	91.50	2.85	36.79	10.34	1.890
152	RJS-9613	38.77	42.38	130.82	2.09	0.66	40.01	2.67	55.86	95.50	2.35	36.68	7.47	0.504
153	RJS-4-79	39.77	43.38	122.48	2.42	1.87	35.67	2.40	58.19	97.50	2.81	40.03	8.49	1.890
154	EC-335000-A	39.77	42.38	126.82	1.76	0.66	31.01	2.60	68.86	97.50	3.15	35.56	10.14	1.630
155	IC-204630	38.77	41.38	105.48	2.76	2.15	15.01	2.60	70.86	96.50	2.85	42.64	6.04	1.260
156	NIC-16264	38.77	42.38	113.15	4.76	2.66	33.67	2.67	63.86	98.50	2.45	44.28	7.83	0.504
157	IC-204137	40.77	43.38	131.82	3.09	0.66	39.67	2.53	58.52	99.50	3.35	35.03	10.95	0.370
158	S-0248	36.77	39.38	156.15	5.42	3.00	56.67	2.70	69.19	92.50	2.47	38.91	12.77	1.630
159	Local-1	37.77	40.38	123.82	2.76	0.66	35.34	2.73	64.52	93.50	2.63	32.44	8.77	1.260
160	IC-205206	39.77	42.38	105.15	2.09	1.58	13.34	2.53	63.86	97.50	2.95	28.76	5.28	0.250
161	Dharand	38.77	44.88	118.32	2.84	1.06	47.26	2.04	61.69	94.75	3.09	35.93	10.52	1.260
162	Kolenyola	38.77	43.88	107.32	3.51	0.73	49.93	2.41	74.36	92.75	2.36	44.20	10.53	0.750
163	GRT-8342	36.77	41.88	119.65	3.84	2.73	52.26	2.34	66.03	88.75	2.31	40.37	9.85	1.630
164	G-20	37.77	43.88	124.99	5.51	3.06	65.26	2.17	71.36	92.75	3.11	38.04	15.56	0.370
165	NIC-8035	37.77	43.88	125.32	3.84	1.06	58.59	2.04	63.03	93.75	3.22	40.92	13.13	0.750

S. No.	Treatment	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC	SYP	OA
166	IS-475	39.77	45.88	132.32	3.84	1.49	62.93	2.17	79.03	96.75	2.66	37.40	14.57	1.630
167	Chagata local	38.77	44.88	113.32	4.51	3.39	44.26	1.97	57.69	94.75	2.48	43.65	8.31	1.260
168	IS-24-P	38.77	43.88	155.99	3.18	1.40	51.26	2.14	56.03	92.75	3.07	46.76	10.39	0.370
169	S-0501	39.77	44.88	137.32	6.18	2.06	74.26	2.17	63.69	95.75	3.16	44.31	15.99	0.750
170	IS-393-1-A	36.02	41.13	121.82	3.17	1.61	39.26	2.39	66.52	92.25	3.20	45.06	12.03	1.008
171	IC-131953	36.77	41.88	125.65	5.51	1.06	62.59	2.07	72.36	89.75	2.87	40.81	14.28	0.750
172	IS-299	36.77	41.88	116.99	3.18	1.40	37.93	2.21	58.69	88.75	3.08	43.93	8.57	1.630
173	SI-3097	37.77	42.88	133.65	4.18	2.39	57.26	2.37	75.03	90.75	3.00	45.88	14.10	0.370
174	IS-564A	38.77	43.88	111.99	2.84	1.06	45.26	2.04	72.03	92.75	3.09	43.65	11.43	0.750
175	KMR-78	39.77	44.88	139.65	5.84	3.06	71.59	2.07	52.36	93.75	2.98	39.78	12.57	1.260
176	SI-2143	39.77	44.88	108.32	3.51	1.73	58.93	2.17	62.03	94.75	3.36	40.11	13.44	1.260
177	KIS-551	37.77	42.88	117.32	5.18	1.73	66.26	2.07	63.03	91.75	3.43	39.62	15.3	0.750
178	GRT-8385	36.77	41.88	108.32	3.18	1.39	42.26	1.64	69.03	88.75	2.64	40.69	9.44	0.250
179	TC-326	36.77	42.88	84.32	2.51	1.93	28.59	2.11	61.69	91.75	2.76	39.37	6.82	1.260
180	NIC-8020	37.77	42.88	87.99	2.84	1.93	33.59	2.01	52.69	92.75	2.96	43.62	7.18	0.250
181	78-831	37.02	42.13	109.82	2.51	0.62	48.93	2.16	63.86	94.25	2.80	40.26	12.23	0.750
182	NIC-8511	38.02	43.13	108.49	3.17	1.61	39.26	1.96	50.52	95.25	3.00	42.41	8.92	1.260
183	MOHUR-3	39.02	44.13	119.15	4.17	0.00	48.93	2.09	68.86	97.25	2.77	36.11	12.97	1.130
184	G-5	38.02	43.13	132.49	4.17	1.28	54.59	1.96	57.52	96.25	2.38	38.04	10.57	0.370
185	SI-7619-B	38.02	42.13	122.82	1.84	0.61	42.93	2.29	64.19	93.25	3.06	40.80	11.99	0.750
186	IS-101-2	37.02	42.13	125.82	3.17	0.28	37.93	1.92	55.86	94.25	2.86	45.05	9.13	1.008
187	IS-470	39.02	44.13	125.49	3.84	2.61	44.93	2.19	65.52	97.25	3.10	36.93	12.78	1.130
188	GRT-8368-I	39.02	42.13	141.82	5.51	1.28	56.59	2.06	53.52	94.25	3.20	48.56	13.10	0.750
189	RJS-8316	36.02	39.13	114.49	4.51	2.28	46.26	2.36	72.86	90.25	3.33	39.12	15.34	0.630

S. No.	Treatment	DFI	DFF	PH	NPB	NSB	NCPP	CL	NSPC	DM	TSW	OC	SYP	OA
190	IS-733	37.02	40.13	144.82	4.84	3.61	71.26	2.29	66.86	91.25	3.40	39.58	20.53	0.630
191	B-223	37.02	40.13	151.82	6.84	3.61	78.59	2.39	71.86	91.25	2.90	39.15	20.71	1.130
192	EC-310425	36.02	39.13	149.82	5.17	3.61	66.93	2.69	63.19	89.25	2.78	34.79	15.47	0.630
193	NIC-8523	38.02	41.13	150.82	3.51	0.61	59.93	2.09	59.52	92.25	2.63	41.62	12.76	1.130
194	10/18/2021	39.02	42.12	145.82	3.51	1.28	51.59	1.92	53.52	94.25	3.10	40.73	11.85	1.630
195	IS-445-I	37.02	43.13	122.15	2.17	0.61	48.26	2.09	59.86	96.25	2.28	41.37	9.61	0.630
196	RJS-738-2-84	38.02	42.13	138.82	3.17	0.95	47.59	2.02	51.86	95.25	3.10	44.35	10.83	0.370
197	IS-431	31.02	34.13	126.82	1.51	0.00	38.59	2.06	70.19	82.25	2.67	44.84	11.14	0.630
198	EC-334968	38.02	41.13	127.15	3.51	0.00	42.93	2.36	72.86	93.25	2.90	46.04	12.92	0.630
199	SI-7178	37.02	40.13	141.15	3.51	1.28	47.59	2.16	56.19	91.25	2.90	44.56	10.99	1.890
200	IS-39-B	37.77	42.88	141.65	4.51	1.41	71.26	2.17	66.69	91.75	3.00	37.83	15.41	0.630
201	TKG-21	39.70	43.10	141.90	3.53	2.01	56.30	3.40	60.70	94.90	3.49	52.24	12.18	-
202	TKG-22	41.20	43.60	143.40	3.82	2.31	56.33	2.91	61.17	95.60	3.13	52.20	12.13	-
203	JTS-8	43.00	45.40	152.90	3.38	3.20	63.03	3.90	66.97	96.30	4.30	50.53	11.85	-
204	GT-10	40.20	42.40	154.07	4.63	4.07	63.37	3.76	68.93	99.20	4.60	51.46	11.89	-

Noted: DFI- Days to flower initiation, DFF- Days to 50% flowering, NPB- Number of primary branches, NSB- Number of secondary branches per plant, NCPP- Number of capsule per plant, PH- plant height, NSPC- Number of seeds per capsule, CL- capsule length, DM- Days to maturity, TSW- Thousand seed weight, OC- Oil content, SYP- Seed yield per plant, OA- Oxalic Acid

Appendix-III

Weekly meteorological data during *Kharif* season, 2020 at Jabalpur (M.P.)

WEEKLY DATA OF JABALPUR - 2020											
Months	T Max.	T Min.	Sun Shine hrs.	Rainfall (mm)	RH (Mor)	RH (Eve)	Wind Speed	Vapour Pressure (MM)		Evapo (mm)	Rainy days
								Mor.	Eve.		
4-10 June	34.2	23.9	6.2	25.8	82.6	49.3	5.3	21.3	19.6	4.0	2
11-17 June	37.0	25.5	5.1	6.4	80.0	54.1	4.1	22.1	22.3	5.3	0
18-24 June	33.8	24.5	1.9	20.4	82.4	55.9	7.0	21.4	21.3	4.3	1
25 June-1 July	33.1	24.6	3.8	21.4	71.3	61.6	4.2	21.5	22.7	5.3	2
2-8 July	32.2	24.6	2.6	204.5	88.1	75.4	3.2	22.9	24.0	5.0	5
9-15 July	32.8	23.6	4.3	7.2	83.0	66.3	4.8	23.3	23.2	4.2	1
16-22 July	33.0	25.1	5.2	38.4	84.0	71.4	4.0	23.1	23.0	4.0	4
23-29 July	32.9	24.6	7.7	24.1	89.4	69.4	3.3	22.8	23.7	3.2	1
30 July-5 Aug	32.7	24.1	4.2	72.2	93.4	72.0	2.9	23.9	23.6	3.5	4
6-12 Aug	29.5	24.6	1.9	201.8	94.1	82.3	3.8	23.4	23.8	3.0	5
13-19 Aug	28.7	24.1	1.1	143.1	94.7	83.9	4.1	22.8	24.3	3.1	7
20-26 Aug	30.0	23.7	3.2	83.5	90.9	76.7	3.6	22.4	22.5	3.8	5
27 Aug-2 Sept	29.7	23.4	4.0	213.0	93.3	74.1	4.9	22.4	21.8	4.7	4
3-9 Sept	33.3	23.9	6.6	50.4	88.3	64.4	2.3	22.5	22.9	4.1	3
10-16 Sept	34.2	24.2	5.7	4.6	87.1	64.7	1.2	23.4	24.2	3.1	1
17-23 Sept	32.7	24.0	4.5	26.4	91.1	74.6	1.2	23.0	24.0	3.2	3
24-30 Sept	30.9	22.8	4.5	68.4	91.6	65.6	1.6	22.0	22.2	3.5	2
1-7 Oct	32.1	20.9	7.4	0.0	85.4	52.3	1.2	18.1	18.3	3.6	0
8-14 Oct	32.3	22.8	5.7	0.0	90.9	58.4	2.0	21.7	20.6	3.0	0
15-21 Oct	33.0	21.2	8.2	0.0	89.3	49.0	3.0	20.0	17.9	3.6	0
22-28 Oct	32.7	16.7	8.7	0.0	85.1	32.9	2.1	14.8	12.0	3.3	0

Source: Department of Physics and Agro-meteorology, College of Agricultural Engineering, J.N.K.V.V., Jabalpur (M.P.)

CURRICULUM VITAE

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The author of this thesis, Sakshi seth D/O Mr. Sanjay Seth and Mrs. Shally Seth, born on 12 September 1996 at Jabalpur (Madhya Pradesh). She has joined the following institutions and successfully completed the degree of M.Sc. (Ag.) during the year 2020-2021.

S.No.	Institution	Degree awarded	University Board	Year
1	JNKVV, College of Agriculture, Jabalpur	M.Sc. (Ag.)	JNKVV, Jabalpur	2021
2	JNKVV, College of Agriculture, Jabalpur	B.Sc. (Ag.)	JNKVV, Jabalpur	2019
3	Christ Church girl's S.S School, Jabalpur	12 th	CBSE BOARD	2015
4	St. Josephs' Convent, S.S. School, Jabalpur	10 th	CBSE BOARD	2013

Scientific Interest

1. Research & Development
2. Breeding of agricultural crops

Awards

For the partial fulfilment of the Master's degree programme, she was allotted a research problem on “**Genetic Assessment for Seed Yield and Quality Traits in Sesame (*Sesamum indicum* L.)**” which was successfully conducted by her and being submitted in the form of the thesis.