DEVELOPING BREEDING LINES OF SESAME SUITABLE FOR CULTIVATION IN KERALA

GREESHMA RAVI
(2022-11-094)

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE VELLAYANI,
THIRUVANANTHAPURAM – 695 522
KERALA, INDIA

2024

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by

GREESHMA RAVI
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THESIS

Submitted in partial fulfilment of the requirement for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture

Kerala Agricultural University

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE VELLAYANI,

THIRUVANANTHAPURAM – 695 522

KERALA, INDIA

2024

DECLARATION

I, hereby declare that this thesis entitled **"Developing breeding lines of sesame suitable for cultivation in Kerala"**is a bonafide work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title of any other University or Society.

Vellayani
Date: 3-12-2024

GREESHMA RAVI
(2022-11-094)

CERTIFICATE

Certified that this thesis entitled **"Developing breeding lines of sesame suitable for cultivation in Kerala"** is a record of research work done independently by Ms. Greeshma Ravi (2022-11-094) under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to her.

Vellayani

Date: 3-12-2024

Dr. Lovely B.

(Major Advisor, Advisory Committee)
Assistant Professor
Department of Genetics and Plant Breeding
College of Agriculture, Vellayani.
Thiruvananthapuram- 695522

CERTIFICATE

We, the undersigned members of the advisory committee of **Ms. Greeshma Ravi** (2022-11-094), a candidate for the degree of **Master of Science in Agriculture**, with major in Genetics and Plant Breeding, agree that the thesis entitled "**Developing breeding lines of sesame suitable for cultivation in Kerala**" may be submitted by **Ms. Greeshma Ravi** (2022-11-094), in partial fulfilment of the requirement for the degree.

Dr. Lovely B
(Major Advisor)
Assistant Professor
Department of Genetics and Plant Breeding
College of Agriculture, Vellayani

Dr. Seeja G.
Professor and Head
Department of Genetics and Plant Breeding
College of Agriculture, Vellayani

Ms. Ninitha Nath C.
Assistant Professor
Department of Genetics and Plant Breeding
College of Agriculture, Vellayani

Dr. Susha S. Thara
Assistant Professor
Department of Plant Pathology
College of Agriculture, Vellayani

ACKNOWLEDGEMENT

“Each moment of gratitude is a whisper of hope echoing through our souls.”

I am deeply grateful to Almighty God for the unwavering support and countless blessings I have received throughout my journey in completing my Master’s program. His guidance and mercy have been my source of strength during challenging times.

I also want to extend my heartfelt gratitude to my family, friends, and mentors, whose encouragement and assistance were invaluable. Their belief in me fueled my determination and made this achievement possible. I recognize that this accomplishment is not solely mine but a shared success, and I am thankful for everyone who played a role in this journey.

With great respect, I would like to express my deep sense of gratitude and indebtedness to my major advisor ***Dr. Lovely B.****, Assistant Professor, Department of Genetics and Plant Breeding, College of Agriculture, Vellayani for her valuable guidance, consistent inspiration and encouragement, critical scrutiny of the manuscript and valuable suggestions which helped me to accomplish the research work successfully. I extend my sincere gratitude for the motherly affection expressed to me which helped me through thick and thin of this work.*

I am in dearth of words to convey my heartfelt thanks to ***Dr. Seeja G.****, Professor and Head, Department of Genetics and Plant Breeding, College of Agriculture, Vellayani for her valuable advice and wholehearted approach right from the beginning, which helped me in the successful completion of the thesis.*

I express my heartfelt gratitude to ***Ms. Ninitha Nath C.****, Assistant Professor, Department of Genetics and Plant Breeding, College of Agriculture, Vellayani for her generous and timely help, support and suggestions during all stages of the study.*

I am grateful to ***Dr. Susha S. Thara****, Professor, Department of Plant Pathology, College of Agriculture, Vellayani for her ingenious suggestions and worthwhile guidance in carrying out the research work.*

I would also like to extend my sincere gratitude to ***Dr. Jayalekshmy V.G.****, retired Professor (RC), Department of Seed Science and technology, College of Agriculture,* *Vellayani for encouraging while TP approval.*

I sincerely express my obligation and respect to teachers of the Department of Genetics and Plant Breeding, ***Dr. G. Gayathri, Dr. Beena Thomas, Smt. Ninitha Nath C.*** *and* ***Smt. Adheena Ram A*** *for their constant encouragement, support, and valuable advice.*

I am grateful to ***Dr. Pratheesh P Gopinath and Dr. Manju Mary Paul,*** *Assistant Professors, Department of Agricultural Statistics for his ingenious suggestions and worthwhile guidance in carrying out the research work.*

I fell short of words while thanking ***Vincy and Athira*** *for their support during field evaluation.*

I would like to express my heartfelt thanks to my dear seniors, ***Balaji chettan, Abirami chechi, Harisha chettan, Bhaskar chettan, Arya chechi****,* ***Aswini chechi, Vishak ettan, Sruthi chechi, Parvathy chechi, Darshana Chechi*** *and* ***Varsha chechi*** *for their help, constant moral support, everlasting patience, valuable suggestions and playing big part in completion of my research work.*

I would like to specially thank my fellow mates ***Amritha, Aiswarya Raj, Aiswarya Chandrahasan, Rajashekhar, Sreeja, Pooja, Kavya, Chandana*** *and* ***Sindhu*** *for their support even in their busy schedule.*

Words are inadequate to express my thanks to my friends ***Shanila, Vishnu, Raseena, Anargha chechi, Abhishek chettan*** *for helping me during my research work.*

Iam incredibly happy to thank ***Ratheesh chettan, Nimisha chechi*** *and* ***Reji chechi*** *for their generous assistance and suggestions during my research work.*

I am thankful to ***Kerala Agricultural University*** *for their technical and financial assistance for carrying out my study and research work, I would like to express thanks to* ***Librarian*** *and* ***library staffs*** *of COA, Vellayani, for their support and assistance during the study period.*

Last but not least I am immensely grateful to my father, ***Raveendran T****, my mother,* ***Anitha Ravi****, my father-in-law,* ***Sunil Kumar****, my mother-in-law,* ***Leena Sunil****, and my better half,* ***Rich Kumar****, for their unwavering support and encouragement throughout my career.*

I express my sincere thanks to the individuals who have helped me directly or indirectly in the successful completion of this thesis work.

Greeshma Ravi

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LIST OF ABBREVIATIONS AND SYMBOLS USED

%	Percent
&	And
ANOVA	Analysis of Variance
C.D	Critical difference
cm	centimetre
CV	Coefficient of Variation
d.f	Degrees of freedom
DAS	Days After Sowing
et al.	Co-authors/And others
Fig.	Figure
g	Gram
GA	Genetic Advance
PCV	Phenotypic Coefficient of variation
GCV	Genotypic Coefficient of variation
H^2	Heritability
KAU	Kerala Agricultural University
Kg	Kilo gram
No.	Number
SD	Standard Deviation
RBD	Randomized Block Design
S. E	Standard Error
%	Per cent
Sl.	Serial
ha	Hectare
<	Less than
>	Greater than
ml	Milli litre

mg	Milli gram
M	Molar
m	Molal
$F_{1,2,3,4}$	Filial generations 1, 2, 3,4
nm	Nano metre
µl	Micro litre
rpm	Revolutions per minute
R	Multiple regression correlation coefficient
R^2	R squared
PCs	Principal components
PCA	Principal component analysis

INTRODUCTION

1. INTRODUCTION

Sesamum (*Sesamum indicum* L.), one of the oldest oil crops, often referred as the 'queen of oilseeds' by virtue of its high-quality oil. It has been under cultivation in Asia for over 5,000 years (Bisht *et al*., 1998). India is very rich in diversity in cultivated sesame. Its domestication started from the wild progenitor *S. malabaricum* in the Indian subcontinent about 5000 years ago (Pathak *et al.*, 2015).

Sesame seeds contain around 50% oil and 18-20% protein. In India, nearly 78% of sesame seed production is directed towards oil extraction, 21.5% for sowing, with the rest used in confectionery and religious ceremonies. About 73% of the oil is utilized for edible purposes, while 8.8% is used in hydrogenation and 4.2% in industrial applications, including paints, pharmaceuticals, and insecticides. Fried sesame seeds are commonly mixed with sugar and enjoyed in various sweets, and sesame oil is an essential cooking ingredient in South India.

According to 2021-22 statistics, sesame cultivation in Kerala covered a total area of 584.76 hectares, yielding 157.8 tonnes. Alappuzha district recorded the highest area and production of sesame in the state. The estimated productivity stands at 270 kg per hectare (Farm Guide 2024). The Onattukara region is traditionally known for its sesame cultivation. However, over the years, farmers have reduced sesame farming due to low yields and insufficient support. In Onattukara, sesame is typically cultivated as a third crop in lowland paddy fields between December and April, and in upland areas from August to December.

Sesame breeding programs primarily aim to improve seed yield, oil quality and quantity, resistance to capsule shattering, seed retention, uniform maturity, and resilience to biotic and abiotic stresses. However, advancements in sesame breeding have been slower compared to crops like groundnut and sunflower. Selection for improved seed yield and yield components remains the key breeding strategy. The main yield-related traits include early and uniform maturity, reduced plant height, higher number of capsules per plant, number of branches per plant, number of seeds per capsule, and heavier 1000-seed weight.

Many investigations reported that the selection in segregating populations within local and exotic populations may give promising results in improving sesame performance. Observed genetic gains in seed yield of sesame were achieved by pedigree selection for two cycles in segregating generations of different populations. An ideal generation to obtain superior transgressive segregants is the F_2 population. The segregation pattern of a cross provides insights on genetic width of the crosses that enables the breeder to identify superior individual plants.

Transgressive segregation refers to appearance of individuals, in the progeny from a hybrid, which exceed either of the two parents of the hybrid with respect to one or more characters. Such plants are produced by accumulation of favourable genes from both the parents as a consequence of segregation and recombination. The occurrence of F_2 or later progenies with phenotypes surpassing the parental range has been described as transgressive segregation by Koide *et al.* (2019). It can provide individuals that exhibit more extreme phenotypes, which might be necessary for achieving significant improvements.

Evaluation of transgressive segregants can lead to the discovery of new genetic variations and traits that were not present in the original parental lines, potentially leading to novel plant varieties with unique characteristics. It can also speed up the process of trait development by providing individuals that already exhibit the desired extreme traits, reducing the time needed to achieve breeding goals.

Handling of the segregating population with wide variation can be challenging to a plant breeder. Identification and selection of the superior genotypes from the population is crucial for achieving notable achievement in the development of a variety. PCA is a dimension reduction method in modern data analysis because it is a simple, nonparametric method for extracting relevant information from confusing data sets. It reduces the dimensionality of the data while retaining most of the variation in the data set. It transforms a number of possibly correlated variables into a smaller number of uncorrelated variables called principal components. PCA facilitates in identifying the most variable principal components which may be given due importance in selecting the genotypes for yield related characters.

Sufficient information to conduct indirect selection for crop improvement strategies is provided by standardised multiple linear regression analysis. It is used for the estimation of relationships between a dependent variable and one or more independent variables. It is an effective way in providing information about the relationship of seed yield and yield components in sesame for indirect selection. This analysis facilitates in deciding minimum number of characteristics, which are effective in improving yield, and will help breeders to handle the number of characteristics in the selection procedure.

The present study entitled “Developing breeding lines of sesame suitable for cultivation in Kerala” was envisaged to evaluate the segregating populations of intervarietal crosses in sesame and to select superior genotypes suitable for cultivation in Kerala.

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

The evaluation of yield potential of a genotype as early as possible after hybridization is defined as early generation selection (Allard, l960). This is more advantageous since the frequency of a superior genotype is greater in early generations than in later ones. Moreover, the selection for quantitatively inherited characters such as yield is not efficient in early generations, mainly attributed to the masking effect of heterosis, the segregation due to heterozygosity and the large environmental influence.

The success of early generation selection depends on a high correlation between the performance of genotypes or families selected in F_2, F_3, or F_4 and the performance of their progeny in later generations. Early generation selection for yield starts in F_2 on a single plant basis and on a family basis as early as F_3. Single plant selection can be attempted because each plants represents a distinct genotype.

A brief review has been made related to development of breeding lines of sesame suitable for cultivation in Kerala is depicted below.

2.1. Genetic parameters

The highest magnitudes of GCV in F_2 generation of sesame was observed for the character number of internodes per plant and the character number of branches per plant recorded the highest magnitudes of GCV in F_3, indicating high amount of variation in number of branches per plant and number of internodes per plant in the above generations (Prasad *et.al,* 2013). High GCV and phenotypic coefficient of variation (PCV) were also noted for seed yield per plant, seed oil content, the number of capsules per plant, plant height, and the number of internodes per plant, suggesting significant variation in these characters in both F_2 and F_3 generations. The differences between GCV and PCV were most notable for the number of branches per plant, followed by the number of internodes per plant and seed yield per plant, indicating environmental influences on these traits. Heritability estimates were high for plant height at harvest (74%) in both generations. Additionally, characters with high heritability and genetic advance showed that simple selection could yield progress in subsequent generations. High heritability and genetic advance were specifically observed for plant height at harvest, the number of internodes per plant, and the number of capsules per plant, implying that these traits are governed by additive gene action, making phenotypic selection effective.

A total of 28 F_2 progenies of sesame were studied for variability, heritability and genetic advance by Bharathi (2019). Highest PCV and GCV were recorded for characters seed yield per plant, number of capsules on secondary branches, number of capsules on primary branches and number of capsules per plant. Moderate PCV and GCV values were recorded for traits like the number of capsules on the main stem, the number of secondary and primary branches, plant height, harvest index, and 1000-seed weight. Traits such as days to 50% flowering, capsule length, days to maturity, and number of seeds per capsule showed low GCV and PCV values. High heritability with high genetic advance as a percent of mean was found in traits like seed yield per plant, the number of capsules on primary branches and total capsules per plant, suggesting these traits are influenced by additive gene action. Moderate heritability with high genetic advance was recorded for the number of capsules on the main stem and secondary branches, while high heritability with moderate genetic advance was observed for plant height, 1000-seed weight, harvest index, and seeds per capsule. High heritability with low genetic advance was observed for days to maturity, and low heritability with low genetic advance was observed for days to 50% flowering.

Bharathi and Reddy (2019) reported that PCV generally exceeded GCV in sesame, indicating environmental influence. Highest GCV and PCV values were recorded for seed yield per plant, the number of capsules on secondary and primary branches, and total capsules per plant. Moderate GCV and PCV values were observed for the number of capsules on the main stem, number of secondary and primary branches, plant height, harvest index, and 1000-seed weight. High heritability was observed for traits like 1000-seed weight, seed yield per plant, days to maturity, plant height, harvest index, the number of capsules on primary branches, and the total number of capsules per plant and seeds per capsule. High heritability coupled with high genetic advance was seen in seed yield per plant, the number of capsules on primary branches and total capsules per plant, supporting the potential for simple selection in these traits. Moderate heritability with high genetic advance was observed for the number of capsules on the main stem and secondary branches, suggesting additive gene action. High heritability with moderate genetic advance was noted for plant height, 1000-seed weight, harvest index, and seeds per capsule, indicating influence from both additive and non-additive gene action. High heritability with low genetic advance was noted for days to maturity, and low heritability with low genetic advance was recorded for days to 50% flowering, suggesting non-additive gene action and limited effectiveness of simple selection.

Evaluation of 24 sesame genotypes was conducted by Manjeet *et.al* (2020) under rainfed conditions to determine the magnitude of variability and to understand the heritable component of variation for 10 agro-morphological characters. Results showed that the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all traits, underscoring environmental influences. High PCV and GCV values were recorded for the harvest index and seed yield per plant, suggesting considerable potential for improvement through hybridization and targeted selection. Broad-sense heritability was high for traits like plant height, the number of branches per plant, the number of seeds per capsule, 1000-seed weight, biological yield per plant, harvest index, and seed yield per plant. The combination of high heritability and genetic advance observed in the number of branches per plant, biological yield per plant, harvest index, and seed yield per plant indicated that these traits are largely influenced by additive genetic effects, suggesting they can be effectively enhanced through phenotypic selection.

In the F_2 population from the OMT 21 A × JLSC 96 sesame cross, Saravanan *et.al* (2020) reported high PCV and GCV values for traits like yield per plant, the number of branches per plant, and the number of capsules per plant. Traits such as the number of branches per plant and 1000-seed weight displayed high heritability along with high genetic advance as a percentage of the mean.

High magnitudes of PCV and GCV were observed for the traits, biological yield per plant, harvest index, productive capsules per plant, oil yield per plant, seed yield per plant, linolenic acid and productive branches per plant by Mohanty *et.al* (2020) in sesame. Traits like stearic acid content, days to first flowering, days to 50% flowering, palmitic acid, oleic acid, linoleic acid and days to maturity showed low PCV values. High heritability coupled with high genetic advance indicating additive gene effects was observed for linoleic acid, oil content, biological yield per plant, productive capsules per plant, harvest index, seed yield per plant, first capsule height, and plant height. Days to maturity and 1000-seed weight exhibited medium heritability estimates.

Phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the characters studied in sesame, indicating the role of environmental variance in the total variance (Kadvani *et.al*, 2020). High GCV and PCV values were found for leaf area per plant, seed yield per plant, and the number of effective branches per plant, while moderate values were recorded for the number of capsules per plant, 1000-seed weight, capsule length per plant, and days to flowering. Low GCV and PCV values were noted for days to maturity and oil content. High heritability paired with high genetic advance as a percentage of mean was observed for leaf area per plant, seed yield per plant, the number of capsules per plant, effective branches per plant, days to flowering, and 1000-seed weight, which are indicative of additive gene action and suggest that selection pressure on these traits could effectively improve them.

A very narrow gap between GCV and PCV indicating very low environmental impact for the traits studied was observed by Hukumchand and Parameshwarappa (2020) in 96 sesame breeding lines. There was a small difference between GCV and PCV for the characters such as days to 50 % flowering, days to maturity, height to first capsule, number of capsules per plant, capsule length, 1000 seed weight, oil content and seed yield per plant, suggesting that the traits were less influenced by the environment and for further advancement selection process can be applied. The PCV and GCV were higher for the trait seed yield per plant, number of capsules per plant and branches per plant indicating significant variability for those traits and are under the genetic control and are less affected by the environment. Days to 50 % flowering, days to maturity, 1000 seed weight and oil content traits exhibited low GCV and PCV. The study also showed high broad sense heritability for traits such as height to first capsule, capsules per plant, 1000 seed weight and seed yield per plant. The traits such as days to 50 per cent flowering, days to maturity, plant height, branches per plant and capsule length were having moderate heritability values while oil content had low heritability value.

Low heritability with low genetic advance as percent of mean was recorded for the characters, days to maturity and capsule length which indicates the presence of non-additive gene action and hence selection would be ineffective for these traits as reported by Kumari *et.al*, (2020) in sesame.

Takele *et.al* (2020) observed that, among 49 genotypes of sesame studied, branches per plant, capsule per plant, biomass yield, harvest index, thousand seed weight and bacterial blight severity showed medium PCV and GCV. Seed yield, biomass yield, capsule per plant, bacterial blight severity and branches per plant showed moderately high heritability with high genetic advance. While, thousand seed weight showed high heritability with moderate genetic advance. Harvest index showed medium heritability and genetic advance.

Twenty-seven sesame breeding lines along with three checks were evaluated by (Vamshi *et.al*, 2021) for twelve different traits viz., days to 50% flowering, days to maturity, number of primary branches per plant, number of capsules per plant, capsule length, capsule width, plant height, harvest index, test weight, seed weight per capsule, oil content and seed yield. Analysis of variance (ANOVA) indicated significant variation among the genotypes for all the characters except for capsule width indicating the presence of substantial amount of variability for selection. High variation was observed for plant height, number of primary branches per plant, number of capsules per plant and seed yield per plot. The GCV for all the characters studied were lesser than the PCV indicating the influence of environment on expression of these traits. High heritability with high genetic advance was observed for plant height, number of primary branches per plant, number of capsules per plant, harvest index, oil content and seed yield per plot indicating additive gene action in the expression of these traits. Simple phenotypic selection may be effective for improving these characters. High heritability coupled with low genetic advance was observed for oil content suggesting involvement of non-additive gene action in the expression of this trait indicating limited scope for further improvement through simple selection.

Sheoran *et.al* (2022) studied genetic variability in 60 sesame accessions. Phenotypic coefficient of variation (PCV) was found to be greater than the genotypic coefficient of variation (GCV) for all the characters studied, which reflected the role of environment in the expression of the observed traits. High PCV & GCV estimates were observed for number of primary and secondary branches per plant, number of capsules per plant, number of seeds per capsule and seed yield per plant. These results suggested that there is considerable possibility of further improvement for these characters through hybridization and phenotypic selection.

High heritability was recorded for all the traits under experiment while genetic advance as percentage of mean recorded low for traits days to flower initiation, days to 50% flowering and days to maturity in sesame (Ranjithkumar *et.al*, 2022). The magnitude of genetic advance was medium for traits oil content (%), plant height and number of seeds per capsule, whereas traits capsule length, number of capsules per plant, thousand seed weight, number of primary branches per plant, seed yield per plant and number of secondary branches per plant recorded high magnitudes.

Roy *et.al* (2022) observed high genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) for number of branches per plant and number of capsules per plant in sesame. A predominant role of additive genetic components for their expression was suggested by the estimates of high heritability coupled with high genetic advance against seed yield per plant, number of branches per plant and capsules per plant indicating better scope for utilization of direct selection for those traits.

Thirty white seeded sesame genotypes were evaluated in a Randomized Block Design (RBD) to determine genetic variability, heritability and genetic advance for twelve biometric and quality characters by Thouseem (2022). The analysis of variance indicated significant variability among the germplasm for the traits examined. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) across all traits, with the highest GCV and PCV observed for seed yield per plant, followed by primary branches per plant, number of capsule leaves per axil, and number of capsules per plant. Most traits showed high heritability, except days to maturity, which exhibited moderate heritability (49.48%). All traits except 1000-seed weight, days to 50% flowering, capsule length, protein content, oil content, and days to maturity had high genetic advance as a percentage of the mean. Seed yield per plant, number of capsule leaves per axil, number of capsules per plant, primary branches per plant, number of seeds per capsule, and plant height showed both high heritability and high genetic advance, suggesting that these traits are largely influenced by additive gene effects, making selection effective.

Analysis of genetic variability for seed yield component traits in 20 sesame (Sesamum indicum L.) revealed significant genotypic variation for all traits (Patel *et.al*, 2023). Among the traits studied, plant height exhibited the highest variability with range of 83.13 to 108.40 cm, while test weight had the least variability having range of 3.00 to 3.51 g. Higher PCV compared to GCV across traits highlighted environmental influences. Seed yield per plant exhibited the highest GCV and PCV (20.32% and 24.07%, respectively), while days to maturity had the lowest (2.07% and 3.15%, respectively). High heritability was observed for capsules per plant, seeds per capsule, biological yield per plant, and seed yield per plant, with genetic gains of 33.46%, 21.29%, 26.19%, and 35.35%, respectively, indicating that these traits are ideal for selection in breeding programs.

Varada (2023) reported that PCV ranged from 5.604% for mean capsule width to 78.672% for number of secondary branches. GCV followed a similar trend as that of PCV, indicating less influence of environmental variation. High GCV (57.295%) was noted for secondary branches, followed by yield (31.149%) and primary branches (30.221%). High heritability paired with high genetic advance was observed for traits including nodes to first flower, primary branches, capsules per plant, capsule length, seeds per capsule, 1000-seed weight, seed yield per plant, oil content, and phenol content. These findings suggest additive genetic effects and make these traits suitable for selection.

Takele and Abera (2023) evaluated genetic variability and trait association of yield and yield related traits of sesame in 5x5 simple lattice design. The analysis of variance showed highly significant differences ($P<0.01$) among the genotypes for all quantitative traits except days to maturity and biomass yield per hectare. Traits like days to flowering, plant height, and capsule length had low PCV, GCV, and genetic advance as a percentage of mean. Branches per plant showed moderate values for PCV, GCV, heritability, and genetic advance. Seed yield per plant, capsule per plant, and seed yield per hectare showed moderate PCV and GCV but high heritability and genetic advance. Traits like biomass yield per plant and harvest index had high values for PCV, GCV, heritability, and genetic advance, indicating their suitability for selection.

Sixty-four sesame genotypes consisting of fifty-nine accessions and five varieties were assessed in order to evaluate sesame genotypes for yield and yield-related traits

(Gedifew, 2023). Analysis of variance revealed significant differences among genotypes (P<0.05) for most traits except internode length and seed shattering. The accession ASARC-ACC-SG-013 had the highest yield, while GK-012 (2) had the highest oil content (60.09%), and 1000-seed weight ranged from 2.00 to 2.75 g. High coefficients of variation for primary branches per plant, number of capsules on the main stem, and total capsules per plant indicated considerable genetic variability. High heritability and genetic advance were noted for plant height to the first branch, capsule length, primary branches per plant, capsules on the main stem, and total capsules per plant, suggesting that these traits are reliable for phenotypic selection.

Rahna *et.al* (2023) reported that number of primary branches, number of capsules per plant and single plant yield were the traits having high PCV and GCV along with high heritability and genetic advance as percent of mean in sesame. These findings suggest considerable variation for these traits among the germplasms and are strongly influenced by genetic factors, making them suitable candidates for effective selection strategies.

In a study on sesame, Sala and Vadivel (2023) observed significant differences among genotypes for traits like days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, number of seeds per capsule, and yield per plant, indicating substantial genetic variability within the population. The traits of branches per plant, capsules per plant, and capsule width showed high genotypic and phenotypic coefficients of variation (GCV and PCV), suggesting their potential for effective selection. The number of seeds per capsule showed moderate GCV and PCV, while days to 50% flowering and days to maturity had low GCV and PCV values. High heritability and genetic advance were observed for seeds per capsule and 1000-seed weight, indicating that these traits are less affected by environmental factors and controlled by additive genetic effects. Moderate heritability and genetic advance were recorded for plant height and capsule length, while days to maturity showed low heritability and genetic advance. Traits like seeds per capsule and 1000-seed weight, with high heritability and genetic advance as a percentage of the mean, are promising for selection to improve yield.

Kumari and Kumhar (2023) observed the maximum magnitudes of phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) for number of primary branches per plant, number of capsules per plant and capsule bearing length (cm). High heritability was recorded for primary branches per plant, days to 50% flowering, seed yield per plant and days to maturity. Traits such as primary branches per plant and seed yield per plant displayed high heritability combined with high genetic advance (5% of the mean), suggesting additive genetic control, making these traits suitable for selection.

In seventeen genotypes of sesame, by assessing nine growths and yield parameters, the number of branches, the height of the first capsules, the number of capsules per plant, and the weight of 1000 seeds all showed a highly significant difference (Idris *et.al*, 2023). No significant differences were found for plant height and days to 50% flowering ($p \geq 0.05$). Traits like number of capsules per plant and seed weight exhibited the greatest genotypic and phenotypic variance, with the highest heritability value seen in 1000-seed weight, while plant height had the lowest. Among the genotypes, Highland produced the highest yield (0.2506 tons/ha). Seed yield (tons/ha) was strongly correlated with seed yield per plant, capsule number per plant, and stem diameter, though there was an inverse, non-significant relationship between height to first capsule and days to flowering.

A field investigation was carried out to study the genetic variations of seventeen yield and yield contributing traits in 36 genotypes of sesame (Kumari *et.al*, 2023). The analysis of variance revealed significant differences among the genotypes for all the studied characters. Phenotypic variances exceeded genotypic variances, with five traits showing high variability suitable for genetic improvement via direct selection. High PCV and GCV values were recorded for seven traits, while five traits showed moderate values. Traits like plant height, stem height to the first branch, capsules per plant, 1000-seed weight, stover yield, biological yield, and protein content exhibited high heritability and genetic advance, indicating minimal environmental influence and predominantly additive genetic control.

Thiyagu *et.al* (2023) assessed genetic parameters such as PCV, GCV, heritability, and genetic advance in 104 F_4 families derived from a cross between OCT 15 and Thirukkattupalli local for yield-related traits, including days to 50% flowering, days to maturity, plant height, number of branches, capsules per plant, seeds per capsule, and 1000-seed weight. Traits like days to 50% flowering and maturity had low PCV and GCV, while plant height and seeds per capsule showed moderate values. Higher PCV and GCV were observed for branches per plant, capsules per plant, 1000-seed weight, and seed yield, all displaying high heritability. Moderate genetic advance was found in days to flowering and maturity, while other traits showed high genetic advance. Traits with high heritability and genetic advance, such as plant height, branches per plant, 1000-seed weight, and seed yield, appear to be influenced by additive genes, making selection effective in stabilizing these traits.

The PCV and GCV levels had very close relationship and higher heritability was observed for the traits like number of capsules, seeds per capsules, 1000 seed weight and seed yield in sesame under rice fallow by Dhandapani *et.al* (2023). Yield responses under rice fallow were very narrow and only few varieties responded to the rice fallow conditions, suggesting strong inherent limitations to adaptation.

High genetic variation was observed for most of the characters studied in sesame were reported by Parvathy (2023). The PCV exceeded the GCV for all characters, highlighting environmental influence. Low variation was found in traits such as days to maturity, capsule length, and days to 50% flowering, suggesting limited potential for improvement through selection. Traits like number of primary branches, capsules per plant, seeds per capsule, plant height, 100-seed weight, seed yield per plant, crude protein content, and oil content showed high heritability. Traits with both high heritability and genetic advance were number of primary branches, capsules per plant, seeds per capsule, 100-seed weight, crude protein and seed yield per plant indicated a strong role of additive genes, supporting direct selection. Traits such as days to flowering initiation, days to 50% flowering, days to maturity, and capsule length had low heritability and genetic advance, indicating high environmental influence. Traits like plant height and oil content showed high heritability but low genetic advance, suggesting non-additive genetic action, where environmental factors rather than genotype drive high heritability. The trait number of secondary branches showed moderate heritability and high genetic advance, while dry pod weight showed moderate heritability and low genetic advance.

Patil (2023) reported high genotypic and phenotypic coefficient variation for traits such as the number of secondary branches per plant, yield per plant (g) and seed yield (Kg/ha) in thirty-four advanced sesame breeding lines. The highest heritability coupled with the greatest genetic advance over the mean was detected for the number of primary branches per plant, suggesting a predominant role of additive genetic components in their expression and indicating a promising avenue for direct selection. The study also developed 31 selection indices through discriminant function analysis, combining traits such as seed yield per plant, days to maturity, productive capsules per plant, 1000-seed weight, and oil content. The index that included all component traits provided the highest expected genetic advance and efficiency.

A study conducted on 30 sesame genotypes recorded larger mean variance range for characteristics such as plant height, number of seeds per capsule, seed output per plant, days to 50% flowering, number of capsules per plant, and 1000 seed weight (Mitkari *et.al*, 2023). High heritability of 80.02% and a genetic advance of 20.55% were noted for seed yield, and traits such as plant height, branches per plant, capsules per plant, and seed output demonstrated high heritability and genetic advance.

Tabrizi (2024) assessed 14 advanced sesame lines and recorded traits like days to flowering, growth period, plant height, capsules per plant, capsule length, 1000-seed weight, seed yield, and oil yield. The PCV and GCV values were moderate for capsules per plant, seed yield, and oil yield, and low for other traits. Moderate heritability and high genetic advance were observed in capsules per plant, seed yield, and oil yield, while phenological traits like days to flowering and growth period had low heritability and genetic advance, suggesting a breeding focus on capsules per plant and yield traits.

Ibrahim and Tahmasbe (2024) noted high heritability for all traits in sesame cultivars except for days to maturity, which had moderate heritability. High general averages were seen in all traits except for 1000-seed weight, days to 50% flowering, capsule length, protein content, oil content, and days to maturity.

The phenotypic variance and phenotype coefficient of variation were relatively higher than the respective genotypic variance and genotypic coefficient of variation for all the characters studied in sesame (Islam *et.al*, 2024). High heritability and genetic advance as a percentage of mean were noted for secondary branches per plant (90.1%), 1000-seed weight (99.31%), and seed yield per plant (97.9%), with moderate heritability observed for days to 50% flowering (59.81%).

The phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation for all the traits (Akkiligunta *et.al*, 2024). High levels of GCV and PCV were observed for seed yield per plant, the number of capsules per plant, and plant height. Heritability was notably high for traits such as seed yield per plant, 1000-seed weight, seeds per capsule, capsules per plant, plant height, days to maturity, and oil content. Genetic advance as a percentage of the mean (GA) was high across all traits, except for days to 50% flowering and days to maturity. Traits like seed yield per plant, 1000-seed weight, seeds per capsule, capsules per plant, plant height, and oil content showed high heritability combined with high genetic advance, suggesting strong additive genetic control.

Durodola *et.al* (2024) recorded high broad-sense heritability and genetic gain for traits such as secondary branches (97.8%; 719.4%), primary branches (96.1%; 142.5%), capsules per plant (97.8%; 141.1%), single plant seed yield (86.87%; 46.03%), capsule length (99.16%; 32%), and 500-seed weight (95.15%; 34.12%). Traits like branching, capsules per plant, capsule length, and seed yield per plant hold promise for selection in breeding programs targeting superior genotypes.

The genetic variability for agronomic characters in the interspecific population developed by hybridization between *Sesamum indicum* (Swetha til) x *Sesamum mulayanum* (IC-43144-1) was studied by Ramya *et.al* (2024). High PCV and GCV were found in total capsules per plant, harvest index and seed yield per plant, supporting selection-based improvement. Traits such as days to emergence, plant height, primary branches, total capsules, harvest index, and seed yield per plant had high heritability and genetic advance, indicating additive genetic effects, suggesting that simple phenotypic selection would be effective for enhancing these traits in breeding programs for interspecific hybrids.

Khuntia *et.al* (2024) reported that the phenotypic coefficient of variation values was generally higher than the genotypic coefficient of variation values for all traits, suggesting that environmental factors contributed to the observed variation along with genetic factors in field conditions. High heritability combined with high genetic advance as a percentage of the mean was observed for traits such as the number of capsules per plant, branches per plant, seed yield per plant, internode length, plant height, and 1000-seed weight, indicating the influence of additive gene action and underscoring these traits as valuable for effective selection.

An experiment was carried out to estimate the heritability and genetic advance in mutant populations of sesame (*Sesamum indicum* L.) with regard to yield and its components by Sarang *et.al* (2024). In the GT-10 cultivar, seed yield per plant displayed the highest GCV, followed by branches per plant. The highest PCV values were recorded for seed yield per plant, followed by branches per plant, capsules per plant, and seeds per capsule. For cultivar TKG-22, high GCV was observed for seed yield per plant, followed by capsules per plant, while the highest PCV values were also noted for seed yield per plant, followed by capsules per plant, branches per plant, and seeds per capsule. In the Gophya Local cultivar, a moderate GCV was observed for capsules per plant, followed by seed yield per plant and seeds per capsule, whereas high PCV was noted for capsules per plant and seed yield per plant. In GT-10, traits such as seed yield per plant, branches per plant, capsule length, and seeds per capsule showed high heritability with significant genetic advance as a percentage of the mean. Similarly, in TKG-22, seed yield per plant and capsules per plant exhibited high heritability along with substantial genetic advance as a percentage of the mean, indicating additive gene action and suggesting that phenotypic selection for these traits would be effective in future breeding programs.

Aye *et.al* (2024) reported high heritability values for traits such as days to 50% flowering, days to maturity, height of the first capsule bearing node, primary branches per plant, capsule length, capsule width, seeds per capsule and 1000-seed weight across 54 sesame genotypes. Moderate heritability values were noted for plant height, capsules per plant, and seed yield per plant.

2.2. Correlation analysis

The study conducted by Saravanan *et.al* (2020) for evaluation of the F_2 population of sesame showed a high significant positive correlation of yield per plant with the number of capsules per plant followed by 1000 seed weight, plant height and the number of branches per plant which indicated that these characters were vital yield components. A negative correlation was observed between days to first flowering and yield per plant, with days to first flowering also showing a strong negative association with the number of capsules per plant.

In an evaluation of four sesame lines and six testers using a line × tester mating design, Disowja *et.al* (2020) found that yield per plant showed a significant positive association with the number of capsules per plant, the height at which the first capsule forms, plant height, and 1000-seed weight, at both genotypic and phenotypic levels. Additionally, 1000-seed weight had a significant positive correlation with capsule length at both levels, and a significant negative association with days to reach 50% flowering at the genotypic level.

According to Kiruthika *et.al* (2020), traits such as days to 50% flowering, days to maturity, the number of primary and secondary branches per plant, top petiole length, capsule length, capsule width, and seed weight are significant contributors to yield, as they are correlated with individual plant yield and oil content. This suggests that selecting plants with shorter capsule lengths and higher seed weights could enhance overall seed yield.

In a study involving 24 sesame hybrids, it was found that yield per plant had a positive and significant correlation with factors such as the height to the first capsule, overall plant height, the number of capsules per plant, and thousand seed weight (Disowja *et.al*, 2020). The number of capsules per plant showed a strong positive correlation, both genotypically and phenotypically, with yield per plant. Conversely, days to maturity demonstrated a negative relationship with yield per plant.

Seed yield per plant exhibited significant positive correlations with thousand seed weight, the number of seeds per capsule, and the number of capsules per plant, while showing a significant negative correlation with days to maturity at both genotypic and phenotypic levels in sesame (Bhattacharjee *et.al*, 2021). This indicates that seed production is primarily influenced by these traits, whereas early maturity is linked to the timing of flowering.

Vivek *et.al* (2022) reported significant and high positive correlation value for number of productive branches, number of capsules per plant, number of seeds per capsule and days to maturity with seed yield per plant in sesame.

Thirty-three sesame genotypes including three checks were grown in Randomized Block Design in three replications for evaluation of yield and yield attributing traits by Kumar *et.al*, (2022). Correlation exhibited significant and high positive for number of productive branches, number of capsules per plant, number of seeds per capsule and days to maturity with seed yield.

Patel *et.al* (2022) reported that in 45 sesame genotypes, the characters days to 50% flowering, plant height, branches per plant, capsules per plant, seeds per capsule, test weight, harvest index and oil content showed significant and positive association with seed yield per plant. Therefore, selection for these characters may be useful in increasing seed yield in sesame.

The extent of genetic variation and its relationship to yield and 19 yield components of sesame was studied by Hassen (2022) and correlation analysis revealed that the length of capsule bearing zone and first capsule, capsule per main axis, number of capsules per plant, harvest index and oil content were all related to seed yield in a positive and significant association.

Pratyusha *et.al* (2022) reported that in a study of 38 genotypes of sesame, correlation coefficient exhibited significant and high positive correlation for number of productive branches, number of capsules per plant, number of seeds per capsule and days to maturity.

A study was conducted to evaluate genetic variability and trait association of yield and yield related traits of sesame in 5x5 simple lattice design by Takele and Abera (2023). Both phenotypic and genotypic correlation coefficient analyses showed positive and significant association of seed yield with seed yield per plant and harvest index.

Mahdy *et.al* (2023) reported that in a base population of sesame consisted of 185 families at the F_3-generation. Number of capsules per plant gave sizeable genotypic (0.52) and phenotypic (0.49) correlations with seed yield per plant. Broad sense heritability was very high ranged from 0.79 to 1. Tall plants had a higher number of capsules per plant, which showed strong genotypic (0.52) and phenotypic (0.49) correlations with seed yield per plant. Selection for early flowering was more effective when guided by seed yield per plant. The most significant enhancement in seed yield per plant from the mid-parent was observed when selection for oil content was restricted by seed yield per plant, followed by selection for 1000-seed weight and early flowering when restricted by seed yield per plant.

Thiyagu *et.al* (2023) evaluated 104 F_4 families of the cross OCT 15 X Thirukkattupalli local for seed yield and attributing traits viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, number of seeds per capsules, and 1000-seed weight. Days to maturity and plant height were recorded positive and significant correlation with seed yield. Number of seeds per capsule had a negative correlation with seed yield.

Kumari and Shah (2023) reported that in 36 diverse genotypes of sesame, correlation studies indicated that seed yield per plant was significantly and positively associated with traits, i.e. plant height, internodal length, number of capsules per plant, number of branches per plant, stover yield per plant and harvest index both at genotypic and phenotypic levels which indicate the importance of these traits in selection for enhancing the seed yield.

By examining the relationships between seed yield and yield-attributing characters in sesame, Madhu *et.al* (2023) revealed that that number of capsules per plant (0.806) and 1000-seed weight (0.657) showed positive correlation with seed yield per plant. The study also revealed that the traits viz., number of capsules per plant and 1000 seed weight association was highly desirable as the improvement in any of the yield components results into overall increase in seed yield. Selection among genotypes based on this analysis can be made for further improvement in seed yield per plant and its contributing characters.

Varada (2023) observed that seed yield per plant had highly significant positive correlation with number of capsules per plant, 1000 seed weight and oil content. Highly significant negative correlation was observed for number of nodes to first flower and number of primary branches with seed yield per plant. Significant negative association was also unveiled between phenol, plant height and seed yield per plant.

Highly significant positive correlation was observed for days to flowering, days to 50% flowering, number of capsules per plant, number of seeds per capsule, dry pod weight and 100 seed weight with seed yield per plant in sesame as reported by Parvathy (2023). It shows that these are vital yield contributing characters. The results clearly indicate that the increase in 100 seed weight, dry pod weight and number of capsules per plant will increase seed yield. This suggests that more emphasis should be given for these characters while selecting for yield improvement.

A field experiment was conducted with forty-three sesame genotypes and it was revealed that there was a significant variation among the genotypes for the traits studied (Islam, 2024). The significant positive correlation with seed yield per plant was found for plant height, days to 50% flowering, days to 80% maturity, number of primary branches, number of capsules per plant, number of seed per capsule, height of first capsule and 1000 seed weight.

Tabrizi (2024) reported a strong positive correlation of capsule number is observed with seed yield and oil yield, which could reach maximum efficiency, with which it provided the high-yielding genotypes that were needed for its breeding program.

The correlation coefficient analysis revealed that seed yield per plant had a significant positive correlation with plant height, days to 50% flowering, days to 80% maturity, number of primary branches per plant, number of capsules per plant, number of seeds per capsule, height of the first capsule, and 1000-seed weight as reported by Islam *et.al* (2024).

Khuntia *et.al* (2024) identified traits like 1000-seed weight, capsule width, number of capsules per plant and capsule length as the key components for exercising meaningful selection in sesame through correlation studies in twenty sesame genotypes.

Correlation analysis using 369 sesame core accessions under five environments by Wang *et.al* (2024) suggested that seven yield-related traits, including capsule number per plant, capsule stem length, thousand-seed weight, plant height, initial flowering stage and were the key factors associated with seed yield in sesame ($P < 0.01$).

The number of primary branches per plant, number of capsules per plant and number of seeds per capsule were reported to be strongly correlated with seed yield per plant by Aye *et.al* (2024) in 54 sesame genotypes.

Evaluation of genetic diversity and character association of sesame revealed that seed yield per plant was positively correlated with the capsules per plant, biological yield per plant and harvest index, while negative correlation was observed with days to 50% flowering and days to maturity (Patel *et.al*, 2024).

2.3. Principal Component Analysis

PCA is a dimension reduction method in modern data analysis because it is a simple, nonparametric method for extracting relevant information from confusing data sets. It reduces the dimensionality of the data while retaining most of the variation in the data set.

Tripathi *et.al* (2013) evaluated hundred sesame accessions collected from diverse ecologies of India to study principal components analysis and showed association in PC1 with days to 50% flowering and number of secondary branches per plant; PC2 with plant height and days to maturity; PC3 with capsule length and PC4 with seed yield per plant. Thus, re-structuring plant type with early flowering, more number of secondary branches per plant, plant height and capsule length would obviously generate plants with high seed yield.

Ismaila and Usman (2014) evaluated thirteen sesame genotypes to study principal components analysis of the genotypes across the three locations and revealed that the first three PCs (PC1 to PC3) gave Eigen-values > 1.0 and cumulative variation accounted for 73.86%. PC1 accounting for 33.15% of the total variation, while PC2 responsible for 27.02% and PC3 contributing 13.69%. The variation in PC1 was mainly associated with height at maturity, capsule length and weight of seeds per capsule. PC2 variation was associated with yield per hectare, number of capsules per plant and number of branches per plant, in PC3 the contributing attributes were days to 50% flowering and 1000 seed weight. This indicates a high degree of variation for these characters among the first three PCs.

A study was carried out at three locations of Northern Ethiopia and thirteen sesame genotypes were evaluated by Baraki *et.al* (2015). Eight Principal Components (PCs) were extracted from the eight agronomic traits of sesame and the first three PCs accounted for 88.49% of the total variance (45.05, 28.25 and 15.20% for PC1, PC2 and PC3, respectively). These three PCs were considered as significant.

Shim *et.al* (2016) evaluated 250 sesame germplasm accessions and classified the germplasm based on variation in morphological traits using principal component (PC). The sesame germplasm was grouped based 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. They constructed a scatter diagram of the first two PCs (PC1 vs. PC2), revealing four distinct groups of eigen vectors.

Aristya *et.al* (2017) evaluated eighteen sesame mutant lines for eleven quantitative traits. Principal component analysis after varimax rotation method in sesame mutant lines was carried out. Factor loadings (greater than 0.5) were considered important for interpretation of data. Factor 1 was strongly associated with number of primary branches, number of secondary branches, number of capsules per plant, biomass yield per plant and seed yield per plant. These variables had positive values and indicates the direction of the relationship between the factor and the variable in factor 1. Factor 2 consisted of plant height, stem height from base to first branch, stem height from base to first capsule and are associated with quantitative traits. All these variables had positive loadings. These types of traits might be influenced by the same gene or genes and therefore could be beneficial for suitable sesame lines screening. Factor 3 was strongly associated with number of nodes per plant. Factor 4 was strongly associated with number of nodes to first flower and 1000-seed weight. Four principal component axes were required to provide a useful separation of the lines and these traits would be effective for the identification of best sesame mutant lines.

Ozcinar and Sogut (2017) evaluated 107 diverse sesame accessions collected from Mediterranean, Aegean and Southeastern Anatolia of Turkey. Principal component analysis (PCA) revealed that 25% or more of the total variation might be explained by the first two or three-axis. The number of seeds per capsule contributed highest towards the divergence followed by number of capsules per plant. Seed yield, number of capsules per plant, plant height and 1000 seed weight are the important contributing factors. There was a positive relationship between number of seeds per capsule, capsule number per plant and seed yield per plant. This study showed a positive relationship between plant height, number of branches and seed production.

Tanwar and Bisen (2017) conducted a study to identify the minimum number of components, which can explain maximum variability out of the total variability and also to rank 96 sesame germplasm on the basis of PC scores using Principal Component Analysis (PCA). Out of them, only nine principal components (PCs) exhibited more than 0.5 eigen value and showed 95.19% total variability among the characters. These nine PCs were given due importance for further explanation. Rotated component matrix revealed that the PC1, which accounted for the highest variability was mostly related to yield related traits like plant height, number of capsules per plant, number of primary branches per plant and seed yield per plant. PC2 was also dominated by yield related traits like number of secondary branches per plant, 1000 seed weight and capsule length. PC3 was dominated by physiological and quality related traits like days to maturity and oil content. While, PC4 was more related to physiological traits like days to 50% flowering. On the basis of Principal Component Analysis, 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.

Sensory evaluation of thirty-five sesame pastes in the market was carried out by Wang *et.al* (2017). Their chemical components including crude fat, crude protein, crude fiber, sterolin, calcium, and phosphorus contents were determined as well. Principal component analysis (PCA) was used for comprehensive assessment. A comprehensive score for each sample was obtained by PCA and sensory evaluation. The results showed that color and texture had significant effects on sensory scores for both white and black sesame pastes. In general, white sesame paste had higher sensory scores than black sesame paste. The chemical components of sesame pastes showed different degrees of variation. While water content and acid value showed bigger degrees of variation, the variations in crude fat and crude protein contents were smaller. The first six principal components identified based on PCA were mineral, lignan, crude protein, acid value and sterol, accounting for 75.33% of the total variability. The ranking orders of comprehensive scores of the principal components and sensory evaluation were basically consistent. Out of 35 samples tested, six (17.14%) were unqualified mainly in terms of acid value, water content and oil content.

The genetic divergence available in the sesame germplasm was evaluated using seventy-five sesame genotypes based on the Mahalanobis distance and cluster analysis by Singh *et.al* (2018). PCA yielded twelve PCs from the twelve agronomic traits of sesame out of which seven PCs showing about 83.193% variability. Results revealed that the genotypes *viz.*, S-0644, KMS-5361, T-1-A, NIC-16214, SI-1125, NIC-8080-A have highest PC values for characters number of capsules per plant, number of seeds per capsule, number of primary branches per plant, number of secondary branches per plant, 1000 seed weight and seed yield per plant.

Dash *et.al* (2020) conducted principal component analysis in sesame to identify important characters in order to explain their differences for further use in cultivar development program. The study revealed that the first three principal components accounted for 65.93% of total variations. Among the nine morphological traits, seed yield per plant, branches per plant, capsules per plant and plant height were the greatest contributors to variability. Based on the study it was suggested that due weightage should be given to these four characters when designing a hybridization program.

Baraki *et.al* (2020) grouped sesame genotypes in to four clusters and cluster-II was characterized as the high yielding cluster and it was also associated with grain yield, pods per plant, branches per plant and thousand seed weight. Branches per plant, pods per plant and thousand seed weight may be the most crucial determinants in developing high yielding sesame varieties. This finding recommends that G4 and G6 are desirable genotypes and can be used for irrigation production.

Gupta *et.al* (2021) reported that in a study with sesame genotypes, only the first 3 PCs showed Eigen values more than one, and they cumulatively explained 67.48% variability. The first PC explained 35.29 per cent of the total variation, and the remaining 2 PCs explained 18.96 and 13.23 per cent variation, respectively. It revealed that the first principal component (PC1) which accounted for the highest variation (35.29%) was mostly related traits are seed yield per plant, capsules bearing length and seeds per capsule. The second principal component (PC2) was dominated by traits *viz.*, days to maturity, number of primary branches per plant and 1000-seed weight while, PC3 consisted mainly of plant height and harvest index. These studies also suggest that it was possible to reduce large number of variables into only three principal factors and identify different lines better for different combinations of characters. Hence, indirect selection for seed yield based on component traits may lead to create better genetic recombinants for improving yield and yield attributing characters in sesame.

The analysis of principal components revealed that the first three principal components had eigenvalues more than one and accounts for most of the variability among the sesame population (Sasipriya *et.al,* 2022). The first component (PC1) had the highest eigenvalue (3.796) contributing about 47.46% of the total variance. The PC2 had an eigenvalue of 1.418 contributing 17.73% towards the variability and PC3 had an eigenvalue of 1.024, with 12.80% of the variability. The three major principal components explained 78.00% of the total variability of the population. From the data of individual trait scores, it was clear that test weight (0.471), the number of seeds per pod (0.457) and seed yield per plant (0.383) were positively influenced by the first principal component. The second principal component had a negative impact on traits such as seed yield, test weight and number of pods per plant. Plant height, pod length and number of branches per plant were the traits with a relatively higher contribution towards the second principal component. The third component had a negative influence on most of the characters especially the days to fifty per cent flowering and seed yield per plant. Pod length was the trait which was largely and positively influenced by principal component 3. The fourth principal component with eigenvalue 0.718 and a relative contribution of 8.98% of variability can also be considered informative. The component had a positive influence on pod length (0.692) and a strong negative influence.

A total of 55 sesame genotypes were evaluated for 16 quantitative traits related to seed yield and were subjected to principal component analysis (PCA) and cluster analysis (Durge *et.al*, 2022). The results showed that seed yield had a high positive correlation with the number of capsules per plant and a high negative correlation with days to maturity. The PCA revealed six components contributing to the total variance, which were components 1 (plant height, the number of primary branches, leaf length and leaf width), 2 (seed yield per plant and thousand seed weight in the positive direction and days to maturity in the negative direction), 3 (days to flower initiation and days to 50 per cent flowering), 4 (capsule width and seeds per capsule), 5 (the number of capsules per plant) and 6 (the number of seeds per capsule) in the order of importance. Cluster analysis showed five clusters of genotypes in accordance with the phenotypic traits. Overall results indicated that the number of capsules per plant, the number of seeds per capsule and thousand seed weights were the most critical traits for selecting high yielding genotypes in sesame.

In the summer season 2021, 328 sesame genotypes were evaluated with augmented block design by Bisen *et.al* (2023). All the twelve quantitative traits taken into consideration had significant variability. On the basis of PCA, 5 PCs obtained more than one eigen value. Overall results revealed that traits and genotypes studied have a considerable level of variability which can be exploited in future breeding programmes.

Hassan and Endale (2023) reported that PCA1 represented the most important variation in the data and PCA2 represented the second most variation in the data in a study with sesame genotypes. Seed yield in kilogram per hectare strongly contributed in dimension one (PCA1) followed by thousand seed weight and numbers of pods per plant, and positively associated for each other. Although plant height had a weak effect on PCA2, days to maturity strongly contributed to PCA2 and were negatively correlated with others, indicating that as the days to maturity increased, the yield and yield components decreased due to a short rainy season. Therefore, early maturing material is used to avoid the short rainy season of the region.

Principal component analysis (PCA) was applied to evaluate the grouping nature of the 93 sesame seed samples, the concentrations of 10 mineral elements in sesame by Hika *et.al* (2023). The results revealed significant differences by ANOVA test which were subjected to PCA. The dataset was Pareto scaled before the construction of the PCA model. Then from the PCA result, three principal components (PCs) with eigenvalues exceeding one were extracted, which accounted for 70 % (PC1, 34 %, PC2, 27 % and PC3 9 %) of the total variance. All the 10 elements employed were loaded on the three components (PC1, PC2 and PC3).

Mukthambica *et.al* (2023) conducted a study using seventy genotypes of sesame based on yield and its contributing traits and also using Principal Component Analysis. On the basis of Principal component analysis, out of fourteen components, only 4 principal components (PCs) exhibited more than 1.00 Eigen value and showed about 68.6 % variability among the traits studied. The PC1 had the highest variability (38.3%) followed by PC2 (12.2%), PC3 (10.2%) and PC4 (7.9%) for traits under study. Rotated component matrix revealed that the first principal component (PC1) was mostly related with traits such as days to 50% flowering, days to maturity, length to first capsule, plant height, secondary branches per plant and seed yield per plant. The second principal component (PC2) was related to the traits *viz.*, capsule number per plant, number of leaf axils in main stem, capsule length, test weight and oil content while PC3 was consisting of traits *viz.*, days to emergence and days to flower session. Fourth principal component was related to primary branches per plant. The genotypes like, Paiyur, VRI-3, TMV-6, TMV-3, DS-5, PKDS-8, Rajeshwari and JLT-408 were identified as putative genotypes and length to first capsule, plant height, primary branches per plant, secondary branches per plant and seed yield per plant are identified as main yield attributes.

Research conducted over 96 exotic sesame accessions with five checks, to identify the minimum number of components, using Principal Component Analysis (PCA) revealed that among the studied traits, Component 1 had the contribution from the traits *viz.*, number of primary branches per plant, number of capsules per plant, number of seeds per capsule, oil content and seed yield/plant, which accounted 30.71% to the total variability (Sonaniya *et.al*, 2023). Days to flower initiation and days to 50% flowering had contributed 17.11% to the total variability in component 2. The remaining variabilities of 11.26%, 9.94%, 7.48% and 6.73% were consolidated in PC3, PC4, PC5 and PC6 respectively by various traits like number of secondary branches per plant, capsule length, days to maturity, thousand seed weight and plant height. The cumulative variance of 83.23% of total variation among 12 characters was explained by the first six axes.

2.4. Regression Analysis

Standardized multiple linear regression analysis provides sufficient information to conduct indirect selection for crop improvement strategies. Standardized multiple linear regression is the most effective way in providing information about the relationship of seed yield and yield components in sesame for indirect selection. This analysis facilitates in deciding minimum number of characteristics, which are effective in improving yield, and will help breeders to handle the number of characteristics in the selection procedure.

An investigation was carried out to understand interrelationship and degree of dependence of seed yield on its components by Parimala and Mathur (2006) in sesame. The multiple correlation coefficient between seed yield and all seven characters in equation was very high (R=0.9754). The step-wise regression analysis revealed that the number of capsules per plant was the most important character having r=0.9687 and could explain 93.84% of the total variation of seed yield. The relative importance of the characters for seed yield per plant could be in the order of number of capsules per plant> capsule length> number of branches per plant> plant height> number of seeds per capsule> 1000-seed weight and > days to first flowering.

El-Mohsen *et.al* (2008) carried out a field experiment to compare five statistical procedures including: simple correlation, path analysis, multiple linear regression, stepwise regression and factor analysis in determining the relationship between sesame seed yield and its contributing traits using thirty sesame genotypes. The characters flowering date, plant height, number of fruiting branches, stem height to the first capsule, fruiting zone length, number of capsules on main stem, number of capsules per plant, capsule density on main stem, 1000-seed weight and seed yield per plant were studied. Stepwise multiple regression analysis showed that 77.25% of the total variation in seed yield could be explained by the variation in number of capsules per plant and flowering date in sesame. It could be concluded that the five of statistical analysis techniques, agreed upon that high yield of sesame plants could be obtained by selecting breeding materials with high number of capsules on main stem, number of capsules per plant, plant height and increasing capsule density on the main stem.

In sesame, multiple stepwise regression analysis was conducted to find the contribution of root and shoot morphological characters on root length, seed yield per plant and number of seeds per capsule (Narayanaswamy *et.al*, 2012). Regression model was fitted with characters namely root length, seed yield per plant and number of capsules per plant as dependent variable. The independent variables used were root and shoot characters. The study revealed that significant contribution of root, shoot length, plant height, capsule length and number of seeds per capsule on seed yield per plant.

A study was conducted to formulate the relationship among five independent growth variables in sesame crop with a dependent variable by Atalou *et.al* (2014). Multiple regression analysis was carried out for the root bulk (X_1), capsule number per plant (X_2), capsule length (X_3), 1000 seed weight (X_4) and seed yield (X_5); and oil yield (OY) as a dependent variable. The stepwise regression analysis was carried out for to test the significance of the independent variables affecting the oil yield. Analysis of variance indicated that effect of studied treatments on root bulk, seed yield and oil yield was significant at 5%, and on capsule number per plant and capsule length was significant at 1% probability levels. The stepwise regression analysis verified that the root bulk, capsule number per plant and seed yield had a marked increasing effect on the sesame oil yield.

Aristya *et.al* (2017) reported that standardized multiple linear regression analysis was strongly associated seed yield with number of primary branches (x_2), number of secondary branches (x_3), number of capsules per plant (x_8), and biomass yield per plant (x_9) in sesame, thus providing a powerful method to analyse multivariate data.

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The principal focus of the research is titled "Developing breeding lines of sesame suitable for cultivation in Kerala". The major objective of the study was to evaluate segregating population of intervarietal crosses in sesame for selecting superior genotypes. The study was conducted in the Department of Genetics and Plant Breeding, College of Agriculture, Vellayani, Thiruvananthapuram, during the period 2022-2024.

3.1. MATERIALS

3.1.1 Experiment I

The experimental material consisted of the F_2 segregating populations of three superior F_1 lines namely, Thilak X Ayali 1(TA1), Thilathara X Ayali 2 (TTA2) and Thilak X Ayali 5 (TA5), selected based on a previous work done in the Department of Genetics and Plant Breeding, College of Agriculture, Vellayani (Plate 1). Observations were recorded on the various biometric characters of the F_2 populations and superior lines were identified and seeds collected after selfing (Plate 2).

3.1.2. Experiment II

The seeds of selected F_2 lines namely, TA1-5, TA5-2, TA5-4, TA5-5 and TA5-32 were proceeded to F_3 generation (Plate 3) and observations recorded on various yield related and biochemical parameters.

3.2. METHODS

3.2.1. Layout and conduct of experiment

The F_2 of three superior F_1 lines namely, Thilak X Ayali 1(TA1), Thilathara X Ayali 2 (TTA2) and Thilak X Ayali 5 (TA5) were space planted in the field during December 2023. Altogether 200 plants were maintained. Normal cultural methods as per the package of practices Recommendations - Crops (KAU, 2016) were adopted.

In experiment II, the seeds of the selected five F_2 segregants namely, TA1-5, TA5-2, TA5-4, TA5-5, TA5-32 were laid out in compact family block design during April 2024. Altogether 200 plants were maintained. Normal cultural methods as per the Package of Practices Recommendations - Crops (KAU, 2016) were adopted.

3.2.2. Observations

In experiment I, 200 seeds were sown, but only 169 germinated. Biometric observations were recorded from 169 plants and in experiment II biometric observations were recorded from 200 plants and biochemical traits were evaluated for selected plants.

3.2.2.1. Biometric observations

Days to first flowering

Number of days taken for the first flowering to occur in each genotype was recorded

Number of primary branches

The no of productive primary branches produced by the plant 75 days after sowing was recorded

Number of capsules per plant

The total number of capsules present in the single plant was recorded

Capsule length (cm)

The length of randomly selected 10 capsules from the bottom, middle and top portions of each plant were measured at maturity of the crop.

Capsule width(cm)

The width of randomly selected 10 capsules from the bottom, middle and top portions of each plant were measured at maturity of the crop.

Number of seeds per capsules

The total number of seeds present in 10 randomly selected capsules of each plant was recorded

Days to maturity

The days to maturity was planned to measure after the first lower capsules turned mature and also after the yellowing of lower leaves but due to the erratic rains the crop growth was prolonged which made the measurement difficult.

Plant height (cm)

The height of the plant 75 days after sowing, was measured from the ground level.

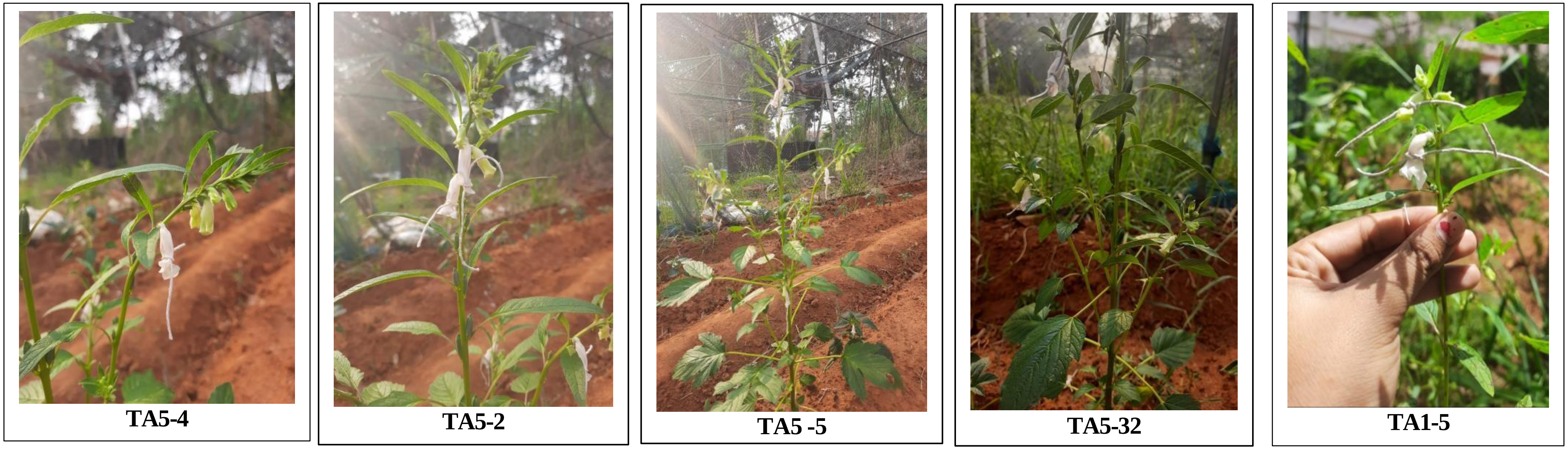
Plate 1. Field view of the F_2 population

At 15 days after planting

At 30 days after planting

At 40 days after planting

Plate 2. Selfing conducted on F_2 plants



TA5-4

TA5-2

TA5 -5

TA5-32

TA1-5

Plate 3. Field view of F_3 population

At 30 days after planting

At 40 days after planting

Seed yield per plant (g)

Seeds from all the capsules of a plant were weighed and recorded

Seed Colour

Colour of seed is evaluated visually

3.2.2.2. Biochemical parameters

Oil content (%)

The oil from 2 g sesame seeds for each genotype was extracted using cold hexane extraction method. Two grams of seeds were ground using pestle and mortar and wrapped in a filter paper and placed inside the thimble portion of the Soxhlet apparatus. The Soxhlet apparatus was kept run for around 1 hour by allowing it to make 6-7 siphoning process. After oil extraction, the remaining hexane was removed by keeping the extract in room temperature for 24 hours.

Crude protein content (%)

Crude protein content was estimated as per the procedure described by AOAC (2000). The Kjeldahl method was used to determine the nitrogen content, involving two major procedures: distillation and titration. For each accession, five millilitres (5 ml) of the digested samples were measured and placed into 50 ml conical flasks. A purple colour was produced after five millilitres (5 ml) of a 2% boric acid solution were added. The digestion tube was then fixed to the distilling end in the presence of 5 ml of NaOH solution, changing the sample’s colour from purple to light green. After this, the distillate was titrated against 0.1 M HCl until a colour change was observed. The titre values were noted for each accession. The entire process was repeated using pure water free of ammonia as the blank.

The percentage nitrogen was calculated using the formula:

$$\%\mathrm{N}= \frac{titre\ value X 0.01 X 14 X V X 100}{100 X W X aliquot\ pipetted}$$

Where, N represents nitrogen, V is the extraction volume (100 ml), and W is the weight of the powdered sample (0.1 g). The percentage of crude protein was then calculated using the formula:

%Crude Protein=%N×6.25%

Peroxidase assay

The crude enzyme extraction was done by grinding 400 mg of leaf sample with 2ml of sodium phosphate buffer at pH 6.5 using a mortar and pestle. The sample was subjected to centrifugation for 10 minutes at 10,000 rpm. The supernatant was collected and used as crude enzyme extract for both peroxidase and polyphenol oxidase enzyme activity measurement.

The procedure as per Sadasivam and Manickam (1996) with some modifications was adopted. The enzyme activity was measured using spectrophotometer under 420 nm which measures the absorbance of the product produced by the peroxidase enzyme. 1ml of 0.05m pyrogallol and 50 µl of enzyme extract was filled in the test cuvette which was placed inside the spectrophotometer. The reaction was started by adding 1ml of 1% hydrogen peroxide. The absorbance value was recorded for 3 minutes at an interval of 30 seconds. A blank reading was recorded using 1ml sodium phosphate buffer (pH 6.5).

Polyphenol oxidase

Polyphenol oxidase activity was estimated according to the method given by (Mayer *et.al.,* 1966). The procedure for enzyme extraction was similar to that of the procedure given for peroxidase enzyme. The reaction mixture consisting of 1ml of 0.1 molar sodium phosphate buffer and 50 µl of enzyme extract was filled in the test cuvette which was placed inside the spectrophotometer. The reaction was initiated by adding 1ml of 0.01m catechol. The absorbance value was recorded for 3 minutes at an interval of 30 seconds. A blank reading was recorded using 1ml sodium phosphate buffer (pH 6.5).

3.2.3. Statistical analysis

The mean values obtained for all the biometric traits were subjected to statistical scrutiny. The following statistical methods were employed for data interpretation. The statistical analysis was done using the statistical software GRAPES (Gopinath *et al.,* 2020) powered by Kerala Agricultural University.

3.2.3.1. Analysis of Variance of factorial Compact Family Block Design

The mean values of each character observed in the progeny lines of five families in the F_3 generation underwent analysis of variance using the Compact Family Block Design method outlined by Chandel (1964). This analysis was conducted in two phases.

(a) First, the variance between families and the corresponding pooled error was determined using the data from the main plots, treating the experiment as a unified entity within simple randomized blocks. The structure of ANOVA for families is given below:

Source	Degrees of freedom	Mean Squares	Expected mean squares
Replications	(r-1)	M_1	$\sigma^2{}_e{}^1 + \sigma^2 r$
Families	(f-1)	M_2	$\sigma^2{}_e{}^1 + \sigma^2 f$
Error	(r-1) (f-1)	M_3	$\sigma^2{}_e{}^1$

Where, r = Number of replications; f = Number of families; M_1 = Mean sum of squares due to replications; M_2 = Mean sum of squares due to families; M_3 = Mean sum of squares due to main plot error; $\sigma^2{}_e{}^1$= Error variance for families; $\sigma^2 r$ = Variance between replications; $\sigma^2 f$ = Variance between families

(b) The analysis for the progenies under each family was done separately for each character using the data of subplots to give the variance between different selection procedures and corresponding errors. The structure of ANOVA for progenies within the family is shown below:

Source	Degrees of freedom	Mean Squares	Expected mean squares
Replications	(r-1)	M_4	$\sigma^2{}_e{}^2 + p\sigma^2{}_r$
Progenies within families	(p-1)	M_5	$\sigma^2{}_e{}^2 + r\,\sigma^2{}_p$
Error	(r-1) (p-1)	M_6	$\sigma^2{}_e{}^2$

Where, r = Number of replications; p = Number of progenies within each family; M_4 = Mean sum of squares due to replications; M_5 = Mean sum of squares due to families; M_6 = Mean sum of squares due to main plot error; $\sigma^2{}_e{}^2$ = Error variance for progenies; $\sigma^2 r$ = Variance between replications; $\sigma^2 p$ = Variance between progenies

Before comparisons, a test was conducted to assess the homogeneity of error variance for each character using Bartlett's test of homogeneity (Bartlett, 1964). Bartlett's test is computed through the following procedure: the pooled variance is calculated using the formula,

$$S_p^2 = \sum \frac{(n_i - 1)s_i^2}{N - a}$$

Where,

S_p^2 = pooled variance

n_i = number of samples of the ith treatment

S_i^2 = Variance of ith treatment

N = total number of samples

a = total number of treatments

Using the pooled variance, the ‘q’ value is calculated with the following formula,

$$q = (N - a)\log S_p^2 - \sum ((n_i - 1) \log s_i^2$$

With the help of the ‘q’ value, the ‘c’ value is calculated by inserting q value in the following formula,

$$c = 1 + \frac{1}{3(a-1)} (\sum (n - 1)^{-1} - (N - a)^{-1})$$

By using the ‘c’ value, Bartlett test statistic is calculated using the formula,

$$\chi_0^2 = 2.3026 \frac{q}{c}$$

After calculating the Bartlett test statistic, it is compared with the critical value of χ at required degrees of freedom. If the Bartlett test statistic is greater than this critical value, there is a significant difference in the variances. If the Bartlett test statistic is less than this critical value, there is no significant difference in the variances.

From the above ANOVA tables, the following statistics were computed

(1) Standard error of the mean (S.Em) $=\sqrt{M6/r}$

(2) Critical difference (C.D.) = S.Em x$\sqrt{2}\ t(0.05)$at error degree of freedom

(3) Coefficient of variation (C.V.) % = $\frac{\sqrt{\frac{M6}{r}} \times 100}{Mean\ of\ progenies}$

3.2.3.2. Coefficient of Variation

Variability that existed in the population for various characters were apportioned using the estimates of coefficient of variation.

For the character $X_{i,}$

Phenotypic coefficient of variation, PCV = $\frac{\sigma pi}{xi}$ x 100

Genotypic coefficient of variation, GCV = $\frac{\sigma gi}{xi}$ x 100

Environmental coefficient of variation, ECV = $\frac{\sigma ei}{xi}$ x 100

Where σ_{pi}, σ_{gi} and σ_{ei} are the phenotypic, genotypic and environmental standard deviations respectively.

3.2.3.3. Heritability

Jain (1982) proposed the mathematical relationship of variance estimates on computation of heritability, which is usually expressed as a percentage.

Heritability (broad sense), H^2 = $\frac{\sigma gi\ 2}{\sigma pi2}$ x 100

The heritability % were categorized as suggested by Robinson *et al.* (1949) namely, low (0-30), moderate (30-60) and high (above 60).

3.2.3.4. Genetic Advance Under Selection

Genetic advance as percentage of mean was calculated as per the formula given by Lush (1949).

Genetic advance, GA = $\frac{k\ H2\ \sigma pi}{xi}$ x 100

H^2 - heritability in broad sense

σ_{pi} - phenotypic standard deviation

k - selection differential that is 2.06 % in case of 5 % selection in large samples (Miller *et al.*, 1958).

Genetic advance as percentage were categorized into low (< 20 %), moderate (10-20 %) and high (> 20%) as suggested by Robinson *et al*. (1949).

3.2.3.5. Correlation Analysis

The correlation coefficients between two characters done using Karl Pearson's coefficient of correlation (1895), also known as Pearson's *r*, is a statistical measure of the linear relationship between two variables. The coefficient is calculated by dividing the co variance of the two variables by the product of their standard deviations:

$$r_{XY} = \frac{cov(X,Y)}{\sigma X.\sigma Y}$$

r_{XY}: The Pearson correlation coefficient

$cov(X,Y)$: The covariance between X and Y

σ_X: The standard deviation of X

σ_Y: The standard deviation of Y

3.2.3.6. Principal Component Analysis

Principal Component Analysis (PCA) (Karl Pearson,1901) is a multivariate statistical method that attempts to describe the total variation in a multivariate sample with fewer variables than in the original data set.

The original mean values of characters were transformed into uncorrelated variables using the pivotal condensation method and these uncorrelated variables were utilized to compute the sum of squares and products and later for working out the principal components. For this, the first approximation for getting the principal component (PC 1) was only the column total of the dispersion matrix, which was reduced by dividing with the highest quantity for the set. Each row of the matrix was multiplied with this third vector. The newly derived vector was a better approximation than the trial one. The process was continued until stable values were obtained. Then, by the square root of their sum of squares, the standardized values of the first vector were calculated. The value of the second component (PC 2) was worked out by subtracting the (i, j)th elements of matrix A (carrying the approximate power) from the product of PC 1 (carrying the same power of matrix A), Xith element and Xjth element of the first vector to obtain reduced matrix. The process of selecting a trial vector and finding a better approximation was repeated on the reduced matrix. The principal component scores were estimated from the linear function of the component coefficients.

A principal component is concerned with explaining the variance - covariance structure through a few linear combinations of the original variables. Its general objectives are (1) Data reduction and (2) Interpretation

Algebraically, principal components are particular linear combinations of the p random variables X1, X2, X3........., Xp. Geometrically, these linear combinations represent the selection of a new coordinate system obtained by rotating the original system with X1, X2, X3. , Xp as the coordinate axes. The new axes represent the directions with maximum variability and provide a simpler and more parsimonious description of the covariance structure.

The principal component depends solely on the covariance matrix $\sum$ (or the correlation matrix ρ) of X1, X2, X3. ...., Xp. The eigenvalue and eigenvector pairs created from data matrix is utilized to identify the principal components.

Let the random vector X´ = [X1, X2, X3 ...., Xp] have the covariance matrix ∑ with eigenvalues λ1 ≥ λ2 ≥....... ≥ λp ≥ 0.

Consider the linear combinations

Y1=ℓ1X= ℓ11X1+ ℓ21X2+ ℓ31X3+...... ℓP1XP

Y2=ℓ2X= ℓ12X1+ ℓ22X2+ ℓ32X3+...... ℓP2XP (3.1)

YP=ℓPX= ℓ1PX1+ ℓ2PX2+ ℓ3PX3+...... ℓPPXP

Then,

var (Yi)= ℓi∑ℓi i=1,2, ..., p (3.2)

Cov (Yi, Yk) = ℓi∑ℓk i=1,2,........., p (3.3)

The principal components are those uncorrelated linear combinations Y1, Y2,............... Yp whose variances in (3.2) are larger as possible.

The first principal component is the linear combination with the maximum variance ie, it maximizes Variance (Y1) = ℓ1∑ ℓ1. It is clear that Var (Y1) = ℓ1∑ ℓ1can be increased by multiplying any ℓ1 by some constant. To eliminate this indeterminacy, it is convenient to restrict attention to the coefficient vector of unit length.

Eigen Values and Eigen Vectors

"The Eigen values and Eigen vectors were computed from the data matrix. Eigen values define the amount of total variation that is displayed on principal components. The amount of variation accounted for each principal component (PC) is explained as the Eigen value divided by the sum of Eigen values."

Proportion of total population variance due to p^{th} principal component =

$$\frac{\lambda p}{\lambda\_1+\lambda\_2+\lambda\_(3 \ldots\ldots\ldots +\lambda p)} \quad (p = 1,2, \ldots\ldots. k)$$

$$= \frac{\lambda p}{\text{Trace(s)}}$$

The Eigen vector (loadings) defines the correlation of each variable with the principal components. The correlation between the k^{th} original variable X^k and the i^{th} principal component Y is given by

$$\mathrm{p}y_{i},\ \mathrm{x}_{k} = \frac{\ell_{ki}\sqrt{\lambda_i}}{\sqrt{\sigma_k}} \qquad i, k = 1,2 \ldots\ldots p$$

Here σk is the standard deviation of xk and (λ1, ℓ1), (λ2, ℓ2), ..., (λp, ℓp) are the Eigen value-Eigen vector pairs for ∑.

Once the principal components have been calculated it need to decide how many to keep. Different methods are used to decide which principal components to retain.

1. Choose sufficient principal components account for a particular percentage (e.g.75%) of the total variability in the data.
2. Choose only those principal components with Eigenvalues over 1 (if using the correlation matrix).
3. Use the Scree plot of the eigenvalues. This will indicate whether there an obvious cut off between large and small Eigenvalues.

Selection index

Selection indices were constructed according to Smith (1936).

$$\mathrm{I} = \sum_{j=1}^{n} b_j X_j$$

The values of b were estimated using the relationship of bP = aG

B = aGP^{-1}

In matrix format,

$$\begin{bmatrix} b_1 \\ b_2 \\ b_3 \\ \vdots \\ b_n \end{bmatrix} = \begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ \vdots \\ a_n \end{bmatrix} \times \begin{bmatrix} G_{11} & G_{12} & G_{13} & G_{1n} \\ G_{21} & G_{22} & G_{23} & G_{2n} \\ G_{31} & G_{32} & G_{33} & G_{3n} \\ \vdots & \vdots & \vdots & \vdots \\ G_{n1} & G_{n2} & G_{n3} & G_{nn} \end{bmatrix} \times \begin{bmatrix} P_{11} & P_{12} & P_{13} & P_{1n} \\ P_{21} & P_{22} & P_{23} & P_{2n} \\ P_{31} & P_{32} & P_{33} & P_{3n} \\ \vdots & \vdots & \vdots & \vdots \\ P_{n1} & P_{n2} & P_{n3} & P_{nn} \end{bmatrix}^{-1}$$

where,

P = Phenotypic variances and covariance matrix of traits X_i to X_j

a_i to a_j = Economic weights of each trait X_i to X_j

G = Genotypic variances and covariance matrix

The values along the diagonal and off the diagonal were the phenotypic and genotypic variances and covariance of traits, respectively.

The weightage for each trait was derived based on the PCA loading value separately for each of the treatments. A scale of 0 to 1 was used for weights, in which a single plant yield had given the maximum weightage of 1. The selection index for the recorded data was computed using PB Tools v. 1.3 (PB Tools 2014).

3.2.3.7. Multiple linear regression analysis

Regression analysis is a statistical method used to estimate the relationships between variables that have a cause-and-effect relationship. The primary focus of univariate regression is to examine the connection between one dependent variable and a single independent variable, aiming to establish a linear equation that defines their relationship. When a regression model includes one dependent variable and multiple independent variables, it is referred to as multiple linear regression.

The multiple regression is calculated by following formula;

$$Y = a+b_1x_1+b_2x_2+ \ldots\ldots\ldots\ldots +b_n x_n$$

Where,

Y = Dependent Variable

$X_1 \ldots\ldots X_n$ = Independent variables

a = Constant

$b_1 \ldots\ldots b_n$ = The regression coefficient for respective independent variables

RESULTS

4. RESULTS

The seeds of the selected F_1 of sesame were raised in the field to generate the F_2 segregating generation. Observations on various biometric parameters were recorded from each individual plant and the superior five plants were selected. The selfed seeds were raised to generate the F_3 populations and biometric observations recorded. The collected data underwent suitable statistical analysis, and the findings are detailed in this chapter.

4.1. Evaluation of F_2 segregants in sesame

The segregating population exhibited a wide range for all the characters studied (table 1) as revealed by the high values of coefficient of variation. The character, seed yield per plant recorded the highest CV (43.02%) closely followed by number of capsules per plant (42.66%). The least CV was recorded by number of seeds per capsule (8.71 %) and capsule length (9.12 %).

Mean value for the character, days to first flowering was recorded as 52.32 which ranged from 29-75. The earliest flowering was recorded for TA5-7 (29 DAS) and the late flowering was recorded for TTA2-8 (75 DAS). Mean value for the character, number of primary branches was recorded as 5.15 which ranged from 4-8. The highest number of primary branches was recorded for TTA2-51, TTA2-52, TA5-2, TA5-4, TA5-5, TA5-17, TA5-20, TA5-32, TA5-40, TA5-54, TA5-55, TA5-70, TA5-81 and TA5-82 and the lowest was recorded for TA1-1, TA1-13, TA1-14, TTA2-4, TTA2-6, TTA2-7, TTA2-8, TTA2-10, TTA2-11, TTA2-12, TTA2-14, TTA2-15, TTA2-17, TTA2-18, TTA2-19, TTA2-21, TTA2-23, TTA2-24, TTA2-40, TTA2-45, TTA2-46, TTA2-47, TA5-22, TA5-23, TA5-26, TA5-27, TA5-28, TA5-30, TA5-31, TA5-33, TA5-34, TA5-35, TA5-37, TA5-39, TA5-42, TA5-43, TA5-44, TA5-47, TA5-48, TA5-49, TA5-50, TA5-51, TA5-52, TA5-53, TA5-60, TA5-61, TA5-62, TA5-63, TA5-68, TA5-71, TA5-74, TA5-75, TA5-77, TA5-90, TA5-92, TA5-98, TA5-99, TA5-100 and TA5-101.

Mean value for the character number of capsules per plant was found to be 101.53, with values ranging from 15-178. TTA2-51 showed the highest capsule number, while TA1-13 had the lowest. The mean capsule length was recorded as 2.11, ranging from 1.85 to 2.68, with TA5-2 exhibiting the greatest length and TTA2-15 the smallest.

The mean value for capsule width was recorded as 0.75, ranging from 0.61 to 0.98. The highest capsule width was recorded for TA5-5, and the lowest for TTA2-7. Mean value for the character number of seeds per capsule was recorded as 51.61 which ranged from 45.5-65.5. The highest number of seeds per capsule was recorded for TA5-4 and the lowest was recorded for TA5-101.

Mean value for the character days to maturity was recorded as 103.17 which ranged from 80-126. The earliest maturation was recorded for TA1-3 and the late maturation was recorded for TTA2-8. For the character plant height, the mean value recorded was 96.75, ranging from 37 to 175.5. The highest plant height was recorded for TA5-5 and the lowest was recorded for TA5-49. Mean value for the character seed yield per plant was recorded as 15.45, ranging from 2.28 to 28.24. The highest seed yield per plant was observed for TA5-4, and the lowest for TA1-13.

4.1.1. Correlation

The correlation between the yield and yield related characters in the F_2 segregating population of sesame was estimated using Pearson correlation since simple correlation did not reveal any significance. Path analysis could not be worked out using the obtained data. The correlation coefficients obtained is presented in table 2. Days to maturity recorded a negative correlation with all the characters. A strong positive correlation of 0.990 was observed between days to first flowering and days to maturity. Number of primary branches had a positive correlation with all the characters except days to first flowering and days to maturity. Seed yield per plant recorded a strong positive correlation with all the traits except with days to first flowering and days to maturity.

4.1.2. Principal Component Analysis

PCA was carried out on the data on the biometric observations recorded from the F_2 population. The eigenvalue, percentage variability and cumulative variability of different principal component is depicted in Table 3. Out of the nine PC generated, the first two principal components have their eigenvalue greater than 1 and accounts for > 80% of the variance. The per cent contributions of nine characters towards the first two principal components is shown in Table 4. Rest of the PCs have eigen values < 1 and are of little use in selection. The first principal component captured 71.275% of the variance, which was

Table 1. Performance of the F_2 progenies of sesame

Treatment	Days to first flowering	No. of primary branches	No. of capsules per plant	Capsule length (cm)	Capsule width (cm)	No. of seeds per capsule	Days to maturity	Plant height (cm)	Seed yield per plant (g)	Seed colour
TA1-1	41	4	22	1.97	0.62	46.5	92	81.5	3.34	Brown
TA1-2	44	6	78	2.05	0.71	48.5	95	126	11.85	Brown
TA1-3	29	6	53	2.11	0.78	52.5	80	128	8.05	Brown
TA1-4	32	6	102	2.07	0.75	50.5	85	120	15.51	Brown
TA1-5*	30	6	163	2.34	0.87	59.5	81	158	28.22	Brown
TA1-6	33	5	118	2.21	0.83	54.5	84	117.5	17.93	Brown
TA1-7	32	6	85	2.01	0.72	49.5	85	106.5	12.92	Brown
TA1-8	31	6	87	2.03	0.74	51.5	84	98	13.22	Brown
TA1-9	43	5	124	2.21	0.85	55.5	94	132.5	18.84	Brown
TA1-10	33	6	157	2.04	0.82	54.5	84	132	25.38	Brown
TA1-11	44	5	113	2.15	0.76	52.5	95	124	17.17	Brown
TA1-12	33	5	89	2.41	0.92	58.5	84	147	13.52	Brown
TA1-13	48	4	15	1.9	0.67	47.5	97	80	2.28	Brown
TA1-14	47	4	18	1.92	0.65	46.5	96	81	2.73	Brown
TTA2-1	66	6	132	2.23	0.82	54.5	115	112	20.06	Brown
TTA2-2	68	5	107	2.16	0.73	50.5	117	104	16.26	Brown
TTA2-3	69	5	108	2.13	0.76	52.5	118	106	16.41	Brown
TTA2-4	67	4	67	1.94	0.65	47.5	116	75	10.18	Brown
TTA2-5	70	5	111	1.99	0.68	48.5	120	96	16.87	Brown
TTA2-6	73	4	92	1.96	0.63	46.5	125	89	13.98	Brown
TTA2-7	68	4	22	1.91	0.61	45.5	117	51.5	3.32	Brown

Contd…...

TTA2-8	75	4	43	1.92	0.64	46.5	126	74	6.53	Brown
TTA2-9	72	5	78	1.98	0.66	47.5	124	92	11.85	Brown
TTA2-10	66	4	31	1.93	0.69	49.5	115	67	4.71	Brown
TTA2-11	75	4	104	1.95	0.67	48.5	126	81	15.81	Brown
TTA2-12	69	4	18	1.89	0.62	45.5	118	38	2.73	Brown
TTA2-13	72	5	97	1.95	0.65	47.5	124	87.5	14.74	Brown
TTA2-14	67	4	35	1.88	0.68	48.5	116	54	5.32	Brown
TTA2-15	74	4	27	1.85	0.61	45.5	123	64	4.11	Brown
TTA2-16	63	5	94	1.94	0.64	46.5	114	93	14.29	Brown
TTA2-17	55	4	28	1.97	0.69	49.5	106	59.5	4.25	Brown
TTA2-18	57	4	37	1.91	0.67	48.5	108	68.5	5.66	Brown
TTA2-19	65	4	33	1.92	0.63	46.5	116	56	5.24	Brown
TTA2-20	73	5	103	1.98	0.65	47.5	125	85	15.75	Brown
TTA2-21	60	4	46	1.96	0.62	45.5	109	69	6.99	Brown
TTA2-22	60	5	113	2.01	0.72	49.5	109	93	17.17	Brown
TTA2-23	72	4	109	1.95	0.68	48.5	124	80	16.56	Brown
TTA2-24	68	4	107	2.02	0.75	51.5	117	82	16.26	Brown
TTA2-25	65	6	134	2.14	0.74	51.5	116	120	20.36	Brown
TTA2-26	37	7	142	2.38	0.83	54.5	87	118	21.58	Brown
TTA2-27	55	6	125	2.15	0.76	52.5	106	99	19.11	Brown
TTA2-28	63	6	122	2.12	0.78	53.5	115	95	18.54	Brown
TTA2-29	43	5	107	1.95	0.69	49.5	91	85	16.26	Brown
TTA2-30	34	7	139	2.41	0.93	59.5	85	110	21.12	Brown
TTA2-31	63	5	118	2.06	0.75	51.5	115	93.5	17.93	Brown
TTA2-32	60	6	127	2.28	0.83	54.5	108	112.5	19.31	Brown
TTA2-33	63	5	78	1.99	0.68	48.5	114	81	11.85	Brown

Contd…...

TTA2-34	60	6	142	2.21	0.86	56.5	108	129	21.58	Brown
TTA2-35	63	5	115	1.98	0.67	48.5	114	93	17.48	Brown
TTA2-36	46	7	163	2.35	0.85	55.5	95	135	24.77	Brown
TTA2-37	65	5	34	1.88	0.63	46.5	116	58	5.16	Brown
TTA2-38	70	6	148	2.31	0.83	54.5	121	119.5	22.49	Brown
TTA2-39	69	6	153	2.24	0.86	56.5	120	128	23.25	Brown
TTA2-40	68	4	67	1.99	0.64	46.5	119	75	10.18	Brown
TTA2-41	70	5	123	2.08	0.77	52.5	121	114	18.69	Brown
TTA2-42	74	5	116	2.01	0.74	51.5	125	95	17.63	Brown
TTA2-43	67	5	119	2.05	0.79	53.5	118	99	18.08	Brown
TTA2-44	72	6	138	2.33	0.85	55.5	123	115.5	20.97	Brown
TTA2-45	71	4	27	1.91	0.67	48.5	122	57	4.11	Brown
TTA2-46	66	4	35	1.89	0.63	46.5	117	60	5.32	Brown
TTA2-47	65	4	29	1.95	0.65	47.5	116	58	4.41	Brown
TTA2-48	40	5	104	1.99	0.68	48.5	91	83.5	15.81	Brown
TTA2-49	39	6	149	2.28	0.81	54.5	98	130	22.64	Brown
TTA2-50	38	6	153	2.23	0.86	56.5	97	128	23.25	Brown
TTA2-51	37	8	178	2.29	0.82	54.5	96	125	27.05	Brown
TTA2-52	32	8	175	2.27	0.84	55.5	91	120	26.61	Brown
TTA2-53	37	5	112	2.11	0.78	53.5	96	92	16.81	Brown
TTA2-54	34	5	117	2.18	0.74	51.5	93	94	17.78	Brown
TA5-1	57	6	86	2.21	0.81	54.5	106	105	13.07	Brown
TA5-2*	30	8	168	2.68	0.95	62.5	81	171.5	26.72	Brown
TA5-3	30	6	87	2.06	0.87	56.5	81	98	13.05	Brown
TA5-4*	31	8	170	2.61	0.94	65.5	84	168	28.24	Brown
TA5-5*	32	8	175	2.65	0.98	61.5	85	175.5	27.02	Brown

Contd…...

TA5-6	36	5	115	2.15	0.73	50.5	89	135	17.48	Brown
TA5-7	29	5	119	2.16	0.76	52.5	80	120	18.08	Brown
TA5-8	33	7	125	2.43	0.93	59.5	86	90	19.01	Brown
TA5-9	32	5	130	2.09	0.74	51.5	85	100	19.76	Brown
TA5-10	45	5	156	2.05	0.72	49.5	94	90.5	23.71	Brown
TA5-11	60	5	140	2.08	0.79	53.5	109	104.5	21.28	Brown
TA5-12	61	5	123	2.11	0.77	52.5	110	120	18.69	Brown
TA5-13	37	7	165	2.47	0.95	60.5	90	118	25.08	Brown
TA5-14	33	7	152	2.48	0.94	59.5	86	109	16.58	Brown
TA5-15	32	5	116	2.23	0.85	55.5	85	110	17.63	Brown
TA5-16	33	5	106	2.21	0.84	55.5	86	93	16.112	Brown
TA5-17	34	8	171	2.53	0.96	60.5	87	130	26.11	Brown
TA5-18	37	6	149	2.43	0.97	61.5	90	111	22.64	Brown
TA5-19	42	5	111	2.36	0.84	55.5	93	117.5	16.87	Brown
TA5-20	42	8	168	2.51	0.94	59.5	93	133	25.53	Brown
TA5-21	62	5	96	2.16	0.75	51.5	111	81	14.59	Brown
TA5-22	62	4	98	1.99	0.67	48.5	110	95.5	15.89	Brown
TA5-23	62	4	112	1.95	0.64	46.5	109	82	17.02	Brown
TA5-24	37	7	151	2.45	0.94	59.5	88	95	22.95	Brown
TA5-25	33	5	107	2.07	0.75	51.5	85	101.3	16.26	Brown
TA5-26	35	4	98	1.98	0.67	48.5	86	82	14.77	Brown
TA5-27	38	4	56	1.94	0.65	47.5	89	67	8.51	Brown
TA5-28	37	4	63	1.95	0.62	45.5	88	75	9.57	Brown
TA5-29	34	5	102	1.93	0.64	46.5	85	93	15.51	Brown
TA5-30	33	4	36	1.85	0.61	45.5	85	38	5.47	Brown
TA5-31	44	4	41	1.88	0.63	46.5	95	48	6.23	Brown

Contd…...

TA5-32*	35	8	173	2.63	0.96	63.5	86	165.5	26.65	Brown
TA5-33	35	4	39	1.85	0.65	47.5	86	52	5.92	Brown
TA5-34	46	4	94	1.97	0.68	48.5	95	82	14.28	Brown
TA5-35	45	4	52	1.86	0.63	46.5	94	67.5	7.91	Brown
TA5-36	37	5	136	2.06	0.74	51.5	88	112	20.67	Brown
TA5-37	47	4	47	1.91	0.65	47.5	96	52	7.14	Brown
TA5-38	47	5	114	1.93	0.67	48.5	96	80	17.32	Brown
TA5-39	57	4	99	1.94	0.63	46.5	108	72	15.04	Brown
TA5-40	30	8	166	2.49	0.95	60.5	80	135	25.23	Brown
TA5-41	60	5	121	2.13	0.74	51.5	109	104	18.39	Brown
TA5-42	60	4	83	2.11	0.72	49.5	109	78	12.61	Brown
TA5-43	55	4	51	1.92	0.62	45.5	104	58	7.75	Brown
TA5-44	55	4	27	2.01	0.77	52.5	104	68.5	4.11	Brown
TA5-45	54	5	88	2.02	0.74	51.5	105	95	13.37	Brown
TA5-46	40	5	91	1.91	0.63	46.5	91	90	13.83	Brown
TA5-47	49	4	33	1.96	0.66	47.5	98	59	5.01	Brown
TA5-48	53	4	24	1.87	0.68	48.5	102	48	3.64	Brown
TA5-49	54	4	19	1.85	0.64	46.5	105	37	2.88	Brown
TA5-50	42	4	68	1.92	0.69	49.5	90	72	10.33	Brown
TA5-51	55	4	77	1.96	0.68	48.5	104	80	11.71	Brown
TA5-52	57	4	61	1.94	0.65	47.5	108	73	9.27	Brown
TA5-53	54	4	90	1.99	0.71	49.5	103	87	13.68	Brown
TA5-54	56	8	162	2.51	0.94	59.5	107	120	24.62	Brown
TA5-55	34	8	158	2.48	0.92	58.5	85	133	24.01	Brown
TA5-56	45	6	133	2.24	0.84	55.5	93	108.5	20.21	Brown
TA5-57	60	5	128	2.26	0.87	56.5	109	112	19.45	Brown

Contd…...

TA5-58	43	5	137	2.27	0.85	55.5	91	113	20.82	Brown
TA5-59	55	5	105	2.29	0.83	54.5	104	87	15.96	Brown
TA5-60	60	4	101	1.94	0.66	47.5	109	84	15.35	Brown
TA5-61	65	4	47	1.98	0.69	49.5	114	63	7.14	Brown
TA5-62	55	4	67	1.93	0.64	46.5	104	72	10.18	Brown
TA5-63	47	4	35	1.97	0.68	48.5	95	59	5.32	Brown
TA5-64	62	5	127	1.94	0.65	47.5	113	94	19.31	Brown
TA5-65	66	5	117	1.97	0.62	45.5	117	98	17.78	Brown
TA5-66	70	5	29	1.99	0.71	48.5	119	62	4.41	Brown
TA5-67	36	5	109	2.05	0.72	49.5	87	95	16.56	Brown
TA5-68	33	4	113	2.09	0.77	52.5	84	91	17.17	Brown
TA5-69	63	5	94	2.12	0.79	53.5	114	80	14.28	Brown
TA5-70	66	8	176	2.52	0.94	59.5	117	132	26.41	Brown
TA5-71	67	4	38	2.03	0.72	49.5	118	67.5	5.77	Brown
TA5-72	68	5	113	2.08	0.74	51.5	119	90.5	17.17	Brown
TA5-73	58	5	123	2.23	0.85	55.5	107	111	18.69	Brown
TA5-74	58	4	106	2.04	0.72	49.5	107	82	16.11	Brown
TA5-75	58	4	87	2.07	0.75	51.5	107	79	13.22	Brown
TA5-76	64	5	116	2.14	0.77	52.5	115	92	17.63	Brown
TA5-77	66	4	92	2.05	0.72	49.5	117	85	13.98	Brown
TA5-78	61	5	120	2.12	0.78	53.5	112	117	18.24	Brown
TA5-79	63	6	128	2.25	0.84	55.5	114	121	19.45	Brown
TA5-80	50	5	145	2.26	0.82	54.5	102	116	22.04	Brown
TA5-81	50	8	143	2.46	0.93	59.5	102	154	21.73	Brown
TA5-82	39	8	154	2.47	0.91	58.5	90	140	23.41	Brown
TA5-83	39	7	166	2.38	0.85	55.5	90	130	25.23	Brown

Contd…...

TA5-84	40	7	157	2.35	0.88	57.5	91	131.5	23.86	Brown
TA5-85	42	5	138	2.11	0.74	51.5	93	113	20.97	Brown
TA5-86	43	5	136	2.13	0.72	49.5	94	119	20.67	Brown
TA5-87	43	6	141	2.29	0.82	54.5	94	122	21.43	Brown
TA5-88	66	5	131	2.16	0.74	51.5	117	114	20.04	Brown
TA5-89	68	5	124	2.18	0.77	52.5	119	112.5	18.84	Brown
TA5-90	64	4	105	1.96	0.67	48.5	115	98	15.96	Brown
TA5-91	63	5	108	1.98	0.63	46.5	114	101	16.52	Brown
TA5-92	67	4	113	1.99	0.71	48.5	118	91.5	17.17	Brown
TA5-93	62	5	97	1.97	0.68	48.5	113	109.5	14.74	Brown
TA5-94	69	5	109	2.06	0.74	51.5	120	100	15.47	Brown
TA5-95	61	6	134	2.31	0.83	54.5	112	126.5	20.36	Brown
TA5-96	67	5	111	2.09	0.74	51.5	118	117.5	16.87	Brown
TA5-97	65	5	96	2.11	0.75	51.5	116	93	14.89	Brown
TA5-98	52	4	74	2.12	0.77	52.5	104	85	11.24	Brown
TA5-99	67	4	41	1.94	0.67	48.5	118	59	6.23	Brown
TA5-100	64	4	39	1.97	0.64	46.5	115	55	5.92	Brown
TA5-101	62	4	36	1.93	0.62	45.5	113	58	5.41	Brown
Mean	52.32	5.15	101.53	2.11	0.75	51.61	103.17	96.75	15.45	
Range	29-75	4-8	15-178	1.85-2.68	0.61-0.98	45.5-65.5	80-126	37-175.5	2.28-28.24	
SD	14.02	1.20	43.32	0.19	0.10	4.50	13.44	27.73	6.65	
CV	26.81	23.29	42.66	9.16	13.29	8.71	13.03	28.66	43.02	

Table 2. Correlation matrix of the nine biometric characters in sesame

	X_1	**X_2**	**X_3**	**X_4**	**X_5**	**X_6**	**X_7**	**X_8**	**X_9**
X_1	1.000								
X_2	-0.423	1.000							
X_3	-0.308	0.770	1.000						
X_4	-0.410	0.866	0.783	1.000					
X_5	-0.427	0.828	0.759	0.947	1.000				
X_6	-0.433	0.827	0.758	0.946	0.988	1.000			
X_7	0.990	-0.388	-0.274	-0.387	-0.408	-0.412	1.000		
X_8	-0.388	0.789	0.845	0.822	0.785	0.794	-0.361	1.000	
X_9	-0.310	0.765	0.996	0.778	0.751	0.756	-0.276	0.853	1.000

X_1 - Days to first flowering
X_2 - Number of primary branches
X_3 - Number of capsules per plant
X_4 - Capsule length
X_5 - Capsule width
X_6 - Number of seeds per capsule
X_7 - Days to maturity
X_8 - Plant height
X_9 - Seed yield per plant

Table 3. Principal components showing the Eigen values, proportion of variation and cumulative percentage of variance in F_2 population of sesame

Principal Components	Eigenvalue	Percentage of variance	Cumulative percentage of variance
PC1	6.415*	71.275	71.275
PC2	1.58*	17.557	88.832
PC3	0.535	5.946	94.778
PC4	0.213	2.364	97.142
PC5	0.176	1.953	99.095
PC6	0.057	0.63	99.726
PC7	0.012	0.137	99.863
PC8	0.009	0.101	99.964
PC9	0.003	0.036	100

Table 4. Percentage contribution of variables on PCA in F_2 segregating population of sesame

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Days to first flowering	**4.752**	**43.234**	1.329	0	0.152	0.001	2.314	47.337
Number of primary branches	**12.63**	**0.418**	1.742	75.704	6.289	3.024	0	0.192
Number of capsules per plant	**12.29**	**4.229**	22.781	2.524	8.788	0.095	3.939	1.515
Capsule length	**13.858**	**0.753**	10.574	0.078	0.059	74.511	0.138	0.004
Capsule width	**13.621**	**0.37**	16.905	8.553	0.43	9.255	44.212	1.556
Number of seeds per capsule	**13.684**	**0.333**	16.009	8.821	0.064	12.123	42.765	1.167
Days to maturity	**4.29**	**45.238**	0.913	0.265	0.006	0.068	2.348	45.998
Plant height	**12.623**	**1.282**	5.446	1.399	78.112	0.921	0.132	0.032
Seed yield per plant	**12.253**	**4.143**	24.302	2.656	6.101	0.001	4.151	2.199

Bold values represent principal components with eigen values >1

followed by the second principal component (17.557 %). Both the PCs together captured 88.832% of variance. The third principal component captured 5.946 % of the variance with a cumulative percentage of variance 94.778%. Hence 2 PCs are selected and selection of genotypes present in 2 PCs are desirable.

PC1 was mostly related with the trait capsule length (13.858) closely followed by number of seeds per capsule (13.684), capsule width (13.621), number of primary branches (12.63), plant height (12.623), number of capsules per plant (12.29) and seed yield per plant (12.253). PC2 was related to days to maturity (45.238) and days to first flowering (43.234).

Factor loading of various traits in relation to the principal components is reflected in the Table 5. Loadings with absolute scores greater than 0.300 are considered to contribute profusely to genetic divergence. In PC1 the characters number of primary branches (-0.355), number of capsules per plant (-0.351), capsule length (-0.372), capsule width (-0.369), number of seeds per capsule (-0.37), plant height (-0.355) and seed yield per plant (-0.35) had the absolute value greater than 0.300, indicating that these traits were primarily responsible for genetic divergence among genotypes. In PC2 the traits days to first flowering (0.658) and days to maturity (0.673) recorded high loadings indicating that divergence among genotypes of PC2 was majorly contributed by these traits.

High PC score for a particular genotype in a particular component denotes high value for variables in that genotype. The PC scores for the selected genotypes of the F_2 generation is given in the table 6. The PC scores for the genotypes in PC1 were 4.445 for TA1-5, 6.375 for TA5-2, 6.440 for TA5-4, 6.377 for TA5-5 and 6.202 for TA5-32. Among the plants of the F_2 population, these genotypes exhibited high variability for the traits capsule length, number of seeds per capsule, capsule width, number of primary branches, plant height, number of capsules per plant and seed yield per plant.

The correlation between variables and the principal components is given in table 7. The high loadings of the traits number of primary branches (0.9), capsule length (0.943), capsule width (0.935), number of seeds per capsule (0.937), plant height (0.9), number of capsules per plant (0.888) and seed yield per plant (0.887) indicate that these traits strongly influence the principal component I. PC2 was highly influenced by the characters days to first flowering (0.827) and days to maturity (0.845), while all the other traits exhibited a negligible influence on it.

4.1.3. Multiple linear regression

Linear regression analysis was performed with seed yield per plant as dependent variable and agronomic traits as independent variables. The fitted model has R^2 value of 99.3% which indicates that the model explains 99.30 % of the variability in seed yield. The adjusted R-squared statistic, which is more suitable for comparing models with different numbers of independent variables, is also 99.3%.

The standard error of the estimate shows that the standard deviation of the residuals is 0.568. Since the *P*-value is greater than 0.05, there is no indication of serial autocorrelation in the residuals at the 95.0% confidence level. Table 8 shows the results of fitting a multiple linear regression model to describe the average relationship between seed yield and eight independent variables. The fitted model was:

Seed yield per plant (Y) = $-3.364 + 0.035 X_1 - 0.018 X_2 + 0.150 X_3 - 0.811 X_4 - 15.513 X_5 + 0.346 X_6 - 0.037 X_7 + 0.011 X_8$

It was observed that the characters, viz. days to first flowering, number of primary branches, capsule length and days to maturity were not significant (P value > 0.05) (table 9). Hence, these variables were removed. Stepwise regression, with backward elimination, shows the results of fitting a linear regression model to describe the relationship between seed yield per plant and 4 independent variables. According to this analysis the prediction equation runs as follows:

$(Y) = -5.655 + 0.149 X_3 – 16.007 X_5 + 0.329 X_6 + 0.010 X_8$ (R squared = 99.3 %), where Y, X_3, X_5, X_6 and X_8 represent seed yield per plant, number of capsules per plant, capsule width, number of seeds per capsule and plant height respectively.

The study revealed significant contribution of number of capsules per plant, capsule width, number of seeds per capsule and plant height on seed yield per plant.

Table 5. Principal component analysis for nine yield and related traits of F_2 segregating population in sesame

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Days to first flowering	0.218	0.658	-0.115	0.002	-0.039	0.003	-0.152	0.688	0.094
Number of primary branches	-0.355	0.065	-0.132	-0.87	0.251	0.174	-0.002	0.044	-0.001
Number of capsules per plant	-0.351	0.206	0.477	0.159	0.296	-0.031	-0.198	-0.123	0.662
Capsule length	-0.372	0.087	-0.325	0.028	-0.024	-0.863	0.037	-0.006	-0.016
Capsule width cm.	-0.369	0.061	-0.411	0.292	0.066	0.304	-0.665	-0.125	-0.226
Number of seeds per capsule	-0.37	0.058	-0.4	0.297	0.025	0.348	0.654	0.108	0.224
Days to maturity	0.207	0.673	-0.096	-0.051	-0.008	0.026	0.153	-0.678	-0.094
Plant height	-0.355	0.113	0.233	-0.118	-0.884	0.096	-0.036	-0.018	0.023
Seed yield per plant	-0.35	0.204	0.493	0.163	0.247	0.004	0.204	0.148	-0.665

Table 6. Principle component scores from standardised variables of selected F_2 plants

Genotypes	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
TA1-5	4.445	0.902	-0.806	-0.654	0.714	0.194	0.411	-0.158	-0.180
TA5-2	6.375	0.520	0.529	0.393	0.722	-0.519	0.290	-0.135	-0.003
TA5-4	6.440*	0.279	0.561	0.186	0.525	-0.009	0.846	-0.150	0.037
TA5-5	6.377	0.174	0.425	0.375	0.780	-0.353	-0.067	0.046	-0.052
TA5-32	6.202	0.040	0.653	0.281	0.496	-0.200	0.345	-0.129	0.106

Table 7. Correlation between variables and PC in F_2 segregating population of sesame

Variables	**PC1**	**PC2**	PC3	PC4	PC5	PC6	PC7	PC8
Days to first flowering	**-0.552**	**0.827**	0.084	-0.001	0.016	0.001	0.017	0.066
Number of primary branches	**0.9**	**0.081**	0.097	0.401	-0.105	0.041	0	0.004
Number of capsules per plant	**0.888**	**0.258**	-0.349	-0.073	-0.124	-0.007	0.022	-0.012
Capsule length	**0.943**	**0.109**	0.238	-0.013	0.01	-0.206	-0.004	-0.001
Capsule width	**0.935**	**0.076**	0.301	-0.135	-0.027	0.072	0.074	-0.012
Number of seeds per capsule	**0.937**	**0.073**	0.293	-0.137	-0.011	0.083	-0.073	0.01
Days to maturity	**-0.525**	**0.845**	0.07	0.024	0.003	0.006	-0.017	-0.065
Plant height	**0.9**	**0.142**	-0.171	0.055	0.371	0.023	0.004	-0.002
Seed yield per plant	**0.887**	**0.256**	-0.361	-0.075	-0.104	0.001	-0.023	0.014

Bold values represent principal components with eigen values >1

Table 8. Variables selected by the model of multiple linear regression with their corresponding coefficient values (a_i), standard error (SE), *t* value and significance level (*P*) according to the model used in F_2 population of sesame

Parameter	Estimate	Std. Error	T value	P-value
Intercept	-3.364	1.898	-1.772	0.078
Days to first flowering	0.035	0.023	1.510	0.133
Number of primary branches	-0.018	0.079	-0.224	0.823
Number of capsules per plant	0.150	0.002	72.966	0.000*
Capsule length	-0.811	0.833	-0.973	0.332
Capsule width	-15.513	3.047	-5.091	0.000*
Number of seeds per capsule	0.346	0.067	5.204	0.000*
Days to maturity	-0.037	0.024	-1.526	0.129
Plant height	0.011	0.003	3.212	0.002*

Regression coefficients with P-value <0.05 are significant.

R squared – 0.993; Adj R squared – 0.993; Residual Standard error – 0.568

Table 9. Variables selected by the model of multiple linear regression after stepwise regression with backward elimination according to the model used in F_2 population of sesame

Parameter	Estimate	Std. Error	T value	P-value
Intercept	-5.655	1.283	-4.407	0.000
Number of capsules per plant	0.149	0.002	75.384	0.000*
Capsule width	-16.007	2.925	-5.473	0.000*
Number of seeds per capsule	0.329	0.066	5.009	0.000*
Plant height	0.010	0.003	3.078	0.0024*

Regression coefficients with P-value <0.05 are significant.

R squared – 0.993; Adj R squared – 0.993; Residual Standard error – 0.568

4.2. Evaluation of F_3 segregants in sesame

4.2.1. Genetic variability

The F_3 population exhibited a wide range for all the characters studied (table 10). The coefficient of variation was found to highest for number of capsules per plant (29.40 %) followed by seed yield per plant (28.55 %), plant height (22.40 %) and number of primary branches (21.94 %). The lowest CV was recorded for the characters number of seeds per capsule (4.63 %), capsule length (5.72%) and days to maturity (5.94%).

Mean value for the character days to first flowering was recorded as 57.42 which ranged from 41-74. The earliest flowering was recorded for TA5-32-25 and the late flowering was recorded for TA5-4-18. Mean value for the character number of primary branches was recorded as 4.90 which ranged from 4-8. The highest number of primary branches was recorded for TA1-5-9, TA5-2-2, TA5-2-8, TA5-4-4, TA5-4-7, TA5-4-16, TA5-4-32, TA5-32-7, TA5-32-14 and TA5-32-25 and the lowest was recorded for TA1-5- 4, TA1-5-5, TA1-5-6, TA1-5-7, TA1-5-14, TA1-5-15, TA1-5-16, TA1-5-17, TA1-5-19, TA1-5-22, TA1-5-24, TA1-5-27, TA1-5-28, TA1-5-31, TA1-5-36, TA1-5-37, TA1-5-38, TA1-5-39, TA5-2-1, TA5-2-3, TA5-2-4, TA5-2-6, TA5-2-7, TA5-2-9, TA5-2-12, TA5-2-14, TA5-2-15, TA5-2-16, TA5-2-17, TA5-2-18, TA5-2-19, TA5-2-23, TA5-2-25, TA5-2-26, TA5-2-27, TA5-2-28, TA5-2-30, TA5-2-31, TA5-2-32, TA5-2-33 ,TA5-2-35, TA5-2-37, TA5-2-38, TA5-2-40, TA5-4-1, TA5-4-3, TA5-4-6, TA5-4-8, TA5-4-9, TA5-4-10, TA5-4-12, TA5-4-15, TA5-4-17, TA5-4-18, TA5-4-23, TA5-4-24, TA5-4-25, TA5-4-26, TA5-4-28, TA5-4-34, TA5-4-35, TA5-4-36, TA5-4-38, TA5-4-40, TA5-5-5, TA5-5-6, TA5-5-7, TA5-5-8, TA5-5-13, TA5-5-14, TA5-5-15, TA5-5-18, TA5-5-21, TA5-5-26, TA5-5-28, TA5-5-29, TA5-5-30, TA5-5-31, TA5-5-36, TA5-5-38, TA5-32-4, TA5-32-5, TA5-32-6, TA5-32-11, TA5-32-16, TA5-32-17, TA5-32-19, TA5-32-24, TA5-32-31, TA5-32-34, TA5-32-36 and TA5-32-39.

Mean value for the character number of capsules per plant was found to be 92.54, which ranged from 25-205. The highest number of capsules was recorded for TA5-32-25 and the lowest was recorded for TA5-4-18. For the character capsule length mean value was recorded as 2.27 ranging from 1.82-2.56. The highest capsule length was observed for TA5-32-25 and the lowest was observed for TA5-4-18. Mean value for the character capsule width was recorded as 0.80 which ranged from 0.61-0.94. The highest capsule width was recorded for TA5-4-7 and the lowest was recorded for TA5-4-18.

Mean value for the character number of seeds per capsule was recorded as 54.87 which ranged from 48-61. The highest number of seeds per capsule was recorded for TA5- 4-7 and the lowest was recorded for TA5-4-18. For the character days to maturity mean value was recorded as 108.53 ranging from 92-125. The earliest maturation was observed for TA5-2-2 and the late maturation was observed for TA5-2-31.

Mean value for the character plant height was recorded as 112.90 which ranged from 46-181. The highest plant height was recorded for TA5-4-7 and the lowest was recorded for TA1-5-24. For the character seed yield per plant mean value was recorded as 13.78. It ranged from 3.25-27.75. The highest seed yield per plant was observed for TA5-32-25 and the lowest was observed for TA5-4-18.

4.2.2. Genetic parameters

The data were subjected to pooled analysis of variance using five families and the results are presented in table 11. All the characters recorded significant differences between the five families, while within families only number of primary branches was estimated to have significant difference. The family TA5-2 was found to be significantly exhibiting maximum duration with respect to flowering and maturity. Seed yield per plant, number of capsules per plant, capsule width, seeds per capsule and plant height was significantly higher in the members of the family TA5-32. Number of primary branches among the families were significantly high for the families TA5-5 and TA5-32.

The various genetic parameters namely phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance were estimated are presented in table 12.

Phenotypic coefficient of variation

Phenotypic coefficient of variation (PCV) exhibited a range from 2.903 for the character number of seeds per capsule to 18.055 for the character number of capsules per plant. The characters, plant height and seed yield per plant also had high PCV i.e, 14.219

Table 10. Performance of F_3 progenies of sesame

Treatment	Days to first flowering	Number of primary branches	Number of capsules per plant	Capsule length (cm)	Capsule width (cm)	Number of seeds per capsule	Days to maturity	Plant Height	Seed yield per plant (g)	Seed Colour
TA1-5-1*	50	8	122	2.41	0.87	58	101	143	19.52	Brown
TA1-5-2	52	7	114	2.38	0.85	57	103	135	18.24	Brown
TA1-5-3	53	5	108	2.34	0.83	56	104	129	17.28	Brown
TA1-5-4	57	4	94	2.27	0.81	55	108	115	15.04	Brown
TA1-5-5	54	4	105	2.32	0.83	56	105	126	16.80	Brown
TA1-5-6	62	4	74	2.12	0.76	53	113	95	11.84	Brown
TA1-5-7	56	4	97	2.27	0.81	55	107	118	15.52	Brown
TA1-5-8	53	6	109	2.34	0.85	57	104	130	17.44	Brown
TA1-5-9	46	7	144	2.43	0.89	59	97	157	23.04	Brown
TA1-5-10	55	6	100	2.32	0.83	56	106	121	16.00	Brown
TA1-5-11	57	5	93	2.27	0.81	55	108	114	14.88	Brown
TA1-5-12	54	5	105	2.32	0.83	56	105	126	16.8	Brown
TA1-5-13	49	6	124	2.43	0.87	58	100	145	19.84	Brown
TA1-5-14	57	4	94	2.25	0.81	55	108	115	15.04	Brown
TA1-5-15	65	4	60	2.16	0.73	52	116	81	9.6	Brown
TA1-5-16	58	4	89	2.27	0.81	55	109	110	14.24	Brown
TA1-5-17	54	4	104	2.34	0.83	56	105	125	16.64	Brown
TA1-5-18	56	5	97	2.25	0.81	55	107	118	15.52	Brown
TA1-5-19	64	4	64	2.16	0.73	52	115	85	10.24	Brown
TA1-5-20	60	5	80	2.21	0.79	54	111	101	12.8	Brown
TA1-5-21	53	5	111	2.38	0.85	57	104	132	17.76	Brown

Contd….

TA1-5-22	59	4	84	2.26	0.79	54	110	105	13.44	Brown
TA1-5-23	69	5	44	2.08	0.67	50	120	65	7.04	Brown
TA1-5-24	72	4	32	1.94	0.64	49	123	46	5.12	Brown
TA1-5-25	51	6	117	2.38	0.85	57	102	138	18.72	Brown
TA1-5-26	58	5	89	2.25	0.81	55	109	110	14.24	Brown
TA1-5-27	64	4	66	2.17	0.73	52	115	87	10.56	Brown
TA1-5-28	66	4	59	2.1	0.73	52	117	80	9.44	Brown
TA1-5-29	56	5	99	2.34	0.83	56	107	120	15.84	Brown
TA1-5-30	53	6	111	2.37	0.85	57	104	132	17.76	Brown
TA1-5-31	63	4	70	2.13	0.76	53	114	91	11.2	Brown
TA1-5-32	71	5	38	1.98	0.64	49	122	59	6.08	Brown
TA1-5-33	55	5	102	2.34	0.83	56	106	123	16.32	Brown
TA1-5-34	55	5	103	2.34	0.83	56	106	124	16.48	Brown
TA1-5-35	69	5	45	2.09	0.67	50	120	66	7.2	Brown
TA1-5-36	57	4	93	2.21	0.81	55	108	114.5	14.88	Brown
TA1-5-37	54	4	107	2.34	0.83	56	105	128	17.12	Brown
TA1-5-38	55	4	100	2.34	0.83	56	106	121	16	Brown
TA1-5-39	69	4	46	2.08	0.67	50	120	67	7.36	Brown
TA1-5-40	55	5	100	2.36	0.83	56	106	121	16	Brown
TA5-2-1	63	4	70	2.14	0.76	53	114	91	11.9	Brown
TA5-2-2*	47	8	143	2.42	0.9	59	92	156	24.31	Brown
TA5-2-3	69	4	46	2.04	0.67	50	120	67	7.82	Brown
TA5-2-4	54	4	107	2.32	0.84	56	105	128	18.19	Brown
TA5-2-5	50	6	120	2.43	0.87	58	101	141	20.4	Brown
TA5-2-6	63	4	68	2.12	0.73	52	114	89	11.56	Brown
TA5-2-7	69	4	44	2.04	0.67	50	120	65	7.48	Brown

Contd….

TA5-2-8	47	8	140	2.42	0.9	59	98	154	23.8	Brown
TA5-2-9	59	4	84	2.25	0.79	54	110	105	14.28	Brown
TA5-2-10	62	5	72	2.14	0.76	53	113	93	12.24	Brown
TA5-2-11	70	5	42	2.04	0.67	50	121	63	7.14	Brown
TA5-2-12	65	4	61	2.12	0.73	52	116	82	10.37	Brown
TA5-2-13	60	5	82	2.25	0.79	54	111	103	13.94	Brown
TA5-2-14	62	4	75	2.14	0.76	53	113	96	12.75	Brown
TA5-2-15	64	4	67	2.12	0.73	52	115	88	11.39	Brown
TA5-2-16	53	4	107	2.35	0.84	56	104	128.5	18.19	Brown
TA5-2-17	59	4	87	2.25	0.79	54	110	108	14.79	Brown
TA5-2-18	61	4	77	2.14	0.76	53	112	98	13.09	Brown
TA5-2-19	60	4	80	2.25	0.79	54	111	101	13.6	Brown
TA5-2-20	59	5	84	2.25	0.79	54	110	105	14.28	Brown
TA5-2-21	64	5	67	2.12	0.73	52	115	88	11.39	Brown
TA5-2-22	64	5	66	2.12	0.73	52	115	87	11.22	Brown
TA5-2-23	63	4	69	2.12	0.76	53	114	90	11.73	Brown
TA5-2-24	59	6	86	2.25	0.79	54	110	107	14.62	Brown
TA5-2-25	58	4	89	2.12	0.81	55	109	110	15.13	Brown
TA5-2-26	66	4	59	2.12	0.73	52	117	80	10.03	Brown
TA5-2-27	68	4	49	2.05	0.7	51	119	70	8.33	Brown
TA5-2-28	65	4	62	2.15	0.73	52	116	83	10.54	Brown
TA5-2-29	58	5	88	2.25	0.79	54	109	109	14.96	Brown
TA5-2-30	62	4	73	2.14	0.76	53	113	94	12.41	Brown
TA5-2-31	72	4	34	1.97	0.64	49	125	55	5.78	Brown
TA5-2-32	54	4	107	2.31	0.84	56	105	128	18.19	Brown
TA5-2-33	60	4	82	2.25	0.79	54	111	103	13.94	Brown

Contd…...

TA5-2-34	63	5	70	2.14	0.76	53	114	91	11.9	Brown
TA5-2-35	65	4	61	2.14	0.73	52	116	82	10.37	Brown
TA5-2-36	56	5	99	2.31	0.84	56	107	120	16.83	Brown
TA5-2-37	60	4	83	2.25	0.79	54	111	104	14.11	Brown
TA5-2-38	64	4	67	2.12	0.73	52	115	88	11.39	Brown
TA5-2-39	62	5	74	2.18	0.76	53	113	95.5	12.58	Brown
TA5-2-40	69	4	45	2.04	0.67	50	120	66	7.65	Brown
TA5-4-1	57	4	94	2.24	0.81	55	108	115	12.22	Brown
TA5-4-2	49	6	124	2.43	0.87	58	100	145	16.12	Brown
TA5-4-3	59	4	84	2.23	0.79	54	110	105	10.92	Brown
TA5-4-4	47	8	138	2.45	0.89	59	98	154	17.94	Brown
TA5-4-5	58	5	91	2.24	0.81	55	109	112	11.83	Brown
TA5-4-6	65	4	62	2.12	0.73	52	116	83	8.06	Brown
TA5-4-7*	43	8	201	2.54	0.94	61	94	181	26.13	Brown
TA5-4-8	56	4	97	2.26	0.81	55	107	118	12.61	Brown
TA5-4-9	61	4	76	2.14	0.76	53	112	97	9.88	Brown
TA5-4-10	62	4	73	2.14	0.76	53	113	94	9.49	Brown
TA5-4-11	60	5	82	2.23	0.79	54	111	103	10.66	Brown
TA5-4-12	59	4	87	2.23	0.79	54	110	108	11.31	Brown
TA5-4-13	52	6	114.5	2.31	0.85	57	103	135.5	14.885	Brown
TA5-4-14	67	5	55	2.08	0.71	51	118	76	7.15	Brown
TA5-4-15	62	4	74	2.15	0.76	53	113	95	9.62	Brown
TA5-4-16	44	8	163	2.51	0.92	60	95	169	21.19	Brown
TA5-4-17	56	4	96	2.26	0.81	55	107	117	12.48	Brown
TA5-4-18	74	4	25	1.82	0.61	48	124	53	3.25	Brown
TA5-4-19	64	5	66	2.13	0.73	52	115	87	8.58	Brown

Contd…...

TA5-4-20	62	6	73	2.15	0.76	53	113	94	9.49	Brown
TA5-4-21	54	5	105	2.38	0.83	56	105	126	13.65	Brown
TA5-4-22	68	5	50	2.08	0.71	51	119	71	6.5	Brown
TA5-4-23	53	4	111	2.31	0.85	57	104	132	14.43	Brown
TA5-4-24	58	4	88	2.25	0.79	54	109	109	11.44	Brown
TA5-4-25	64	4	66	2.13	0.73	52	115	87	8.58	Brown
TA5-4-26	61	4	79	2.23	0.79	54	112	100	10.27	Brown
TA5-4-27	61	5	79	2.23	0.79	54	112	100	10.27	Brown
TA5-4-28	48	4	130	2.45	0.89	59	99	151	16.9	Brown
TA5-4-29	58	5	91	2.26	0.81	55	109	112	11.83	Brown
TA5-4-30	58	5	91	2.26	0.81	55	109	112	11.83	Brown
TA5-4-31	54	6	104	2.26	0.83	56	105	125.5	13.52	Brown
TA5-4-32	48	8	129	2.45	0.89	59	99	150	16.77	Brown
TA5-4-33	50	6	123	2.43	0.87	58	101	144	15.99	Brown
TA5-4-34	62	4	74	2.15	0.76	53	113	95	9.62	Brown
TA5-4-35	60	4	80	2.23	0.79	54	111	101	10.4	Brown
TA5-4-36	51	4	119	2.43	0.87	58	102	140	15.47	Brown
TA5-4-37	50	6	122	2.43	0.87	58	101	143	15.86	Brown
TA5-4-38	55	4	102.5	2.38	0.83	56	106	123.5	13.325	Brown
TA5-4-39	55	5	100	2.38	0.83	56	106	121	13	Brown
TA5-4-40	56	4	99	2.38	0.83	56	107	120	12.87	Brown
TA5-5-1*	48	6	128	2.43	0.87	60	99	149	17.92	Brown
TA5-5-2	56	5	99	2.38	0.83	56	107	120	13.86	Brown
TA5-5-3	60	5	81	2.23	0.79	54	111	102	11.34	Brown
TA5-5-4	55	5	101	2.38	0.83	56	106	122	14.14	Brown
TA5-5-5	55	4	102	2.38	0.83	56	106	123	14.28	Brown

Contd…...

TA5-5-6	53	4	108	2.31	0.85	57	104	129.5	15.12	Brown
TA5-5-7	54	4	104	2.38	0.83	56	105	125	14.56	Brown
TA5-5-8	53	4	109	2.35	0.85	57	104	130	15.26	Brown
TA5-5-9	61	6	78	2.15	0.76	53	112	99	10.92	Brown
TA5-5-10	52	6	113	2.31	0.85	57	103	134	15.82	Brown
TA5-5-11	54	6	103	2.38	0.83	56	105	124.5	14.42	Brown
TA5-5-12	50	7	121	2.43	0.87	58	101	142	16.94	Brown
TA5-5-13	53	4	108	2.38	0.83	56	104	129	15.12	Brown
TA5-5-14	60	4	81	2.23	0.79	54	111	102	11.34	Brown
TA5-5-15	55	4	105	2.38	0.83	56	106	126	14.7	Brown
TA5-5-16	58	5	91	2.25	0.81	55	109	112	12.74	Brown
TA5-5-17	67	5	54	2.08	0.71	51	118	75	7.56	Brown
TA5-5-18	67	4	54	2.08	0.71	51	118	75	7.56	Brown
TA5-5-19	53	5	111	2.31	0.85	57	104	132	15.54	Brown
TA5-5-20	50	6	122	2.43	0.87	58	101	143	17.08	Brown
TA5-5-21	55	4	101	2.38	0.83	56	106	122	14.14	Brown
TA5-5-22	66	5	57	2.08	0.71	51	117	78	7.98	Brown
TA5-5-23	64	5	66	2.13	0.73	52	115	87	9.24	Brown
TA5-5-24	52	5	112.5	2.31	0.85	57	103	133.5	15.75	Brown
TA5-5-25	53	5	111	2.31	0.85	57	104	132	15.54	Brown
TA5-5-26	63	4	70	2.15	0.76	53	114	91	9.8	Brown
TA5-5-27	61	5	79	2.23	0.79	54	114	100	11.06	Brown
TA5-5-28	53	4	108	2.38	0.83	56	104	129	15.12	Brown
TA5-5-29	69	4	44	2.02	0.67	50	120	65	6.16	Brown
TA5-5-30	61	4	78	2.15	0.76	53	112	99	10.92	Brown
TA5-5-31	54	4	104	2.38	0.83	56	112	125.5	14.56	Brown

Contd…...

TA5-5-32	50	6	123	2.43	0.87	58	101	144	17.22	Brown
TA5-5-33	54	5	104	2.38	0.83	56	105	125	14.56	Brown
TA5-5-34	68	6	51	2.08	0.71	51	119	72	7.14	Brown
TA5-5-35	63	6	71	2.15	0.76	53	119	92	9.94	Brown
TA5-5-36	63	4	89	2.25	0.81	55	114	110	12.46	Brown
TA5-5-37	50	7	123	2.43	0.87	58	101	144	17.22	Brown
TA5-5-38	58	4	88	2.23	0.79	54	109	109	12.32	Brown
TA5-5-39	58	5	89	2.23	0.81	55	109	110	12.46	Brown
TA5-5-40	50	6	120	2.43	0.87	58	101	141	16.8	Brown
TA5-32-1	59	5	84	2.23	0.79	54	110	105	12.6	Brown
TA5-32-2	58	5	91	2.25	0.81	55	109	112	13.65	Brown
TA5-32-3	51	6	116	2.31	0.85	57	102	137	17.4	Brown
TA5-32-4	58	4	89	2.25	0.81	55	109	110	13.35	Brown
TA5-32-5	56	4	98	2.25	0.81	55	107	119	14.7	Brown
TA5-32-6	53	4	108	2.38	0.83	56	104	129	16.2	Brown
TA5-32-7	43	8	148	2.52	0.92	60	94	169	22.2	Brown
TA5-32-8	53	5	108	2.38	0.83	56	104	129	16.2	Brown
TA5-32-9	58	6	91	2.25	0.81	55	109	112	13.65	Brown
TA5-32-10	50	6	120	2.43	0.87	58	101	141	18	Brown
TA5-32-11	54	4	104	2.43	0.83	56	105	125	15.6	Brown
TA5-32-12	51	6	119	2.48	0.87	58	102	140	17.85	Brown
TA5-32-13	53	5	110	2.31	0.85	57	104	131	16.5	Brown
TA5-32-14	48	8	131	2.48	0.89	59	99	152	19.65	Brown
TA5-32-15	53	5	108	2.38	0.83	56	104	129	16.2	Brown
TA5-32-16	63	4	68	2.14	0.73	52	114	89	10.2	Brown
TA5-32-17	54	4	104	2.38	0.83	56	105	125	15.6	Brown

Contd…...

TA5-32-18	49	6	125	2.43	0.87	58	100	146	18.75	Brown
TA5-32-19	66	4	57	2.08	0.71	51	117	78	8.55	Brown
TA5-32-20	60	5	81	2.23	0.79	54	111	102	12.15	Brown
TA5-32-21	53	6	111	2.31	0.85	57	104	132	16.65	Brown
TA5-32-22	47	6	132	2.48	0.89	59	98	153	19.8	Brown
TA5-32-23	54	5	104	2.38	0.83	56	105	125	15.6	Brown
TA5-32-24	54	4	106	2.38	0.83	56	105	127	15.9	Brown
TA5-32-25*	41	8	205	2.56	0.93	60	94	179	27.75	Brown
TA5-32-26	57	5	92	2.25	0.81	55	108	113	13.8	Brown
TA5-32-27	52	6	114	2.31	0.85	57	103	135	17.1	Brown
TA5-32-28	56	5	96	2.25	0.81	55	107	117	14.4	Brown
TA5-32-29	54	5	107	2.38	0.83	56	105	128	16.05	Brown
TA5-32-30	48	6	128	2.43	0.87	58	99	149	19.2	Brown
TA5-32-31	59	4	84	2.23	0.79	54	110	105	12.6	Brown
TA5-32-32	51	6	116	2.31	0.85	57	102	137	17.4	Brown
TA5-32-33	63	6	71	2.15	0.76	53	114	92	10.65	Brown
TA5-32-34	52	4	114	2.31	0.85	57	103	135	17.1	Brown
TA5-32-35	56	5	96	2.25	0.81	55	107	117	14.4	Brown
TA5-32-36	54	4	104	2.38	0.83	56	105	125	15.6	Brown
TA5-32-37	58	5	89	2.25	0.81	55	119	110	13.35	Brown
TA5-32-38	55	5	100	2.38	0.83	56	106	121	15	Brown
TA5-32-39	53	4	109	2.31	0.85	57	104	130	16.35	Brown
TA5-32-40	53	6	111	2.31	0.85	57	104	132	16.65	Brown
Mean	57.42	4.90	92.54	2.27	0.80	54.87	108.53	112.90	13.78	
Range	41-74	4-8	25-205	1.82-2.56	0.61-0.94	48-61	92-125	46-181	3.25-30.75	
SD	6.32	1.08	27.21	0.13	0.06	2.54	6.45	25.29	3.94	
CV	11.00	21.94	29.40	5.72	7.66	4.63	5.94	22.40	28.55	

Table 11. ANOVA of various yield related characters in F_3 progenies in sesame

Sl. No.	Characters	Mean Sum of Squares		F values	
		Between families Df = 4	Within families Df = 36	Between families	Within families
1.	Days to first flowering	265.693	23.367	11.370*	0.627
2.	No. of primary branches	187.559	12.669	14.805*	9.104*
3.	No. of capsules per plant	4422.131	370.178	11.946*	0.525
4.	Capsule length	0.111	0.011	10.162*	0.720
5.	Capsule width	0.023	0.002	10.880*	0.596
6.	No. of seeds per capsule	41.808	3.544	11.798*	0.581
7.	Days to maturity	246.607	26.346	9.360*	0.691
8.	Plant height	4153.786	344.800	12.047*	0.578
9.	Seed yield per plant	76.878	8.285	9.279*	0.533

Table 12. Genetic parameters of yield related characters in F_3 segregating population in sesame

Characters	PCV (%)	GCV (%)	H^2 (%)	GA (%)
Days to first flowering	7.022	3.214	21	3.031
No. of primary branches	11.377	4.017	12.5	2.922
No. of capsules per plant	18.055*	7.807*	18.7	6.954
Capsule length	3.759	1.561	17.2	1.335
Capsule width	4.412	1.973	20	1.818
No. of seeds per capsule	2.903	1.34	21.3	1.274
Days to maturity	3.705	1.627	19.3	1.472
Plant height	14.219	6.351	20	5.844
Seed yield per plant	17.481	5.761	10.9	3.911

and 17.481 respectively indicating high degree of variation. Days to maturity and capsule length also showed low PCV values of 3.705 and 3.759 respectively.

Genotypic coefficient of variation

The highest genotypic coefficient of variation (GCV) was recorded for number of capsules per plant (7.807) followed by plant height (6.351) and seed yield per plant (5.761) indicating high degree of variation, while low GCV values were recorded for number of seeds per capsule (1.34) followed by capsule length (1.561), days to maturity (1.627) and capsule width (1.973) indicating low degree of variation. Genotypic coefficient of variation showed a range from 1.34 to7.807. The GCV values were relatively lower than the respective PCV values for all the characters suggesting the influence of environment on these characters.

Heritability and genetic advance

The heritability values of the characters studied were in a range from 10.9 (seed yield per plant) to 21.3% (number of seeds per capsule). According to the classification suggested by Hanson *et al*. (1956), the characters days to first flowering, number of primary branches, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, days to maturity, plant height and seed yield per plant has low heritability (< 40%), indicating the characters may be controlled by non-additive genes and selection is ineffective.

The highest estimate of genetic advance was observed for number of capsules per plant (6.954) and lowest for number of seeds per capsule (1.254). According to the classification suggested by Jhonson *et al*. (1955), the characters days to first flowering, number of primary branches, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, days to maturity, plant height and seed yield per plant had low genetic advance (< 20%), indicating the characters may be controlled by non-additive genes and selection is ineffective.

4.2.3. Principal Component Analysis

PCA was carried out on the data on biometric observations recorded from the F_3

population. The eigenvalue, percentage variability and cumulative variability of different principal component is depicted in table 13. Out of the nine PC generated, only the first principal component has their eigenvalue greater than 1 and accounts for > 80% of the variance. The per cent contributions of nine characters towards the first principal components is shown in table 14. Rest of the PCs have eigen values < 1 and are of little use in selection. The first principal component captured 89.935% of the variance. The second principal component captured 7.234 % of the variance with a cumulative percentage of variance 97.169%. Hence only the first PC is selected and selection of genotypes present in PC1 is desirable.

PC1 was mostly related with the traits, plant height (12.243) closely followed by days to first flowering (12.197), number of seeds per capsule (12.171), number of capsules per plant (12.072), days to maturity (11.987), capsule width (11.938), capsule length (11.392) and seed yield per plant (11.189). In PC1 the traits, number of capsules per plant (-0.347), capsule length (-0.338), capsule width (-0.346), number of seeds per capsule (- 0.349), plant height (-0.35), days to first flowering (0.349), days to maturity (0.346) and seed yield per plant (-0.335) had absolute value greater than 0.300, indicating that these traits were primarily responsible for genetic divergence among genotypes.

Factor loading of various traits in relation to the principal components is reflected in the table 15. Loadings with absolute scores greater than 0.300 are considered to contribute profusely to genetic divergence. In PC1 the characters, number of capsules per plant (-0.347), capsule length (-0.338), capsule width (-0.346), number of seeds per capsule (-0.349), plant height (-0.350), days to first flowering (0.349), days to maturity (0.346) and seed yield per plant (-0.335) had the absolute value greater than 0.300, indicating that these traits were primarily responsible for genetic divergence among genotypes. In PC2 the trait number of primary branches (-0.967) alone recorded high loadings indicating that divergence among genotypes of PC2 was majorly contributed by this trait.

High PC score for a particular genotype in a particular component denotes high value for variables in that genotype. The PC scores for the selected genotypes of the F_3 generation is given in the table 16. The PC scores for the genotypes in PC1 were 3.723 for TA1-5-1, 5.441 for TA5-2-2, 7.756 for TA5-4-7, 3.816 for TA5-5-1 and 8.785 for TA5-32-

Table 13. Principal components showing the Eigen values, proportion of variation and cumulative percentage of variance in F_3 population of sesame

Principal Components	Eigenvalue	Percentage of variance	Cumulative percentage of variance
PC1	8.094*	89.935	89.935
PC2	0.651	7.234	97.169
PC3	0.12	1.332	98.501
PC4	0.06	0.672	99.173
PC5	0.035	0.394	99.567
PC6	0.025	0.276	99.843
PC7	0.008	0.093	99.935
PC8	0.004	0.045	99.981
PC9	0.002	0.019	100

Table 14. Percentage contribution of variables on PC in F_3 population of sesame

Variables	**PC1**	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Days to first flowering	**12.197**	0.638	0.408	3.463	4.26	0.574	44.637	1.547
Number of primary branches	**4.811**	93.556	1.112	0.113	0.03	0.306	0.001	0.071
Number of capsules per plant	**12.072**	0.018	2.226	1.772	0.389	73.662	5.665	3.404
Capsule length	**11.392**	2.229	19.695	64.863	1.428	0.144	0.202	0.045
Capsule width	**11.938**	1.766	2.788	3.41	37.24	7.891	5.335	29.561
Number of seeds per capsule	**12.171**	0.524	1.838	2.719	13.463	0.002	1.532	65.119
Days to maturity	**11.987**	0.686	0.123	8.221	42.362	12.764	23.751	0.006
Plant height	**12.243**	0.576	0.401	3.324	0.109	0.238	18.853	0.133
Seed yield per plant	**11.189**	0.007	71.41	12.116	0.718	4.419	0.023	0.115

Bold values represent principal components with eigen values >1

Table 15. Principal component analysis for nine yield and yield related traits of F_3 segregating population in sesame

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Days to first flowering	0.349	-0.08	0.064	-0.186	0.206	-0.076	0.668	-0.124	-0.568
Number of primary branches	-0.219	-0.967	-0.105	-0.034	0.017	0.055	0.004	0.027	-0.002
Number of capsules per plant	-0.347	0.013	0.149	0.133	-0.062	-0.858	0.238	0.184	0.089
Capsule length	-0.338	0.149	-0.444	-0.805	-0.12	-0.038	0.045	0.021	-0.005
Capsule width	-0.346	0.133	-0.167	0.185	0.61	0.281	0.231	0.544	0.027
Number of seeds per capsule	-0.349	0.072	-0.136	0.165	0.367	-0.005	0.124	-0.807	0.162
Days to maturity	0.346	-0.083	0.035	-0.287	0.651	-0.357	-0.487	0.008	0.032
Plant height	-0.35	0.076	-0.063	0.182	-0.033	-0.049	-0.434	-0.036	-0.801
Seed yield per plant	-0.335	0.008	0.845	-0.348	0.085	0.21	-0.015	-0.034	-0.006

Table 16. Principle component scores from standardised variables of selected F_3 plants

Genotypes	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
TA1-5-1	3.723	1.179	0.125	-0.136	0.040	-0.198	0.026	0.066	0.020
TA5-2-2	5.441	1.839	0.908	-0.072	0.123	-0.150	0.005	-0.048	0.042
TA5-4-7	7.756	1.395	0.910	-0.060	-0.054	1.249	-0.354	-0.128	-0.114
TA5-5-1	3.816	0.185	-0.199	0.132	-0.320	0.009	0.126	0.005	0.017
TA5-32-25	8.785*	1.231	1.708	-0.260	-0.020	0.975	-0.250	0.086	-0.071

25. Among the plants of the F_3 population, these genotypes exhibited high variability for the traits capsule length, number of seeds per capsule, capsule width, days to first flowering, days to maturity, plant height, number of capsules per plant and seed yield per plant.

The correlation between variables and the principal components is given in table 17. The high loadings of the traits days to first flowering (-0.994), capsule length (0.96), capsule width (0.983), number of seeds per capsule (0.993), plant height (0.995), number of capsules per plant (0.988), days to maturity (-0.985) and seed yield per plant (0.952) indicate that these traits strongly influence the principal component I. PC2 was highly influenced by the characters number of primary branches (0.78) followed by capsule length (-0.12) and capsule width (-0.107), while all the other traits exhibited a negligible influence on it.

4.2.4. Multiple linear regression

Linear regression analysis was performed with seed yield per plant as dependent variable and other agronomic traits as independent variables. The fitted model has R^2 value of 90.30 % which indicates that 90.30% of the variability in seed yield is explained. The adjusted R^2 statistic, which is more suitable for comparing models with different numbers of independent variables, is also 89.9%.

The standard error of the estimate shows that the standard deviation of the residuals is 1.271. Since the *P*-value is greater than 0.05, there is no indication of serial autocorrelation in the residuals at the 95.0% confidence level. Table 18 shows the results of fitting a multiple linear regression model to describe the average relationship between seed yield and eight independent variables. The fitted model was:

Seed yield per plant (Y) = $50.215 - 0.184 X_1 + 0.095 X_2 + 0.134 X_3 - 2.024 X_4 + 21.535 X_5 - 0.746 X_6 - 0.069 X_7 - 0.026 X_8$

It was observed that the characters, viz. days to first flowering, number of primary branches, capsule length, capsule width, number of seeds per capsule, plant height and days to maturity were not significant (*P* values > 0.05). Stepwise regression, with backward elimination, does not exhibit a major deviation in R^2 value (table 19). Hence the prediction equation model to describe the relationship between seed yield per plant and 7 independent variables is not changed. The character number of capsules per plant only had an estimate of P value < 0.05, suggesting its contribution to seed yield per plant.

4.2.5. Biochemical parameters

The biochemical parameters namely peroxidase activity, polyphenol oxidase activity, crude protein content and oil content of the selected five F_3 individual plants from the population is presented in table 20. The peroxidase activity ranged from 11.6 to 90.1, while polyphenol oxidase activity ranged from 1.7 to 6.63. The genotype TA5-32-25 recorded maximum crude protein content (29.18 %), followed by TA5-4-7 (28.87 %), TA5-2-2 (28.31 %), TA1-5-1 (24.81%) and TA5-5-1 (17.5%). Highest oil content was observed for TA5-4-7 (50.01%) followed by TA5-32-25 (45.0%), TA1-5-1 (41.0 %), TA5- 2-2 (38.0%) and TA5-5-1 (35.0%).

Table 17. Correlation between variables and PCs in F_3 population of sesame

Variables	**PC1**	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Days to first flowering	**-0.994**	0.064	0.022	0.046	0.039	0.012	0.061	0.008
Number of primary branches	**0.624**	0.78	-0.037	0.008	0.003	-0.009	0	-0.002
Number of capsules per plant	**0.988**	-0.011	0.052	-0.033	-0.012	0.135	0.022	-0.012
Capsule length	**0.96**	-0.12	-0.154	0.198	-0.023	0.006	0.004	-0.001
Capsule width	**0.983**	-0.107	-0.058	-0.045	0.115	-0.044	0.021	-0.035
Number of seeds per capsule	**0.993**	-0.058	-0.047	-0.041	0.069	0.001	0.011	0.052
Days to maturity	**-0.985**	0.067	0.012	0.071	0.123	0.056	-0.045	-0.001
Plant height	**0.995**	-0.061	-0.022	-0.045	-0.006	0.008	-0.04	0.002
Seed yield per plant	**0.952**	-0.007	0.293	0.086	0.016	-0.033	-0.001	0.002

Bold values represent principal components with eigen values >1

Table 18. Variables selected by the model of multiple linear regression with their corresponding coefficient values (a_i), standard error (SE), *t* value and significance level (*p*) according to the model used in F_3 population of sesame

Parameter	Estimate	Std. Error	T value	P-value
Intercept	50.215	22.480	2.234	0.027
Days to first flowering	-0.184	0.223	-0.825	0.411
Number of primary branches	0.095	0.114	0.829	0.408
Number of capsules per plant	0.134	0.021	6.275	0.000*
Capsule length	-2.024	2.528	-0.801	0.424
Capsule width	21.535	14.133	1.524	0.129
Number of seeds per capsule	-0.746	0.473	-1.578	0.116
Days to maturity	-0.069	0.097	-0.710	0.479
Plant height	-0.026	0.071	-0.369	0.712

Regression coefficients with P-value <0.05 are significant.

R squared – 0.903; Adj R squared – 0.899; Residual Standard error – 1.271

Table 19. Variables selected by the model of multiple linear regression after stepwise regression with backward elimination according to the model used in F_3 population of sesame

Parameter	Estimate	Std. Error	T value	P-value
Intercept	41.755	20.223	2.065	0.040
Days to first flowering	-0.173	0.107	-1.608	0.109
Number of primary branches	0.105	0.113	0.929	0.354
Number of capsules per plant	0.132	0.019	6.820	0.000*
Capsule width	19.951	13.872	1.438	0.152
Number of seeds per capsule	-0.852	0.446	-1.912	0.057

Regression coefficients with P-value <0.05 are significant.

R squared – 0.902; Adj R squared – 0.900; Residual Standard error – 1.266

Table 20. Biochemical parameters of selected five F_3 progenies in sesame

Progeny	Peroxidase activity	Polyphenol activity	Crude Protein (%)	Oil content (%)
TA1-5-1	4.3	6.63*	24.81	41.0
TA5-2-2	90.1*	6.2	28.31	38.0
TA5-4-7	19.4	1.7	28.87	50.01*
TA5-5-1	1.6	2.4	17.5	35.0
TA5-32-25	33.9	6.6	29.18*	45.0

DISCUSSION

5. DISCUSSION

Breeding gains in sesame are low and stagnant compared to other oilseed crops such as groundnut and sunflower. Selection for improved seed yield and yield components remains the key breeding strategy. The main yield-related traits include early and uniform maturity, reduced plant height, higher number of capsules per plant, number of branches per plant, number of seeds per capsule, and heavier 1000-seed weight. Many investigations reported that the selection in segregating populations may give promising results in improving sesame performance. Observed genetic gains in seed yield of sesame were achieved by pedigree selection for two cycles in segregating generations of different populations. The present study aims at studying the segregating populations of sesame and selecting high yielding lines suitable for cultivation in Kerala.

5.1. Evaluation of F_2 segregants in sesame

The present study was conducted for the assessment of genetic variability for different traits among the F_2 segregating population of three F_1 crosses of sesame. Transgressive segregations in hybrid progenies have been earlier reported by many plant breeders. It refers to appearance of individuals, in the progeny from a hybrid, which exceed either of the two parents of the hybrid with respect to one or more characters. Success in obtaining the desired transgressive segregants depends on obtaining genetic recombination between both linked and unlinked alleles (Briggs and Allard, 1953). The pedigree method of breeding has been designed for utilisation of transgressive segregants (Singh, 2002).

The segregating population exhibited a wide range for all the characters studied as revealed by the high values of coefficient of variation. The character, seed yield per plant recorded the highest CV closely followed by number of capsules per plant. The least CV was recorded by number of seeds per capsule and capsule length. Presence of good amount of variation in segregating populations of sesame was earlier reported by Rajavindran *et al.* (2002), Prasad *et al.* (2013) and Bharathi and Reddy, (2019).

The character, days to first flowering ranged from 29-75 days. The earliest flowering was recorded for TA5-7 and the late flowering was recorded for TTA2-8. The wide range for this character suggests ample scope for improvement with respect to earliness in this crop.

Mean value for the character, number of primary branches was recorded as 5.15

which ranged from 4-8. Among the population, number of capsules per plant ranged from 15-178. A wide range for this character in the segregating population of sesame was earlier reported by Bharathi and Reddy, (2019). While, capsule length and capsule width recorded a very narrow range of 1.85-2.68 and 0.61-0.98 respectively, suggesting limited scope for improvement.

The mean value for the character number of seeds per capsule was recorded as 51.61. It ranged from 45.5-65.5. The highest number of seeds per capsule was recorded for TA5-4 and the lowest was recorded for TA5-101. Days to maturity ranged from 80-126 days suggesting high variation with respect to duration of the crop.

The height of the plants in the segregating population ranged from 37-175.5. The highest plant height was recorded for TA5-5 and the lowest was recorded for TA5-49. Seed yield per plant ranged from 2.28-28.24 g, suggesting ample scope of improvement with respect to economic yield. Rajavindran *et al*. (2002), Prasad *et al.* (2013) and Bharathi and Reddy, (2019) also reported similar results.

5.1.1. Correlation analysis

The correlation between the yield and yield related characters will give valuable insights into the relevant characters for selection. In the present study days to maturity recorded a negative correlation with all the characters except days to maturity. A strong positive correlation of 0.990 was observed between days to first flowering and days to maturity. Number of primary branches had a positive correlation with all the characters except days to first flowering and days to maturity. Seed yield per plant recorded a strong positive correlation with all the traits except with days to first flowering and days to maturity.

Negative correlation of days to flowering and days to maturity with seed yield per plant was earlier reported by Saravanan *et al*. (2020), Disowja *et al*. (2020), Bhattacharjee *et al*. (2021) and Patel *et al*. (2024). While contradictory results of positive correlation were recorded by Kiruthika *et al.* (2020), Vivek *et al*. (2022), Kumar *et al*. (2022), Patel *et al*. (2022), (Islam, 2022), Pratyusha *et al*. (2022), Thiyagu *et al*. (2023), Parvathy (2023) and Islam *et al*. (2024).

Number of primary branches per plant exhibiting a positive correlation with seed yield per plant was earlier recorded by Saravanan *et al*. (2020), Vivek *et al*. (2022), Kumar *et al*. (2022), (Islam, 2022), Pratyusha *et al*. (2022), Kumari and Shah (2023), Islam *et al.*

(2024) and Aiye *et al.* (2024). While a negative correlation was observed by Varada (2023).

Number of capsules per plant exhibiting a positive correlation with seed yield per plant was earlier recorded by Disowja *et al*. (2020), Bhattacharjee *et al*. (2021), Mahdi *et al.* (2023), Kumari and Shah (2023), Madhu *et al*. (2023), Varada (2023), Tabrizi (2024), Wang *et al.* (2024) and Patel *et al*. (2024). Capsule length exhibiting a positive correlation with seed yield per plant was earlier recorded by Kiruthika *et al.* (2020), Hassen (2022) and Khuntia *et al*. (2024). Capsule width exhibiting a positive correlation with seed yield per plant was earlier recorded by Kiruthika *et al.* (2020) and Khuntia *et al*. (2024).

Plant height exhibiting a positive correlation with seed yield per plant was earlier recorded by Saravanan *et al*. (2020), Disowja *et al*. (2020), Patel *et al*. (2022), Islam (2022), Thiyagu *et al*. (2023), Kumari and Shah (2023) and Wang *et al.* (2024). Number of seeds per capsule exhibiting a positive correlation with seed yield per plant was earlier recorded by Bhattacharjee *et al*. (2021), Vivek *et al*. (2022), Kumar *et al*. (2022), Patel *et al*. (2022), Pratyusha *et al*. (2022), Parvathy (2023) and Aiye *et al.* (2024).

Since, seed yield per plant was positively correlated with number of primary branches, capsule length, capsule width, number of seeds per capsule, plant height and number of capsules per plant these characters can be further used for selection for improving yield and related parameters.

5.1.2. Principal Component Analysis

Principal Component Analysis (PCA) is a multivariate analysis statistical procedure used to transform a number of possibly correlated variables into a smaller number of uncorrelated variables called principal components. In the present study, PCA was carried out to identify the most variable principal components which may be given due importance in selecting the genotypes for yield related characters. This technique has been widely used for studying genetic variability in sesame (Teklu *et al.*, 2021; Durge *et al.*, 2022).

Multivariate analysis of the genotypes of the F_2 population showed that the first two PCs (PC1 to PC2) having eigenvalues > 1.0 and cumulatively accounted for 88.832% of the total variation (Fig 1.). From the third PC onwards, the line is almost flat. Hence 2 PCs are selected and selection of genotypes present in 2 PCs are desirable. Evaluation of genetic divergence in sesame germplasm using principal component analysis was done by Ismaila and Usman (2014), Baraki *et al*. (2015), Wang *et al.* (2017), Singh *et al*. (2018), Sasipriya *et al.* (2022), Bisen *et al*. (2023) and Hika *et al*. (2023), which resulted in grouping them into different clusters.

The variation in PC1 was largely correlated with the traits, capsule length, number of seeds per capsule, capsule width, number of primary branches, plant height, number of capsules per plant and seed yield per plant (fig 2.). High contribution of yield related parameters on principal components in sesame was reported by Tanwar and Bisen (2017), Ozcinar and Sogut (2017), Aristya *et al.* (2017), Dash *et al.* (2020), Gupta *et al.* (2021), Sasipriya *et al.* (2022), Durge *et al*. (2022), Sonaniya *et al.* (2023) and Hassan and Endale (2023).

The second principal component was related to days to maturity and days to first flowering as indicated by the fig 2. The high influence of the trait days to first flowering on principal component was also supported by Tripathi *et al*. (2013), Shim *et al*. (2016) and Mukthambica *et al*. (2023).

Figure 3 depicts the biplot created using the first two PCs, which reveals that the genotypes of the segregating population of sesame is scattered in all the four quadrants. The genotypes in the first quadrant had similar capsule length, number of seeds per capsule, capsule width, number of primary branches, plant height, number of capsules per plant and seed yield per plant. The related genotypes can be found closer to each other and nearer to the origin. The traits days to maturity and days to flowering were placed in the second quadrant and hence genotypes belonging to this quadrant have longer duration (Fig 4). While the genotypes in the third and fourth quadrants may be selected for earliness.

The selected F_2 individuals namely TA1-5, TA5-2, TA5-4, TA5-5 and TA5-32, which were positioned in the first and the fourth quadrant indicating their earliness and high yield related parameters. The calculated PC score was also high compared to other genotypes. Selection of genotypes based on PC score were resorted to by many scientists in sesame (Wang *et al.*, 2017; Singh *et al*., 2018; Baraki *et al*., 2020 and Mukthambica *et al*., 2023)

The correlation between variables and the principal components is given in figure 5. The genotypes and variables near to each other are associated to each other while those in opposite direction are negatively associated to each other. The high loadings of the traits number of primary branches, capsule length, capsule width, number of seeds per capsule,

Fig. 1. Scree plot indicating Eigen values and percentage variation in F_2 population of sesame

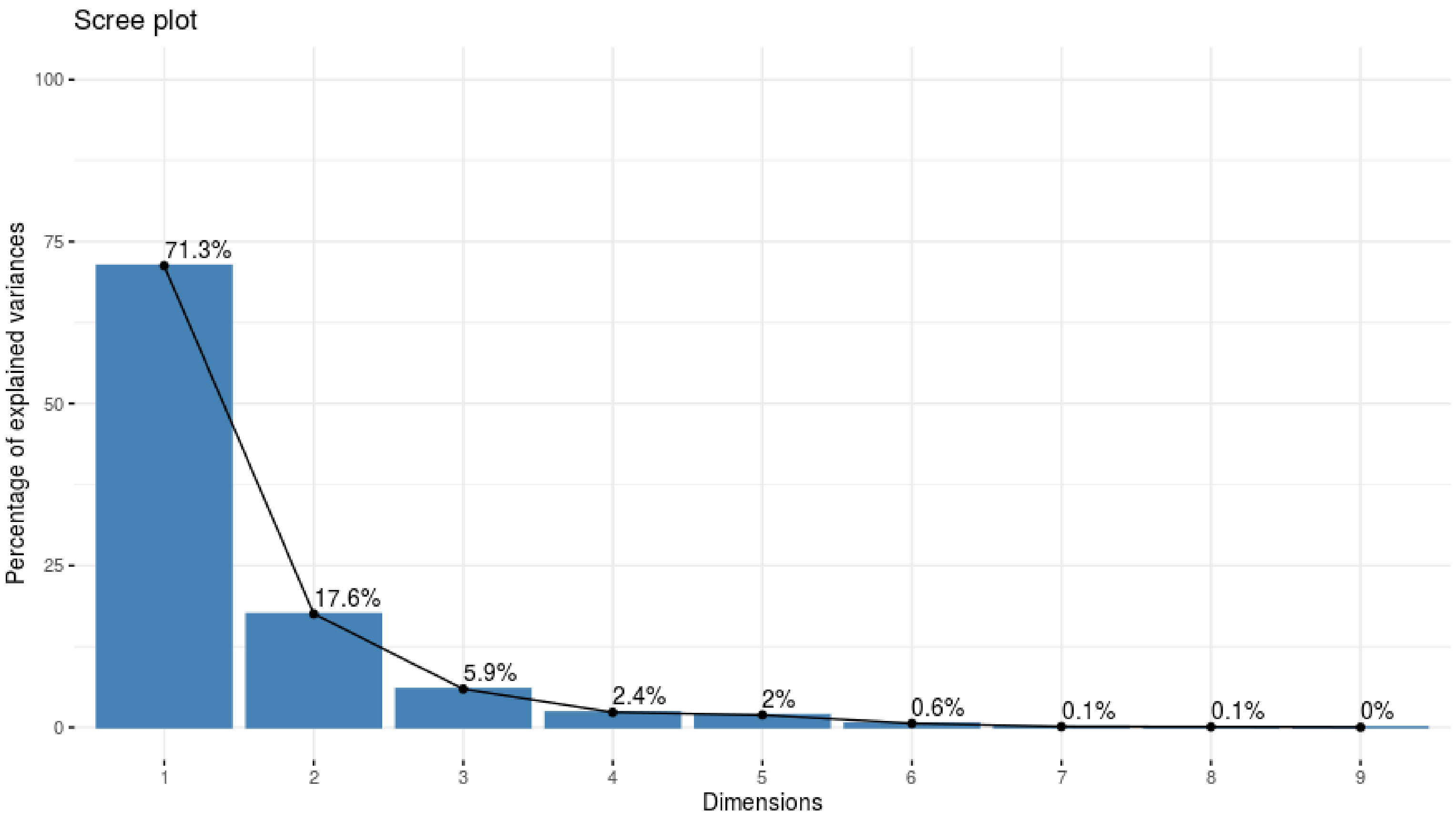


Fig 2. Projection of yield related characters on the first two principal components in F_2 population of sesame

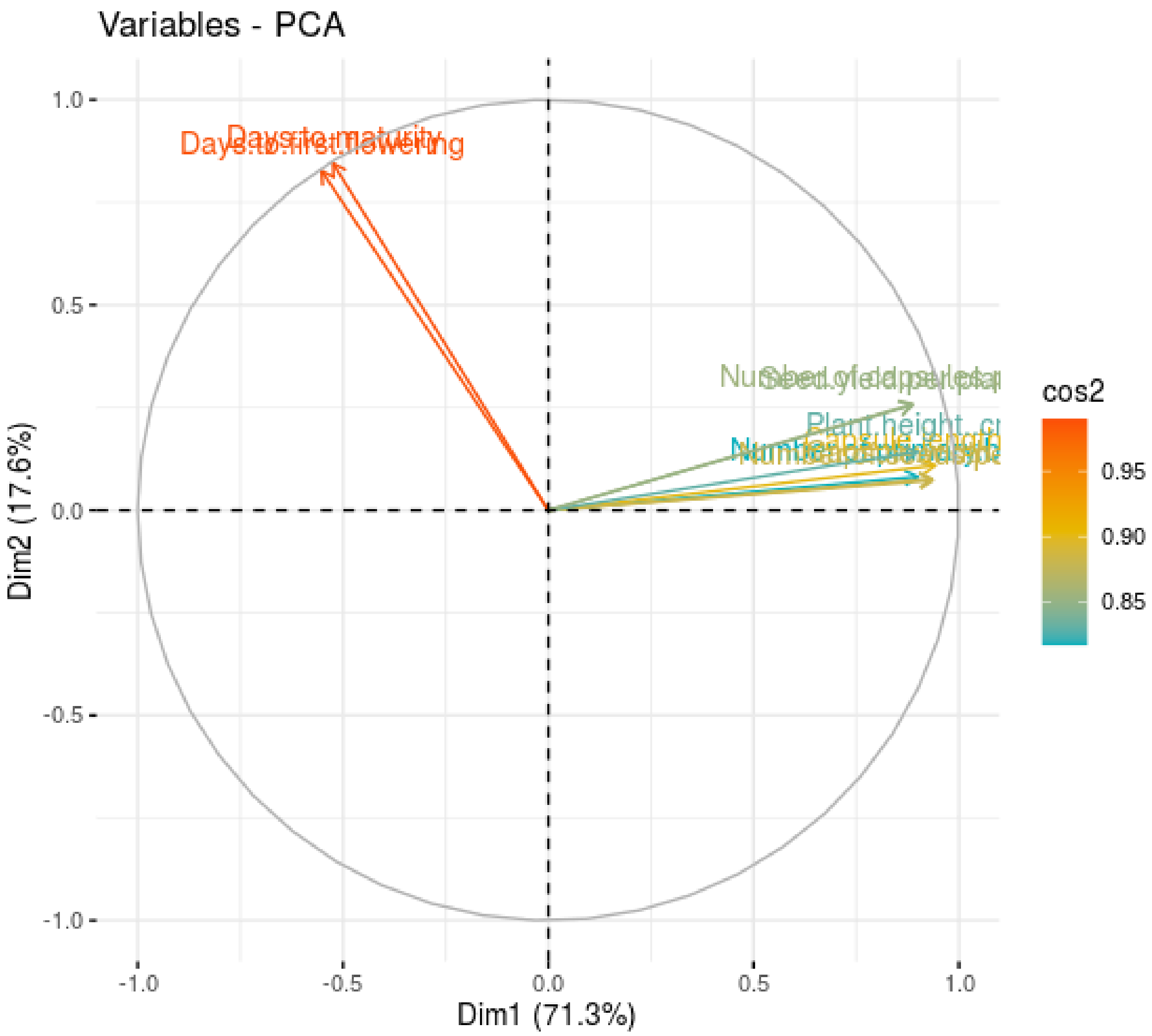


Fig 3. Individual Principal Component Analysis in F$_2$ population of sesame

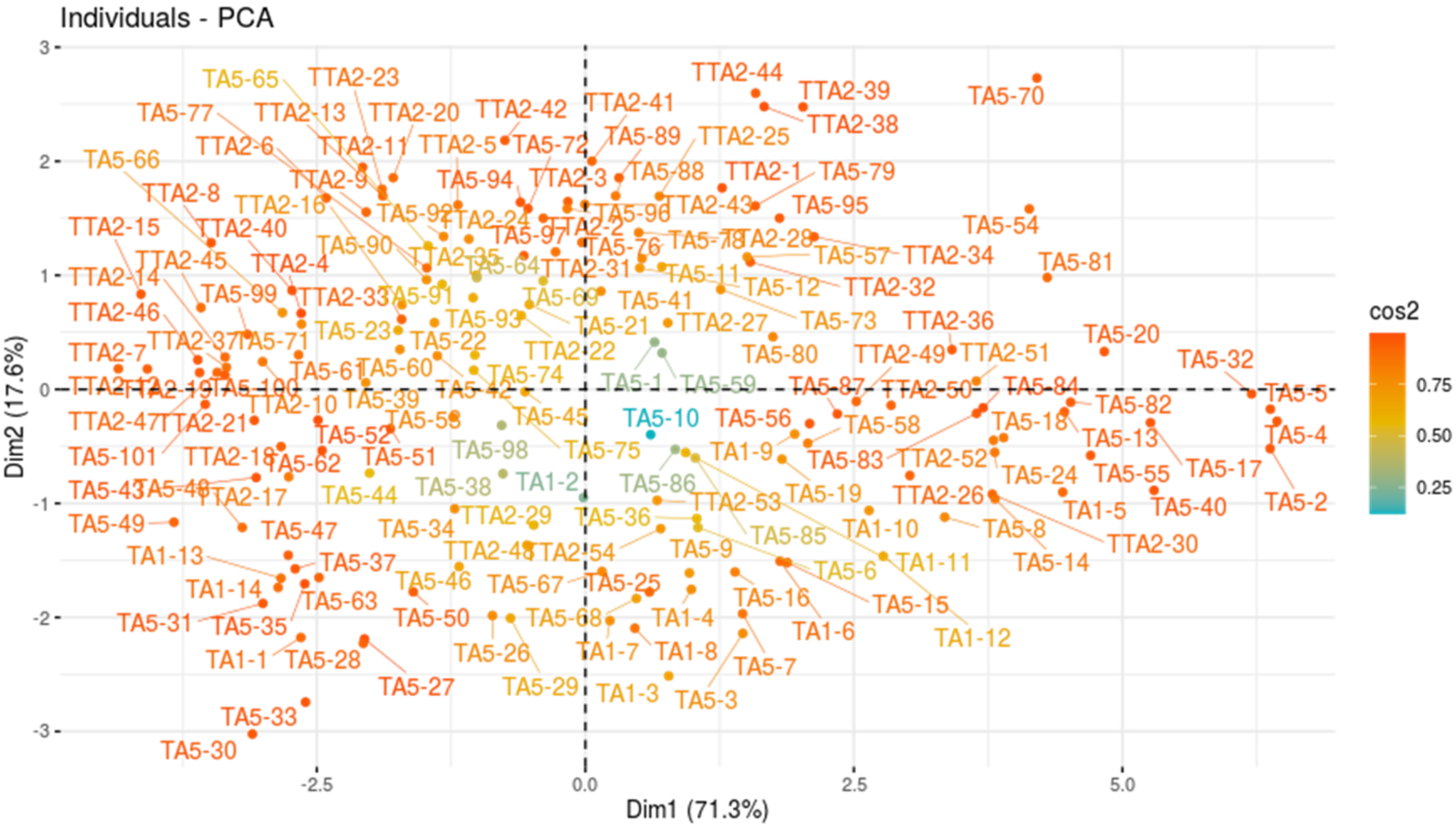


Fig 4. Two dimensional biplot of Principal Component Analysis in F_2 population of sesame

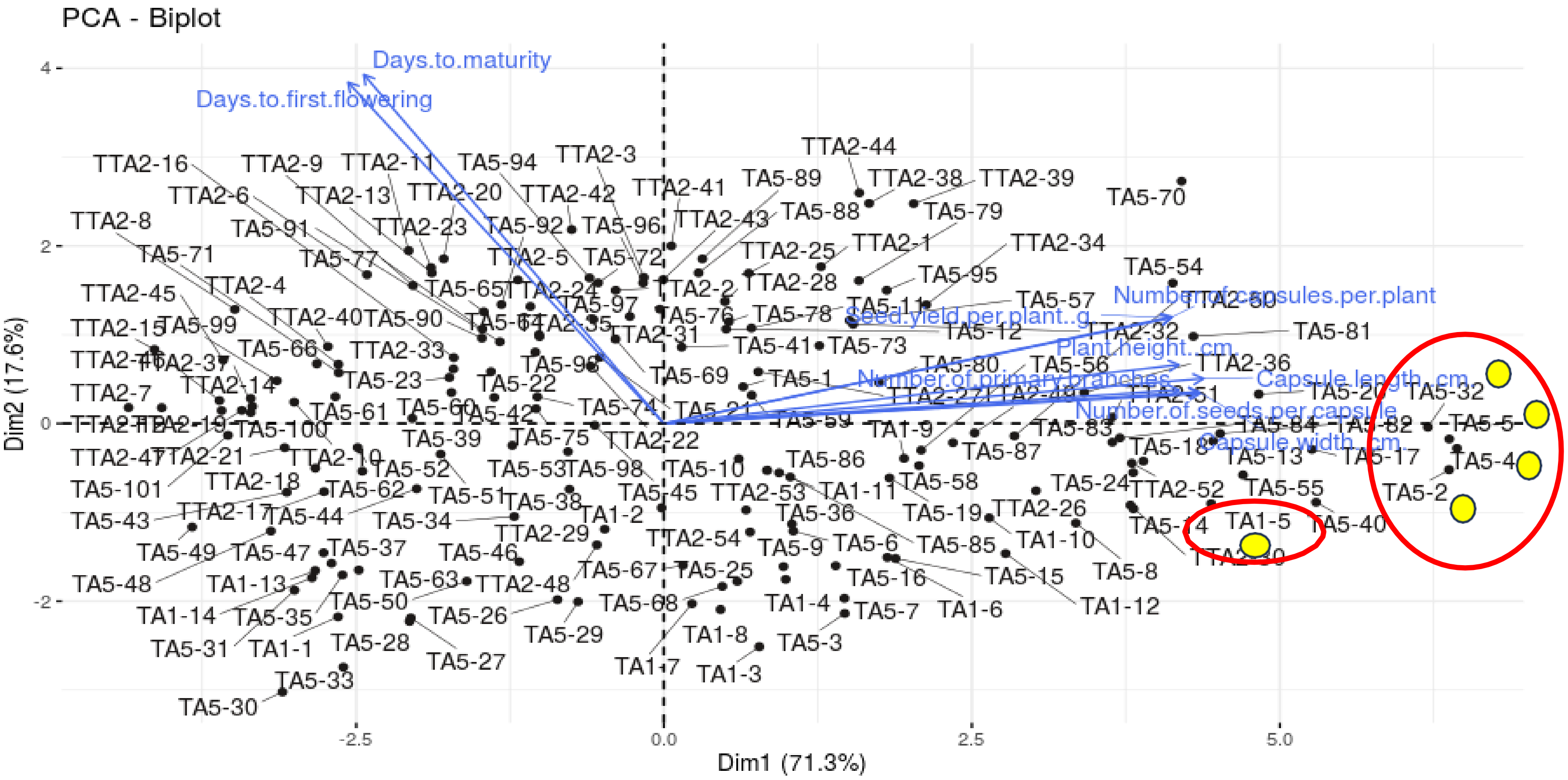
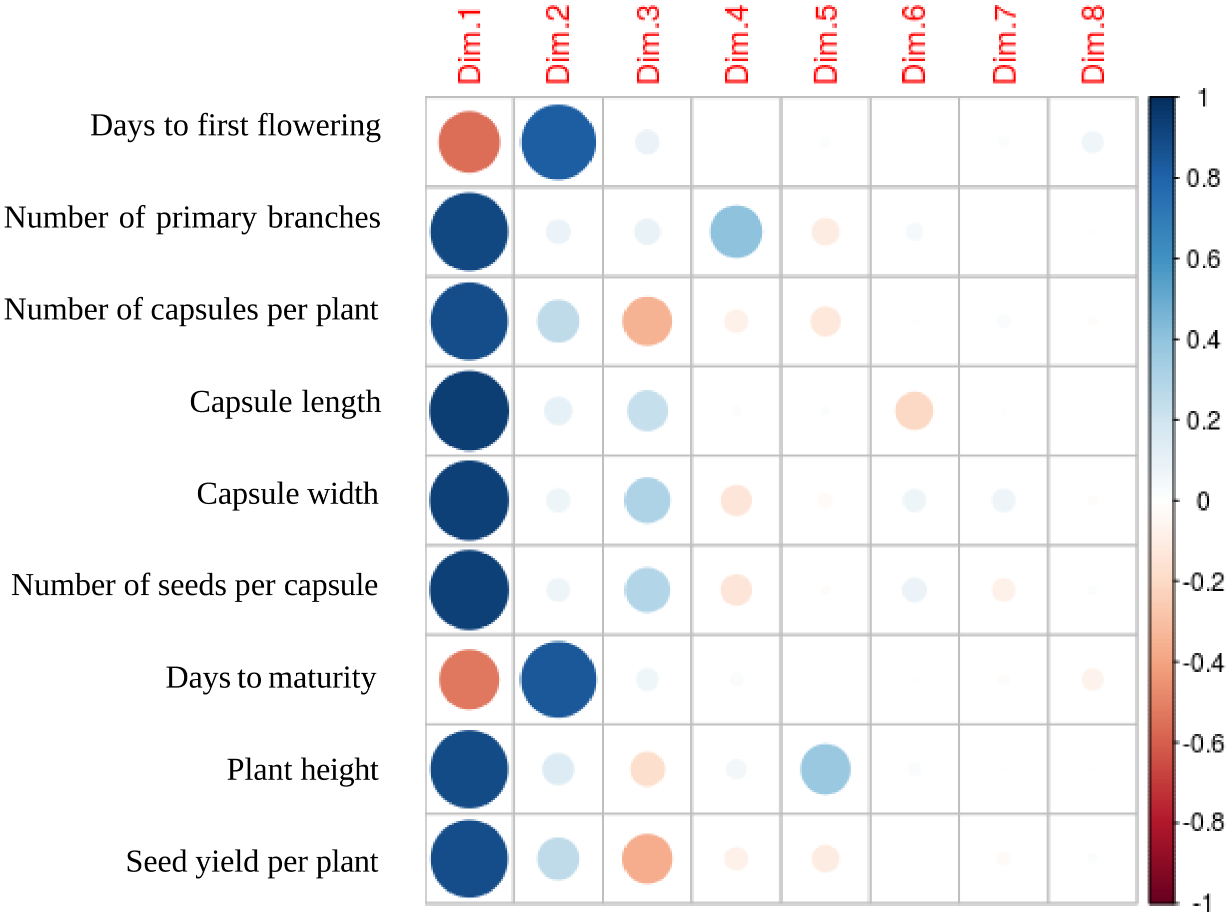


Fig 5. Correlation plot of variables vs PCs in F_2 population of sesame



plant height, number of capsules per plant and seed yield per plant indicate that these traits strongly influence the principal component I. PC2 was highly influenced by the characters days to first flowering and days to maturity, while all the other traits exhibited a negligible influence on it. A positive correlation of yield related parameters on principal components were recorded by Shim *et al.* (2016), Ozcinar and Sogut (2017), Sasipriya *et al.* (2022), Hassan and Endale (2023) and Mukthambica *et al*. (2023). Duration of the crop as indicated by days to flowering and days to maturity were also reported to have a high correlation with PC (Shim *et al.*, 2016; Sasipriya *et al.*, 2022; Hassan and Endale, 2023 and Mukthambica *et al*., 2023)

5.1.3. Multiple linear regression

Regression analysis is a statistical method used for the estimation of relationships between a dependent variable and one or more independent variables. It is useful in assessing the strength of the relationship between variables and for modelling the future relationship between them. Linear regression analysis was performed with seed yield per plant as dependent variable and agronomic traits as independent variables (Fig 6). The analysis revealed significant contribution of number of capsules per plant, capsule width, number of seeds per capsule and plant height on seed yield per plant.

The trait number of capsules per plant being the most important character to explain the total variation on seed yield through regression analysis was also observed by Parimala and Mathur (2006), El-Mohsen *et al*. (2008), Atalou *et al*. (2014) and Aristya *et al.* (2017) in sesame. Narayanaswamy *et al.* (2012) and Parimala and Mathur (2006) reported the importance of the characters plant height and number of seeds per capsule on seed yield per plant in sesame through step-wise regression analysis.

5.2. Evaluation of F_3 segregants in sesame

5.2.1. Genetic variability

The study was conducted to evaluate the genetic variability for various traits within the F_3 segregating population of five F_2 sesame families. All the characters recorded significant differences between the five families, while within families only number of primary branches was estimated to have significant difference. The family TA5-32 can be considered as superior since it recorded significantly different values for the yield related characters namely seed yield per plant, number of capsules per plant, capsule width, seeds per capsule and plant height. The days to first flowering and days to maturity were also found to be the lowest in the same family. This suggests that there is ample scope of selection from the segregating generations of the family TA5-32.

The population displayed a broad range of variation across all traits, as indicated by the high coefficient of variation (CV) values. Number of capsules per plant showed the highest CV, followed closely by seed yield per plant. Conversely, the number of seeds per capsule, capsule length and days to maturity exhibited the lowest CV. Previous studies by Rajavindran *et al*. (2002), Prasad *et al*. (2013), and Bharathi and Reddy (2019) similarly reported significant variation in segregating sesame populations.

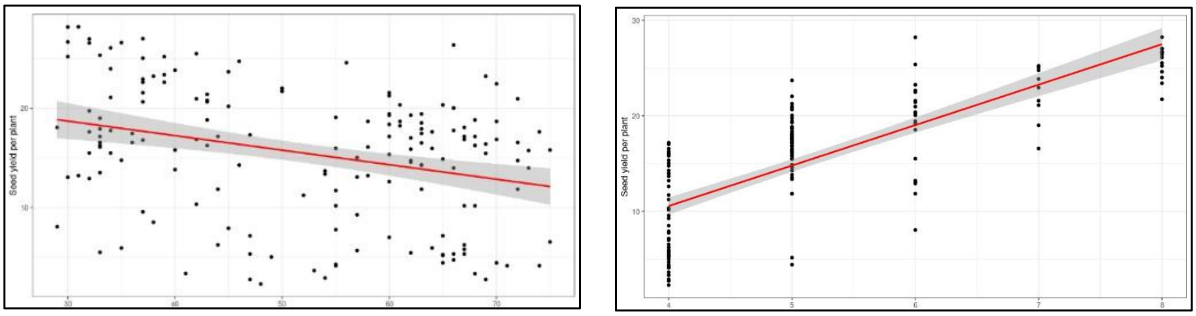
The days to first flowering ranged from 41-74 days, with TA5-32-25 being the earliest flowering and TA5-4-18 the latest. This wide variation suggests there is significant potential for improving earliness in the crop. The mean number of primary branches was 4.90, ranging from 4 to 8. In the population, the number of capsules per plant varied widely, from 25 to 205, a finding consistent with Bharathi and Reddy (2019). In contrast, capsule length (1.82 to 2.56 cm) and capsule width (0.61 to 0.94 cm) showed a narrow range, indicating limited scope for improvement in these traits.

The mean number of seeds per capsule was 54.87, ranging from 48 to 61. The highest number of seeds per capsule was found in TA5-4-7, while the lowest was observed in TA5-4-18. Days to maturity varied from 92 to 125 days, demonstrating considerable variation in crop duration. Plant height in the population ranged from 46 to 181 cm, with TA5-4-7 having the tallest plants and TA1-5-24 the shortest. Seed yield per plant ranged from 3.25 to 27.75 grams, indicating substantial potential for yield improvement. Similar findings were reported by Rajavindran *et al*. (2002), Prasad *et al*. (2013), and Bharathi and Reddy (2019).

5.2.2. Genetic parameters

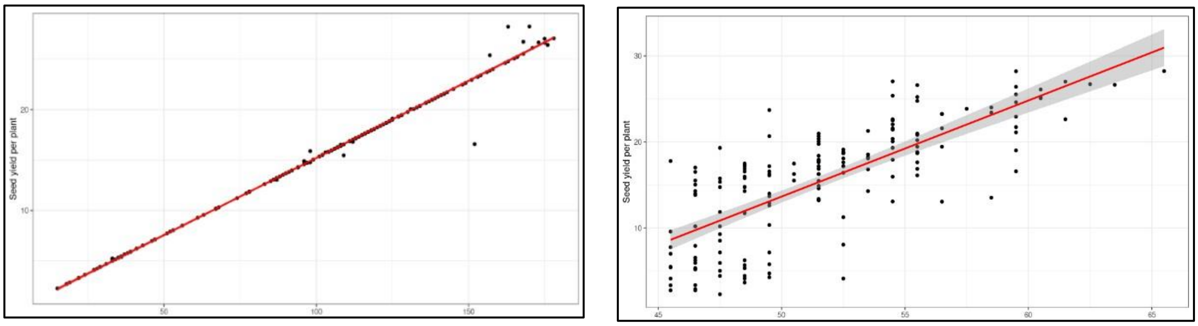
Analysis of variance offers an estimation of phenotypic, genotypic, and environmental variances. Phenotypic variation encompasses both genetic and environmental factors, and thus fluctuates depending on environmental conditions. The coefficient of variation is useful in distinguishing whether the observed variability among genotypes is due to genetic factors or environmental effects. Estimates of the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) revealed a considerable level

Fig 6. Multiple linear Regression of seed yield per plant in F_2 population of sesame



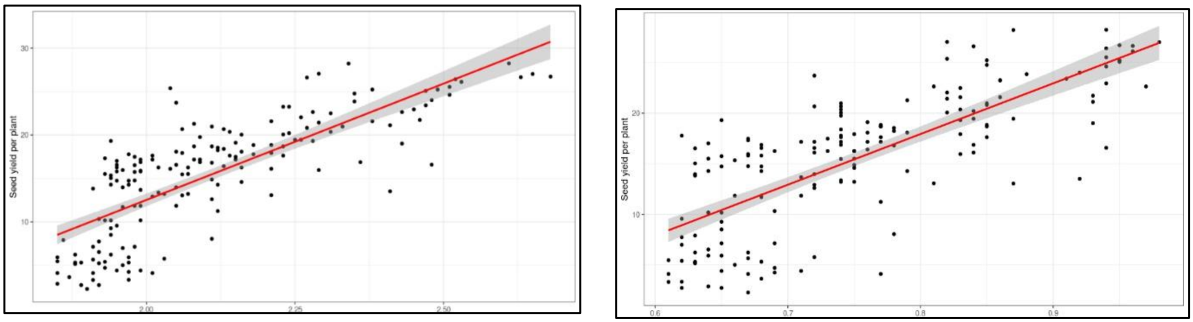
Days to first flowering

Number of primary branches



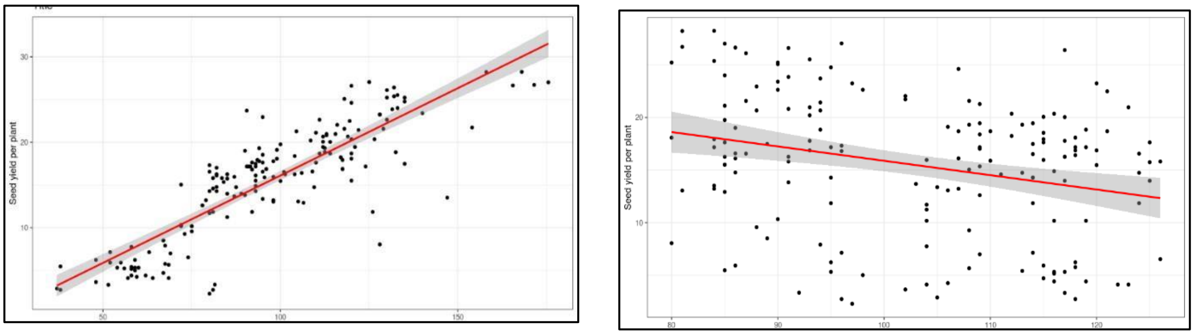
Number of capsules per plant

Number of seeds per capsule



Capsule length

Capsule width



Plant height

Days to maturity

of variation among the genotypes for all the traits examined.

A highly significant variation was observed for traits such as days to first flowering, number of primary branches, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, days to maturity, plant height and seed yield per plant. Similar wide variability in sesame traits was reported by Prasad *et al*. (2013) and Kadvani *et al*. (2020). The phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all traits studied, highlighting the environmental influence on these traits.

Coefficient of variation

The highest PCV and GCV values were noted for the character number of capsules per plant consistent with the findings of Mohanty *et al*. (2020), Hukumchand and Parameshwarappa (2020), Vamshi *et al*. (2021), Sheoran *et al*. (2022), Roy *et al*. (2022), Thouseem (2022), Rahna *et al*. (2023), Sala and Vadivel (2023), Kumari and Kumhar (2023), Idris *et al*. (2023), Thiyagu *et al*. (2023) Dhandapani *et al*. (2023), Parvathy (2023). High PCV and GCV were recorded for number of capsules per plant followed by plant height and seed yield per plant similar to the findings of Bharathi (2019) and Bharathi and Reddy (2019) indicating substantial variability suitable for selection. However, Kadvani *et al*. (2020) and Takele *et al.* (2020) reported only moderate PCV and GCV values for the same trait. High PCV and GCV values for seed yield per plant align with the results of Manjeet *et al.* (2020), Mohanty *et al*. (2020), Kadvani *et al*. (2020), Akkiligunta *et al.* (2024), Ramya *et al*. (2024) and Sarang *et al*. (2024).

Conversely, traits like days to maturity, capsule length, and number of seeds per capsule showed low coefficients of variation, indicating limited variability and restricting the potential for crop improvement through selection. Low PCV and GCV values for number of seeds per capsule align with results of Sala and Vadivel (2023). Low PCV and GCV values for days to maturity align with results of Kadvani *et al*. (2020), Hukumchand and Parameshwarappa (2020), Patel *et al*. (2023), Sala and Vadivel (2023), Thiyagu *et al*. (2023) and Parvathy (2023). Low PCV and GCV values for capsule length align with results of Takele and Abera (2023) and Parvathy (2023).

The environment had a significant impact on all traits, as indicated by the higher PCV compared to GCV. The substantial difference between PCV and GCV for traits such as the number of capsules per plant and number of seeds per capsule further emphasizes the strong environmental influence on these characteristics since it was a segregating population.

Heritability and genetic advance

Heritability and genetic advance are key parameters for selection. Heritability refers to the proportion of phenotypic variance that is inherited, expressed as the ratio of genotypic variance to total variance. While heritability alone provides some insight, combining it with genetic advance offers a more accurate prediction of selection gains. It is not always the case, however, that traits with high heritability also exhibit high genetic advance. Heritability serves as a valuable index for assessing the transmission of traits from parents to offspring, assisting breeders in selecting superior genotypes from diverse populations.

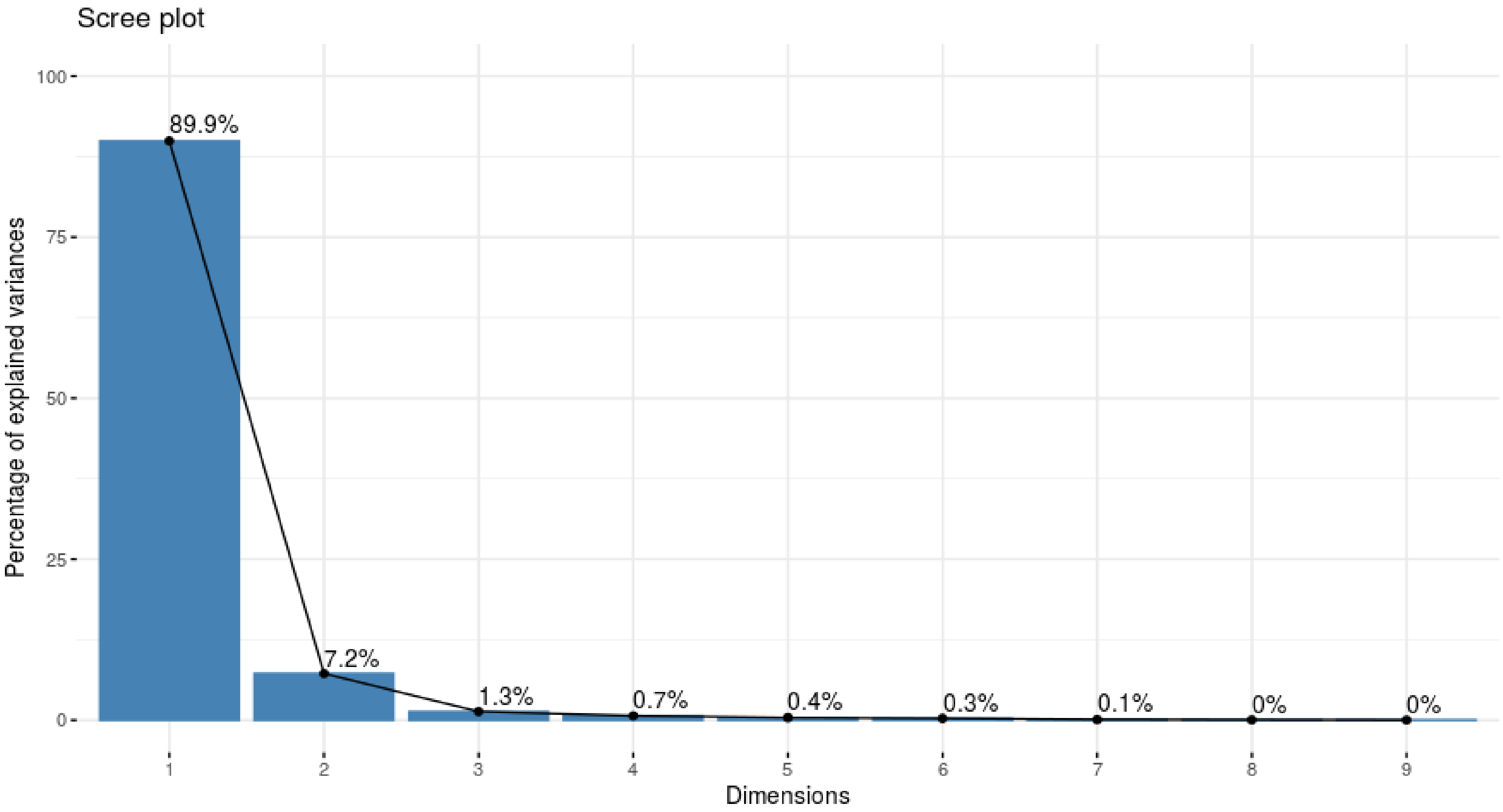
Heritability was calculated for 9 traits, including days to first flowering, number of primary branches, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, days to maturity, plant height and seed yield per plant. All the characters exhibited low heritability coupled with low genetic advance as percent mean since they were segregating population.

Several studies have consistently reported low heritability combined with low genetic advance for key agronomic traits, suggesting limited potential for improvement through selection. Bharathi (2019) and Bharathi & Reddy (2019) observed this for days to 50% flowering, while Kumari *et al*. (2020) noted it for days to maturity and capsule length. Similarly, Takele & Abera (2023) found this trend for days to flowering, plant height, and capsule length. Sala & Vadivel (2023) reported it for days to maturity, and Parvathy (2023) confirmed the same pattern for days to first flowering, days to maturity, and capsule length. These findings suggest that traditional breeding methods may be less effective for these traits, and alternative approaches may be needed to enhance genetic improvement.

5.2.3. Principal Component Analysis

PCA was carried out on the data on the biometric observations recorded from the F_3 population. Out of the nine PC generated, only the first principal component has their eigenvalue greater than 1 and accounts for > 80% of the variance (Fig 7). The first principal component captured 89.935% of the variance. From the third PC onwards, the line is almost flat. Hence only the first PC is selected and selection of genotypes present in PC1 is desirable.

Fig 7. Scree plot indicating Eigen values and percentage variation in F_3 population of sesame



Evaluation of genetic divergence in sesame germplasm using principal component analysis was done by Ismaila and Usman (2014), Baraki *et al.* (2015), Wang *et al.* (2017), Singh *et al.* (2018), Sasipriya *et al.* (2022), Bisen *et al.* (2023) and Hika *et al.* (2023), which resulted in grouping them into different clusters.

PC1 was mostly related with the traits, plant height closely followed by days to first flowering, number of seeds per capsule, number of capsules per plant, days to maturity, capsule width, capsule length and seed yield per plant (fig 8). High contribution of these characters on principal components in sesame was reported by Tanwar and Bisen (2017), Dash *et al.* (2020), Gupta *et al.* (2021), Sasipriya *et al.* (2022), Durge *et al.* (2022), Sonaniya *et al.* (2023), Hassan and Endale (2023) and Mukthambica *et al.* (2023).

Figure 9 depicts the biplot created using the first two PCs, which reveals that the genotypes of the segregating population of sesame is scattered in all the four quadrants. The genotypes in the first quadrant had similar number of primary branches, plant height, number of capsules per plant and seed yield per plant. In the second quadrant genotypes with similar days to maturity and days to flowering were incorporated. The genotypes with similar capsule length, number of seeds per capsule and capsule width were placed in the fourth quadrant.

High PC score for a particular genotype in a particular component denotes high value for variables in that genotype. The selected genotypes of the F_3 generation were TA1-5-1, TA5-2-2, TA5-4-7 and TA5-32-25. Among the plants of the F_3 population, these genotypes exhibited high variability for the traits capsule length, number of seeds per capsule, capsule width, days to first flowering, days to maturity, plant height, number of capsules per plant and seed yield per plant. These genotypes were positioned in the first quadrant indicating high values of yield related characters (fig 10.).

The correlation between variables and the principal components is given in figure 11. The high loadings of the traits days to first flowering, capsule length, capsule width, number of seeds per capsule, plant height, number of capsules per plant, days to maturity and seed yield per plant indicate that these traits strongly influence the principal component I. PC2 was highly influenced by the characters number of primary branches followed by capsule length and capsule width, while all the other traits exhibited a negligible influence on it.

A positive correlation of yield related parameters on principal components were recorded by Shim *et al.* (2016), Ozcinar and Sogut (2017), Sasipriya *et al.* (2022), Hassan and Endale (2023) and Mukthambica *et al*. (2023). Duration of the crop as indicated by days to flowering and days to maturity were also reported to have a high correlation with PC (Shim *et al.*, 2016; Sasipriya *et al.*, 2022; Hassan and Endale, 2023 and Mukthambica *et al*., 2023)

5.2.4. Multiple linear regression

Linear regression analysis was performed with seed yield per plant as dependent variable and other agronomic traits as independent variables (fig12.). The fitted model has R^2 value of 90.30 % which indicates that 90.30% of the variability in seed yield is explained. The adjusted R-squared statistic, which is more suitable for comparing models with different numbers of independent variables, is also 89.9%.

It was observed that the characters, viz. days to first flowering, number of primary branches, capsule length, capsule width, number of seeds per capsule, plant height and days to maturity were not significant (P values > 0.05). The character number of capsules per plant only had an estimate of P value < 0.05, suggesting its contribution to seed yield per plant.

The trait number of capsules per plant being the most important character to explain the total variation on seed yield through regression analysis was also observed by Parimala and Mathur (2006), El-Mohsen *et al*. (2008), Atalou *et al*. (2014) and Aristya *et al.* (2017) in sesame.

5.2.5. Biochemical parameters

Sesame is rich in oil (50%) and protein (18-20%). Development of a high yielding variety in sesame should also consider the oil content of the genotype. Studies related to biochemical changes in plants caused by phytoplasma infection can change the level of some compounds in plant tissues. Development of an antioxidant defense system in plants protects them against oxidative stress damage. Phyllody infected plants and healthy plants of sesame, show significant differences with respect to the activity of antioxidant enzymes, peroxidase and poly phenol oxidase.

The selected genotype TA5-32-25 recorded maximum seed yield per plant (27.75 g/plant) along with maximum crude protein content (29.18 %), high oil content (45 %), high

Fig 8. Projection of yield related characters on the first two principal components in F_3 population of sesame

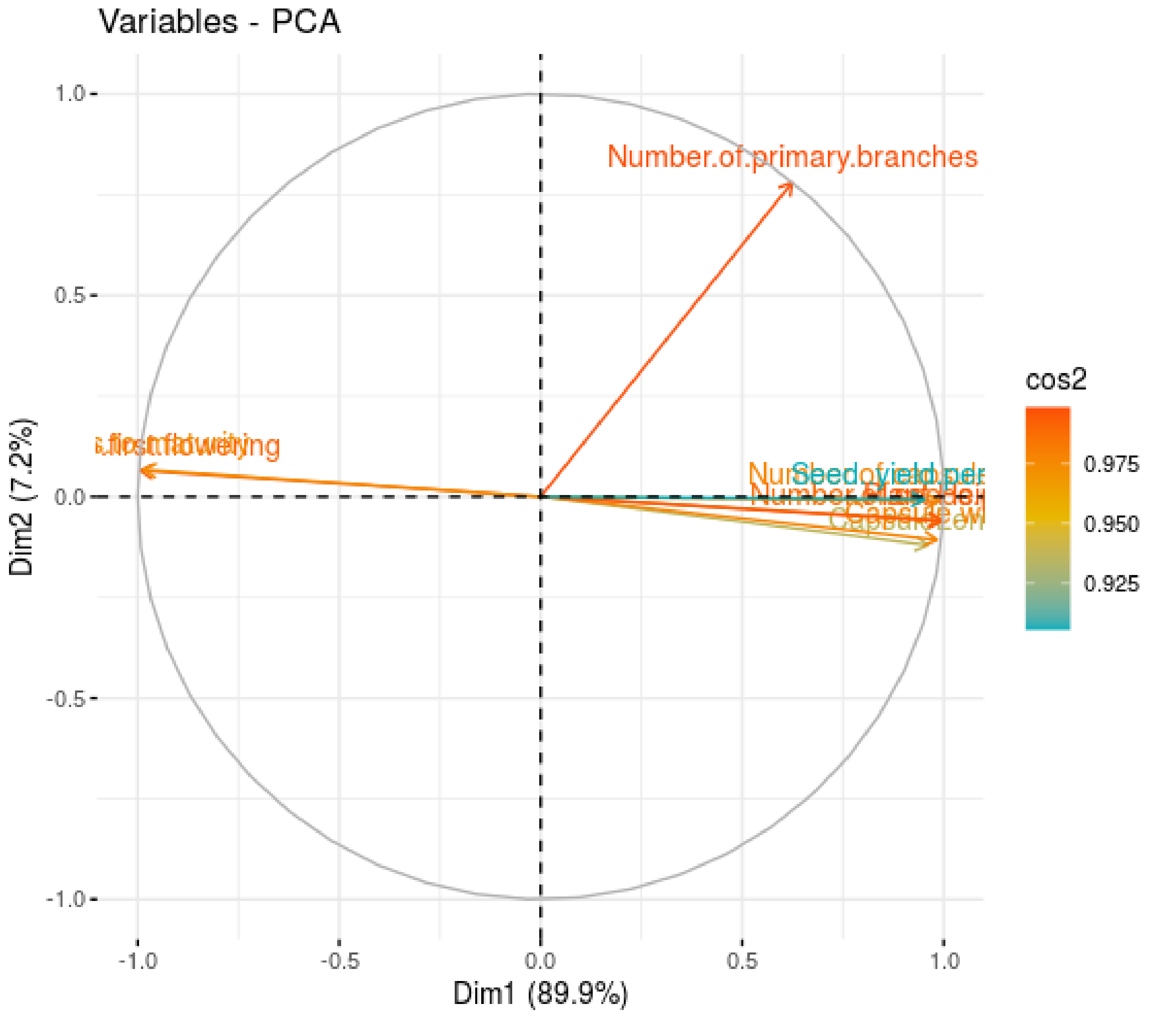


Fig 9. Individual Principal Component Analysis in F$_3$ population of sesame

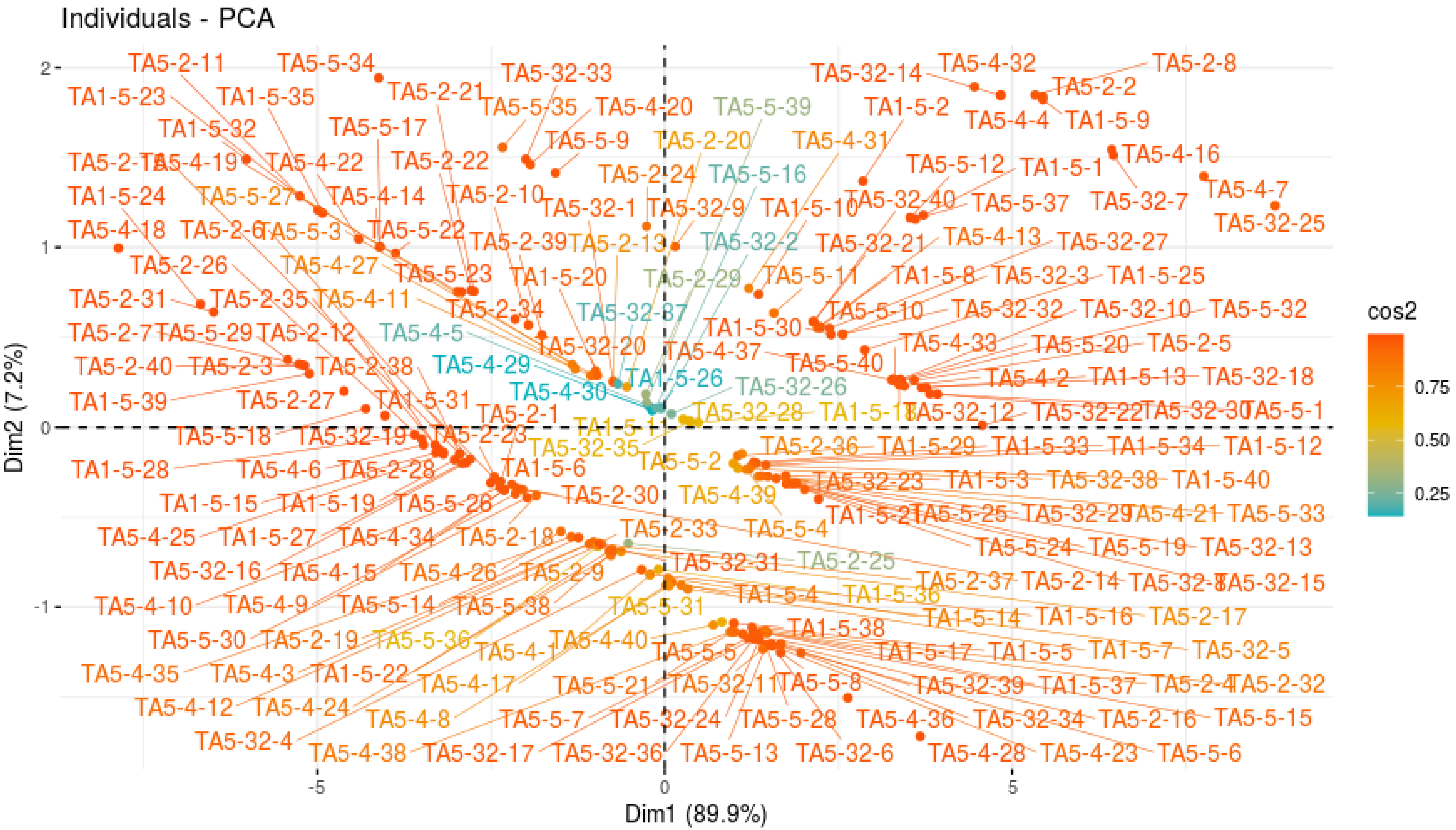


Fig 10. Two dimensional biplot of Principal Component Analysis in F_3 population of sesame

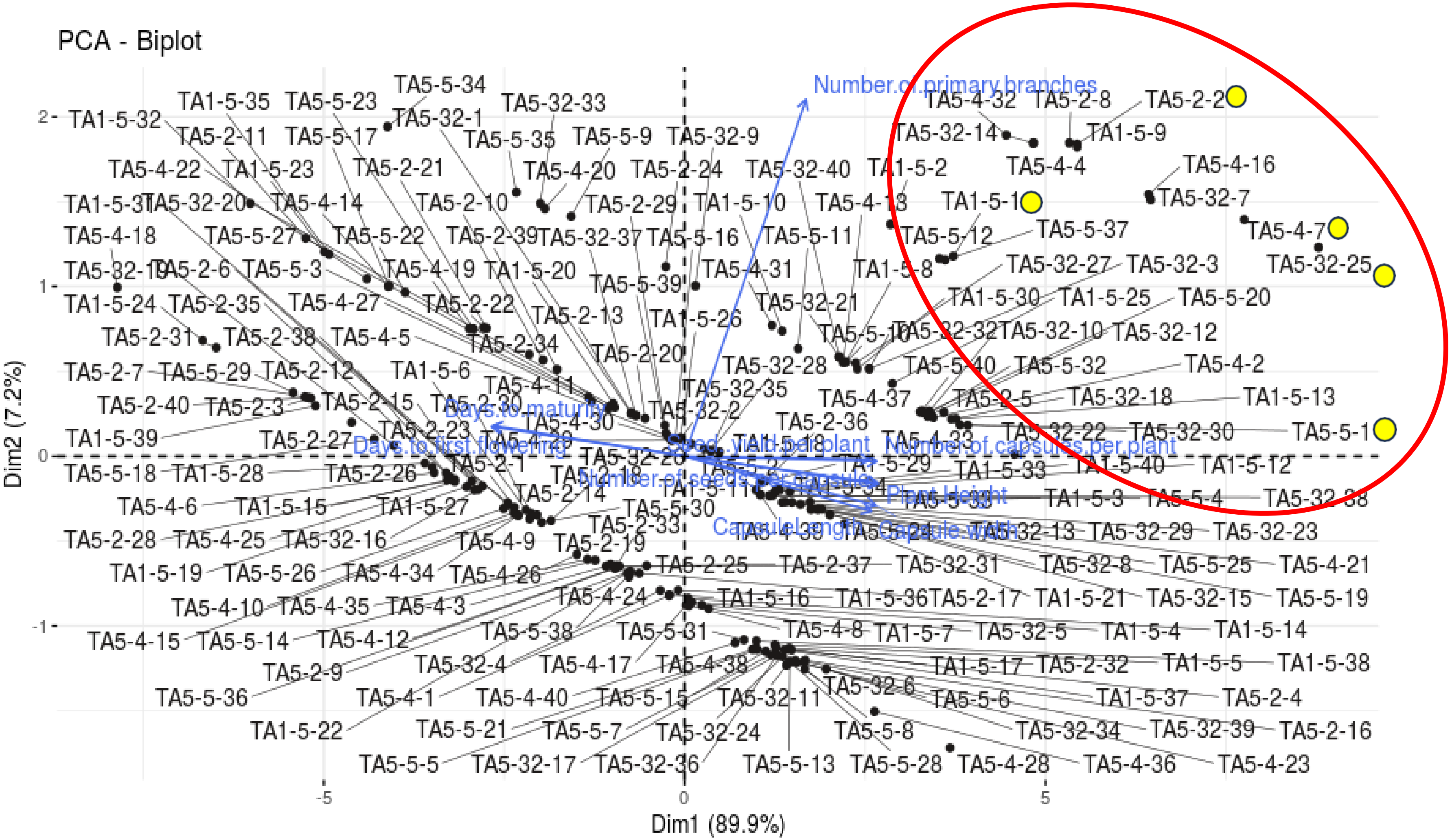


Fig 11. Correlation plot of variables vs PCs in F_3 population of sesame

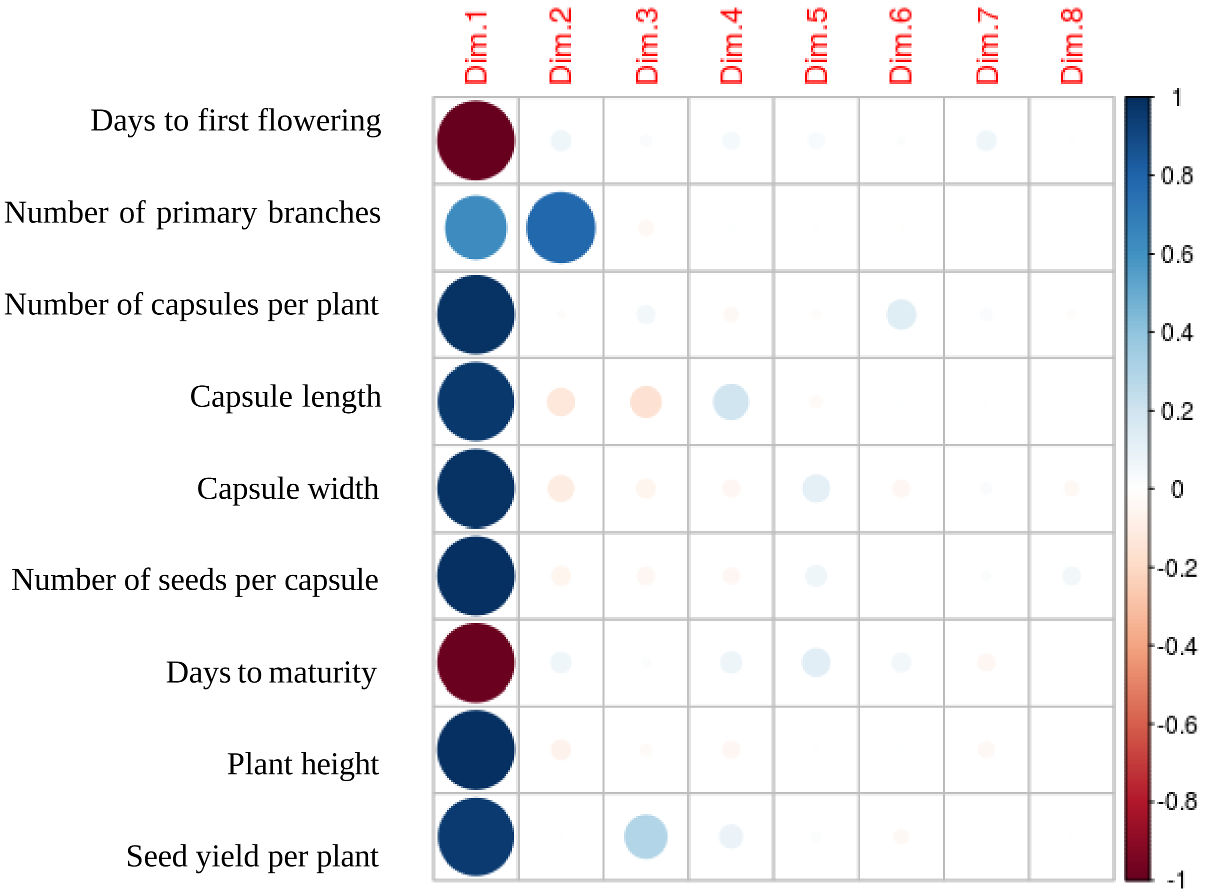
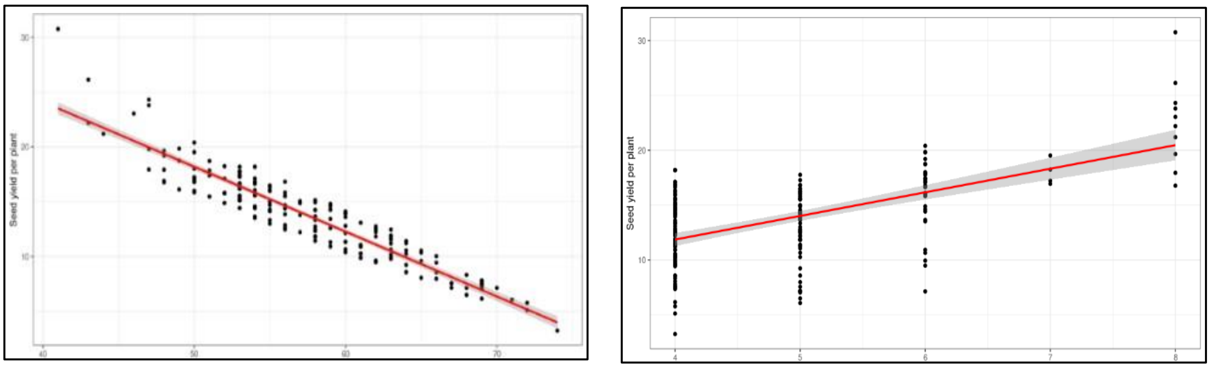
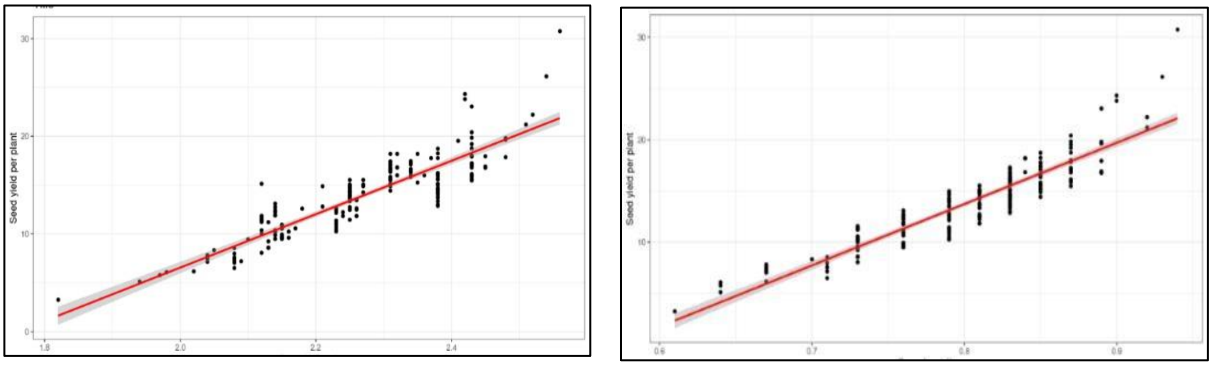


Fig 12. Multiple linear Regression of seed yield per plant in F$_3$ population of sesame



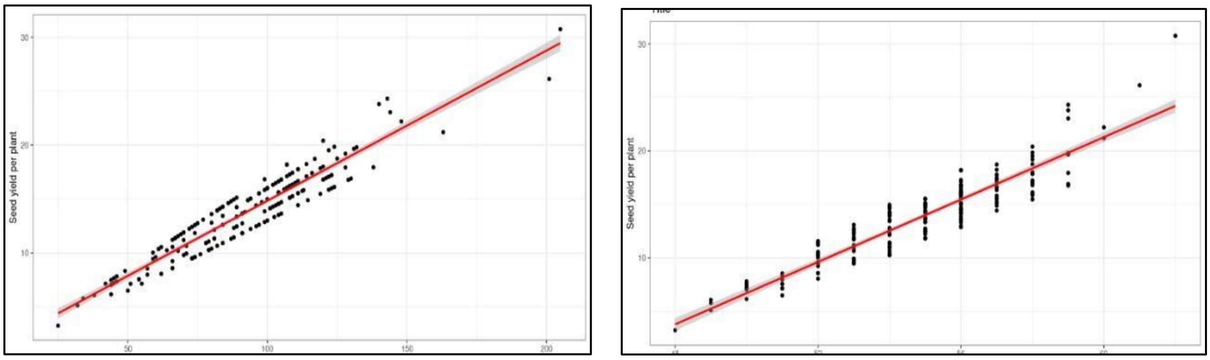
Days to first flowering

Number of primary branches



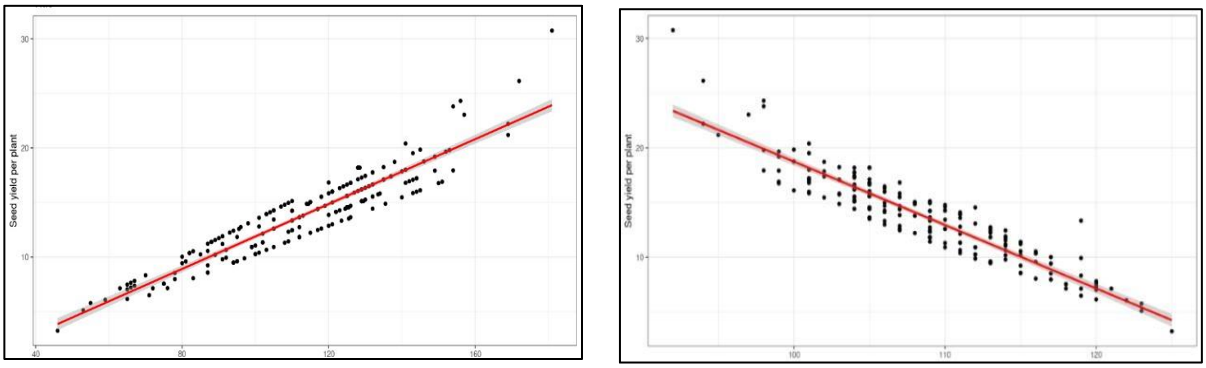
Capsule length

Capsule width



Number of capsules per plant

Number of seeds per capsule

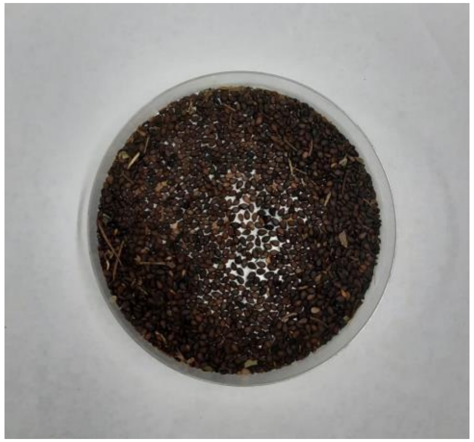


Plant hieght

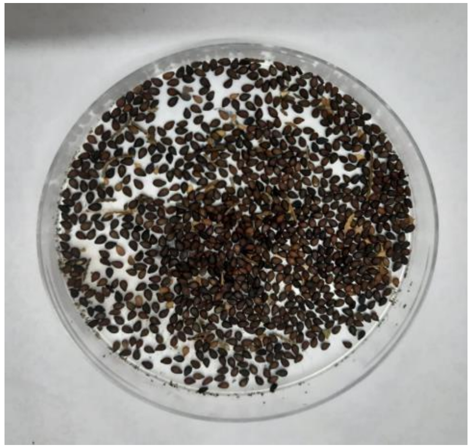
Days to maturity

peroxidase activity (33.9) and high polyphenol oxidase activity (6.6). The genotype TA5-4-7 had maximum oil content (50.01 %), with seed yield of 26.13 g/plant, crude protein of (28.87 %), peroxidase activity of 19.4 and polyphenol oxidase activity of 1.7. The genotype with maximum peroxidase activity (90.1) was TA5-2-2, which recorded a seed yield of 24.31 g/plant, oil content of 38 %, crude protein of 28.31% and polyphenol oxidase activity of 6.2. Maximum polyphenol oxidase activity (6.63) was expressed by TA1-5-1, which recorded a seed yield of 19.52 g/plant, oil content of 41 %, crude protein content of 24.81 % and peroxidase activity of 14.3. The genotype TA5-5-1 recorded a seed yield of 17.92 g/plant, oil content of 35 %, crude protein of 17.5 %, peroxidase activity of 11.6 and polyphenol oxidase activity of 2.4. The seeds of the selected five lines namely TA5-5-1, TA5-2-2, TA5-4-7, TA1-5-1 and TA5-32-25 is given in plate 4.

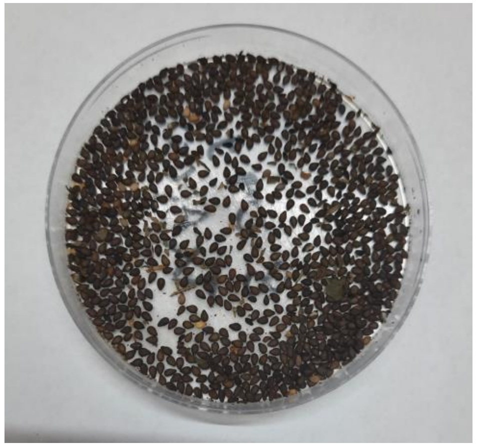
Plate 4. Seeds of selected F_3 plants



TA5-5-1



TA5-2-2



TA5-4-7

TA1-5-1

TA5-32-25

SUMMARY

6. SUMMARY

The research programme entitled ‘Developing breeding lines of sesame suitable for cultivation in Kerala’ was carried at the Department of Genetics and Plant Breeding, College of Agriculture, Vellayani during the period 2022-2024 with the objective of evaluating the segregating population of intervarietal crosses in sesame for selecting superior genotypes.

Sesamum indicum L., often referred to as the ‘queen of oilseeds,’ has a rich history of cultivation in Asia for over 5,000 years, originating from its wild progenitor, *S. malabaricum*. Renowned for its high oil content (50%) and protein levels (18-20%), sesame seeds are primarily used for oil extraction, with 78% of production directed towards this purpose, while the rest is utilized for sowing and in confections. Breeding programs focus on improving seed yield, oil quality, and resilience to biotic and abiotic stresses, although gains in sesame breeding have been lower compared to other oilseed crops. This study aims to evaluate segregating sesame populations and identify high-yielding lines suitable for cultivation in Kerala, contributing to the enhancement of sesame production in the region.

The experimental material of the present study consisted of the F_2 segregating populations of three superior F_1 lines namely, Thilak X Ayali 1(TA1), Thilathara X Ayali 2 (TTA2) and Thilak X Ayali 5 (TA5), selected based on a previous work done in the Department of Genetics and Plant Breeding, College of Agriculture, Vellayani. The present study assessed genetic variability among the F_2 and F_3 segregating populations of sesame, revealing significant variation across various traits. The occurrence of transgressive segregants, where individuals exceed the performance of both parents, supports the potential for improving desirable traits in breeding programs. The observed high coefficients of variation for traits like seed yield per plant and the number of capsules per plant indicate ample opportunities for selection and improvement. The range in days to first flowering (29-75 days in F_2 and 41-74 days in F_3) and days to maturity (80-126 days in F_2 and 92-125 days in F_3) suggests considerable potential for enhancing earliness and crop duration, which is critical for adaptability in diverse agro-ecological conditions. Traits such as plant height, which ranged from 37-175.5 cm in F2 and 46-181 cm in F_3, and seed yield per plant (2.28-28.24 g in F2 and 3.25-27.75 g in F3) further highlight the genetic diversity present in these populations. However, traits like capsule length and width showed limited variation, indicating less scope for improvement in these areas. These findings are consistent with previous studies, emphasizing the need for targeted selection strategies in sesame breeding to enhance yield and other economically important traits.

Transgressive segregation plays a crucial role in plant breeding, particularly in enhancing desirable traits in hybrid populations. The analysis of variance in this study revealed substantial phenotypic, genotypic, and environmental variances, providing insights into the traits suitable for selection. A highly significant variation was observed for traits such as days to first flowering, number of primary branches, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, days to maturity, plant height, and seed yield per plant. The higher phenotypic coefficient of variation (PCV) compared to genotypic coefficient of variation (GCV) for all traits indicates a strong environmental influence. However, traits such as days to maturity and capsule length displayed low coefficients of variation, indicating limited potential for improvement through selection.

Heritability, when combined with genetic advance, gives a clearer picture of the potential for trait selection. The study showed low heritability and genetic advance for most traits, including days to first flowering and seed yield per plant. Low heritability and genetic advance suggest limited gains from traditional breeding for these traits, emphasizing the need for alternative breeding approaches to enhance genetic improvement in sesame.

The correlation analysis in the present study provides crucial insights into the relationship between seed yield and other agronomic traits, which are essential for selection in sesame breeding. Seed yield per plant exhibited a strong positive correlation with key traits such as the number of primary branches, capsule length, capsule width, number of seeds per capsule, plant height, and the number of capsules per plant. In contrast, days to first flowering and days to maturity demonstrated a negative correlation with seed yield. Overall, the positive correlations observed in this study suggest that selecting for traits like the number of primary branches, capsule dimensions, plant height, and the number of capsules per plant could be effective in improving seed yield in sesame breeding programs.

Principal Component Analysis (PCA) serves as a powerful statistical tool in the evaluation of genetic diversity within sesame germplasm, as evidenced by various studies that have highlighted its utility in elucidating relationships between yield-related traits. The current study demonstrates that the first two principal components (PC1 and PC2) account for a significant portion of the total variation in the F_2 population, indicating that these components are critical for selecting desirable genotypes. The high correlation of PC1 with traits such as capsule length, number of seeds per capsule, and seed yield suggests that these parameters play a crucial role in enhancing yield potential. Furthermore, the identification of genotypes exhibiting earliness and high yield attributes in specific quadrants of the biplot underscores the potential for targeted breeding strategies. The substantial contributions of traits associated with maturity and flowering times to PC2 further enrich our understanding of the genetic architecture of sesame, revealing how these traits can be effectively leveraged in breeding programs to develop superior genotypes. Overall, the findings align with previous research emphasizing the importance of PCA in optimizing genetic selection processes, ultimately aiding in the development of high-yielding sesame varieties.

The results of the Principal Component Analysis (PCA) conducted on the biometric observations from the F_3 population highlight the significance of the first principal component (PC1) in capturing the majority of the variance, accounting for 89.935% of the total variability. This finding suggests that PC1 is essential for identifying and selecting desirable genotypes, as it correlates predominantly with key yield-related traits, including plant height, days to first flowering, and seed yield per plant. The biplot analysis reveals that genotypes clustered in various quadrants exhibit distinct trait similarities, further emphasizing the potential for targeted selection based on high PC scores, which indicate favorable phenotypic traits. Selected genotypes TA1-5-1, TA5-2-2, TA5-4-7, and TA5-32-25 stand out due to their high variability in critical traits such as capsule length, number of seeds per capsule, and seed yield, positioning them advantageously within the first quadrant. The strong influence of traits on PC1 aligns with previous findings in sesame, underscoring the effectiveness of PCA in guiding breeding strategies for yield improvement. Overall, this analysis confirms the utility of PCA as a robust tool in selecting high-yielding sesame genotypes, reinforcing its relevance in genetic research and crop improvement efforts.

The regression analysis conducted in this study underscores the significant relationships between agronomic traits and seed yield per plant in sesame, with the number of capsules per plant identified as the most influential variable. This finding highlighted the critical role of this trait in explaining the variation in seed yield. These results emphasize the relevance of these agronomic traits in developing strategies for enhancing seed yield in sesame, providing valuable insights for breeders aiming to improve crop productivity.

The linear regression analysis conducted in this study revealed that the fitted model accounted for a substantial 90.30% of the variability in seed yield per plant, as indicated by the R^2 value. The adjusted R^2 value of 89.9% further supports the robustness of the model, making it suitable for comparison with other models that include different independent variables. Notably, among the various agronomic traits examined, only the number of capsules per plant demonstrated a statistically significant contribution to seed yield, with a P-value less than 0.05. In contrast, traits such as days to first flowering, number of primary branches, capsule length, capsule width, number of seeds per capsule, plant height, and days to maturity did not show significant effects (P-values > 0.05). These results highlight the importance of focusing on the number of capsules per plant in breeding programs aimed at improving sesame yield.

Sesame is rich in oil (50%) and protein (18-20%). Development of a high yielding variety in sesame should also consider the oil content of the genotype. Studies related to biochemical changes in plants caused by phytoplasma infection can change the level of some compounds in plant tissues. Development of an antioxidant defense system in plants protects them against oxidative stress damage. Phyllody infected plants and healthy plants of sesame, show significant differences with respect to the activity of antioxidant enzymes, peroxidase and poly phenol oxidase.

The selected genotype TA5-32-25 recorded maximum seed yield per plant (27.75 g/plant) along with maximum crude protein content (29.18 %), high oil content (45 %), high peroxidase activity (33.9) and high polyphenol oxidase activity (6.6). The genotype TA5-4-7 had maximum oil content (50.01 %), with seed yield of 26.13 g/plant, crude protein of (28.87 %), peroxidase activity of 19.4 and polyphenol oxidase activity of 1.7. The genotype with maximum peroxidase activity (90.1) was TA5-2-2, which recorded a seed yield of 24.31 g/plant, oil content of 38 %, crude protein of 28.31% and polyphenol oxidase activity of 6.2. Maximum polyphenol oxidase activity (6.63) was expressed by TA1-5-1, which recorded a seed yield of 19.52 g/plant, oil content of 41 %, crude protein content of 24.81 % and peroxidase activity of 14.3. The genotype TA5-5-1 recorded a seed yield of 17.92 g/plant, oil content of 35 %, crude protein of 17.5 %, peroxidase activity of 11.6 and polyphenol oxidase activity of 2.4.

The family **TA5-32** can be considered as superior since it recorded significantly different values for the yield related characters which suggests ample scope for selection from its segregating generations. Based on the performance of the F_3 genotypes, five superior lines were identified *viz.*, **TA5-32-25, TA5-4-7, TA5-2-2, TA1-5-1** and **TA5-5-1** which exhibited significant variations in seed yield, oil content, protein content, and antioxidant enzyme activities, which are key traits in sesame breeding programs. These lines can be proceeded further to the next generations for development of high yielding varieties in sesame. Development of short duration varieties in sesame can also be resorted to, due to the high variation observed in days to first flowering and days to maturity.

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DEVELOPING BREEDING LINES OF SESAME SUITABLE FOR CULTIVATION IN KERALA

by

GREESHMA RAVI
(2022-11-094)

ABSTRACT

Submitted in partial fulfilment of the
requirement for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture

Kerala Agricultural University

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE VELLAYANI
THIRUVANANTHAPURAM - 695 522
KERALA, INDIA

2024

ABSTRACT

The research programme entitled ‘Developing breeding lines of sesame suitable for cultivation in Kerala’ was carried at the Department of Genetics and Plant Breeding, College of Agriculture, Vellayani during the period 2022-2024 with the objective of evaluating the segregating population of intervarietal crosses in sesame for selecting superior genotypes.

Sesamum indicum L., an important edible oilseed crop is self-pollinating with varying degrees of cross-pollination depending on the environment. Breeding programs focus on improving seed yield, oil quality, and resilience to biotic and abiotic stresses, although gains in sesame breeding have been lower compared to other oilseed crops. The experimental material of the present study consisted of the F_2 segregating populations of three superior F_1 lines namely, Thilak X Ayali 1(TA1), Thilathara X Ayali 2 (TTA2) and Thilak X Ayali 5 (TA5), selected based on a previous work done in the Department of Genetics and Plant Breeding, College of Agriculture, Vellayani.

The occurrence of transgressive segregants, where individuals exceed the performance of both parents, supports the potential for improving desirable traits in breeding programs. The observed high coefficients of variation for traits like seed yield per plant and the number of capsules per plant indicate ample opportunities for selection and improvement. The range in days to first flowering (29-75 days in F_2 and 41-74 days in F_3) and days to maturity (80-126 days in F_2 and 92-125 days in F_3) suggests considerable potential for enhancing earliness and crop duration, which is critical for adaptability in diverse agro-ecological conditions.

Traits such as plant height, which ranged from 37-175.5 cm in F_2 and 46-181 cm in F_3, and seed yield per plant (2.28-28.24 g in F_2 and 3.25-27.75 g in F_3) further highlight the genetic diversity present in these populations. However, traits like capsule length and width showed limited variation, indicating less scope for improvement in these areas. These findings are consistent with previous studies, emphasizing the need for targeted selection strategies in sesame breeding to enhance yield and other economically important traits.

The analysis of variance revealed highly significant variation for traits such as days to first flowering, number of primary branches, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, days to maturity, plant height, and seed yield per plant. The higher phenotypic coefficient of variation (PCV) compared to genotypic coefficient of variation (GCV) for all traits indicates a strong environmental

influence. However, traits such as days to maturity and capsule length displayed low coefficients of variation, indicating limited potential for improvement through selection. The study showed low heritability coupled with low genetic advance for most traits, including days to first flowering and seed yield per plant since it was a segregating population.

The correlation analysis in the present study provides crucial insights into the relationship between seed yield and other agronomic traits, which are essential for selection in sesame breeding. Seed yield per plant exhibited a strong positive correlation with key traits such as number of primary branches, capsule length, capsule width, number of seeds per capsule, plant height, and the number of capsules per plant. In contrast, days to first flowering and days to maturity demonstrated a negative correlation with seed yield.

Principal Component Analysis (PCA) enabled to identify the key traits contributing to genetic variability in sesame, with a focus on yield-related characters. In the F_2 population, PC1 and PC2 account for a significant portion of the total variation, underlining their importance in selecting desirable genotypes. PC1 is highly correlated with yield-related traits such as capsule length, number of seeds per capsule, and seed yield, while PC2 is linked to maturity and flowering times. Meanwhile, in the F_3 population, PC1 alone explains 89.935% of the total variability, emphasizing its dominance in capturing genetic variation. PC1 correlates predominantly with plant height, days to first flowering, and seed yield, with a stronger emphasis on plant height and flowering time. Biplot analysis in the F_2 population shows genotypes with early maturity and high yield traits in specific quadrants, suggesting potential for targeted breeding strategies.

The regression analysis conducted in this study underscores the significant relationships between agronomic traits and seed yield per plant in sesame. In both the F_2 and F_3 populations, the number of capsules per plant emerged as the most influential variable affecting seed yield.

The family **TA5-32** can be considered as superior since it recorded significantly different values for the yield related characters which suggests ample scope for selection from its segregating generations. Based on the performance of the F_3 genotypes, five superior lines were identified *viz.*, **TA5-32-25, TA5-4-7, TA5-2-2, TA1-5-1** and **TA5-5-1** which exhibited significant variations in seed yield and oil content. These lines can be proceeded further to the next generations for development of high yielding varieties in sesame.

സംഗ്രഹം

വെള്ളായണി കാർഷിക കോളേജിലെ ജനിതക ശാസ്ത്ര സസ്യ പ്രജനന വിഭാഗത്തിൽ 'കേരളത്തിലെ കൃഷിക്ക് അനുയോജ്യമായ എള്ളിന്റെ ബ്രീഡിങ് ലൈൻസ് വികസിപ്പിക്കൽ' എന്ന ഗവേഷണ പരിപാടി 2022-2024 കാലയളവിൽ നടത്തിയിരുന്നു. ഉയർന്ന ജനിതകരൂപങ്ങൾ തിരഞ്ഞെടുക്കുന്നതിനായി എള്ളിലെ ഇന്റർവെറൈറ്റൽ ക്രോസുകളുടെ സെഗ്രെഗേറ്റിംഗ് പോപുലേഷൻ വിലയിരുത്തുക എന്നതായിരുന്നു ലക്ഷ്യം.

ഒരു പ്രധാന ഭക്ഷ്യ എണ്ണക്കുരു വിളയായ എള്ളിൽ (സെസാമം ഇൻഡികം എൽ.) സ്വയ പരാഗണത്തോടൊപ്പം പര പരാഗണവും വലിയ അളവിൽ ഉണ്ട്. മറ്റ് എണ്ണക്കുരു വിളകളെ അപേക്ഷിച്ച് എള്ള് പ്രജനനത്തിലെ നേട്ടങ്ങൾ കുറവാണെങ്കിലും, വിത്ത് വിളവ്, എണ്ണ ഗുണനിലവാരം, ജൈവ , അജൈവ സമ്മർദ്ദങ്ങൾക്കുള്ള പ്രതിരോധം എന്നിവയിൽ പ്രജനന പരിപാടികൾ ശ്രദ്ധ കേന്ദ്രീകരിക്കുന്നു. വെള്ളായണി കാർഷിക കോളേജിലെ ജനിതക ശാസ്ത്ര സസ്യ പ്രജനന വിഭാഗത്തിലെ ഗവേഷണ പഠനത്തിന്റെ അടിസ്ഥാനത്തിൽ തിരഞ്ഞെടുത്ത തിലക് x ആയാളി 1 (ടിഎ1), തിലക് x ആയാളി 2 (ടിടിഎ2), തിലക് x ആയാളി 5 (ടിഎ5) എന്നിങ്ങനെ മൂന്ന് മികച്ച എഫ്1 ലൈനുകളാണ് ഇപ്പോഴത്തെ പഠനത്തിന്റെ പരീക്ഷണാത്മക സാമഗ്രികൾ.

വ്യക്തിഗത സസ്യങ്ങൾ രണ്ട് മാതാപിതാക്കളുടെയും പ്രകടനത്തെ മറികടക്കുമ്പോഴാണ് ട്രാൻസ്ഗ്രെസ്സീവ് സെഗ്ഗ്രെകന്റ്സ് ഉണ്ടാകുന്നത്, ഇവ പ്രജനന പരിപാടികളിൽ അഭികാമ്യമായ പ്രതീകങ്ങളെ മെച്ചപ്പെടുത്തുന്നതിനുള്ള സാധ്യതയെ പിന്തുണയ്ക്കുന്നു. ഓരോ ചെടിയുടെയും വിത്ത് വിളവ്, ഓരോ ചെടിയുടെയും ക്യാപ്സ്യൂളുകളുടെ എണ്ണം തുടങ്ങിയ സവിശേഷതകൾ ഉയർന്ന കോഎഫിഷ്യന്റ് ഓഫ് വേരിയേഷൻ തിരഞ്ഞെടുക്കുന്നതിനും മെച്ചപ്പെടുത്തുന്നതിനുമുള്ള ധാരാളം അവസരങ്ങളെ സൂചിപ്പിക്കുന്നു. ആദ്യത്തെ പൂവിടുന്ന ദിവസം മുതൽ (എഫ് 2-ൽ 29-75 ദിവസം, എഫ് 3-ൽ 41-74 ദിവസം) ചെടിയുടെ കാലയളവ് (എഫ് 2-ൽ 80-126 ദിവസം, എഫ് 3-ൽ 92-125 ദിവസം) വരെയുള്ള ദിവസങ്ങൾ ഒരു ചെടിയുടെ നേരത്തെ പാകമാകാനുള്ള കഴിവിനെ

സൂചിപ്പിക്കുന്നു.

എഫ് 2-ൽ 37-175.5 സെന്റീമീറ്റർ വരെയും എഫ് 3-ൽ 46-181 സെന്റീമീറ്റർ വരെയും ഉള്ള ചെടികളുടെ ഉയരം, ഓരോ ചെടിയുടെയും വിത്ത് വിളവ് (എഫ് 2-ൽ 2.28-28.24 ഗ്രാം, എഫ് 3-ൽ 3.25-27.75 ഗ്രാം) എന്നിങ്ങനെയുള്ള പ്രതീകങ്ങൾ ജനിതക വൈവിധ്യത്തെ കൂടുതൽ എടുത്തുകാട്ടുന്നു. എന്നിരുന്നാലും, ക്യാപ്സ്യൂൾ നീളവും വീതിയും പോലെയുള്ള പ്രതീകങ്ങൾ പരിമിതമായ വ്യതിയാനങ്ങൾ കാണിച്ചു, ഈ മേഖലകളിൽ മെച്ചപ്പെടാനുള്ള സാധ്യത കുറവാണ്. ഈ കണ്ടെത്തലുകൾ മുമ്പത്തെ പഠനങ്ങളുമായി പൊരുത്തപ്പെടുന്നു.

അനോവ വിശകലനം ചെയ്തപ്പോൾ, ആദ്യത്തെ പൂവിടുന്ന ദിവസങ്ങൾ, പ്രാഥമിക ശാഖകളുടെ എണ്ണം, ഒരു ചെടിയിലെ ക്യാപ്സ്യൂളുകളുടെ എണ്ണം, കാപ്സ്യൂളിന്റെ നീളം, കാപ്സ്യൂൾ വീതി, കാപ്സ്യൂളിലെ വിത്തുകളുടെ എണ്ണം, ചെടിയുടെ കാലയളവ്, ചെടിയുടെ ഉയരം, വിത്ത് വിളവ് തുടങ്ങിയ പ്രതീകങ്ങൾക്ക് വളരെ പ്രധാനപ്പെട്ട വ്യത്യാസം കണ്ടെത്തി. എല്ലാ പ്രതീകങ്ങൾക്കും വേണ്ടിയുള്ള ജിനോടൈപ്പിക് കോഫിഫിഷ്യന്റ് ഓഫ് വേരിയേഷനുമായി (ജിസിവി) താരതമ്യപ്പെടുത്തുമ്പോൾ ഉയർന്ന ഫിനോടൈപ്പിക് കോഫിഫിഷ്യന്റ് ഓഫ് വേരിയേഷൻ (പിസിവി) ശക്തമായ പാരിസ്ഥിതിക സ്വാധീനത്തെ സൂചിപ്പിക്കുന്നു. എന്നിരുന്നാലും, ചെടിയുടെ കാലയളവ്, ക്യാപ്സ്യൂൾ ദൈർഘ്യം തുടങ്ങിയ സവിശേഷതകൾ കുറഞ്ഞ കോഎഫിഷ്യന്റ് ഓഫ് വാരിയേഷൻ പ്രദർശിപ്പിക്കുന്നു, ഇത് തിരഞ്ഞെടുക്കുന്നതിലൂടെ മെച്ചപ്പെടുത്താനുള്ള പരിമിതമായ സാധ്യതയെ സൂചിപ്പിക്കുന്നു. സെഗ്രെഗേറ്റിംഗ് പോപുലേഷനായതിനാൽ ആദ്യത്തെ പൂവിടുന്ന ദിവസങ്ങൾ മുതൽ വിത്ത് വിളവ് ഉൾപ്പെടെ, മിക്ക പ്രതീകങ്ങൾക്കും കുറഞ്ഞ പാരമ്പര്യവും കുറഞ്ഞ ജനിതക മുന്നേറ്റവും പഠനം കാണിക്കുന്നു.

നിലവിലെ പഠനത്തിലെ പരസ്പര ബന്ധ വിശകലനം വിത്ത് വിളവും മറ്റ് കാർഷിക പ്രതീകങ്ങളും തമ്മിലുള്ള ബന്ധത്തെക്കുറിച്ചുള്ള നിർണായക ഉൾക്കാഴ്ചകൾ നൽകുന്നു, അവ എള്ള് പ്രജനനത്തിൽ തിരഞ്ഞെടുക്കുന്നതിന് അത്യന്താപേക്ഷിതമാണ്. ഒരു ചെടിയുടെ വിത്ത് വിളവ്, പ്രാഥമിക

ശാഖകളുടെ എണ്ണം, ക്യാപ്സ്യൂൾ നീളം, കാപ്സ്യൂൾ വീതി, ഒരു കാപ്സ്യൂളിലെ വിത്തുകളുടെ എണ്ണം, ചെടിയുടെ ഉയരം, ഓരോ ചെടിയുടെയും കാപ്സ്യൂളുകളുടെ എണ്ണം എന്നിങ്ങനെയുള്ള പ്രധാന പ്രതീകങ്ങളുമായി ശക്തമായ പോസിറ്റീവ് പരസ്പരബന്ധം പ്രകടമാക്കി. നേരെമറിച്ച്, ആദ്യം പൂവിടുന്ന ദിവസങ്ങളും, ചെടിയുടെ കാലയളവും വിത്ത് വിളവുമായി ഒരു നെഗറ്റീവ് പരസ്പരബന്ധം പ്രകടമാക്കി.

പ്രിൻസിപ്പൽ കോംപോണന്റ് അനാലിസിസ് (പിസിഎ) വിളവുമായി ബന്ധപ്പെട്ട പ്രതീകങ്ങളിൽ ശ്രദ്ധ കേന്ദ്രീകരിച്ച് എള്ളിലെ ജനിതക വ്യതിയാനത്തിന് കാരണമാകുന്ന പ്രധാന പ്രതീകങ്ങൾ തിരിച്ചറിയാൻ പ്രാപ്തമാക്കി. എഫ് 2 പോപ്പുലേഷനിൽ, പിസി 1 ഉം പിസി 2 ഉം മൊത്തം വ്യതിയാനത്തിന്റെ ഒരു പ്രധാന ഭാഗമാണ്, അഭികാമ്യമായ ജനിതകരൂപങ്ങൾ തിരഞ്ഞെടുക്കുന്നതിൽ അവയുടെ പ്രാധാന്യം അടിവരയിടുന്നു. കാപ്സ്യൂൾ നീളം, കാപ്സ്യൂളിലെ വിത്തുകളുടെ എണ്ണം, വിത്ത് വിളവ് തുടങ്ങിയ വിളവുമായി ബന്ധപ്പെട്ട പ്രതീകങ്ങളുമായി പിസി 1 വളരെ ബന്ധപ്പെട്ടിരിക്കുന്നു, അതേസമയം പിസി 2 ചെടിയുടെ കാലയളവും പൂവിടുന്ന സമയവുമായി ബന്ധപ്പെട്ടിരിക്കുന്നു. അതേസമയം, F3യിൽ, PC1 മാത്രം മൊത്തം വ്യതിയാനത്തിന്റെ 89.935% വിശദീകരിക്കുന്നു, ജനിതക വ്യതിയാനം പിടിച്ചെടുക്കുന്നതിൽ അതിന്റെ ആധിപത്യം ഊന്നിപ്പറയുന്നു. പിസി 1 പ്രധാനമായും ചെടിയുടെ ഉയരം, ആദ്യത്തെ പൂവിടുന്ന ദിവസങ്ങൾ, വിത്ത് വിളവ് എന്നിവയുമായി ബന്ധപ്പെട്ടിരിക്കുന്നു, ചെടിയുടെ ഉയരത്തിലും പൂവിടുന്ന സമയത്തിലും ശക്തമായ ഊന്നൽ നൽകുന്നു. എഫ് 2 പോപുലേഷനിലെ ബൈപ്ലോട്ട് വിശകലനം, നിർദ്ദിഷ്ട ക്വാഡ്രന്റുകളിൽ നേരത്തെ പാകമാകുന്ന ചെടികളെയും ഉയർന്ന വിളവ് നൽകുന്ന ചെടികളെയും സൂചിപ്പിക്കുന്നു.

ഈ പഠനത്തിൽ നടത്തിയ റിഗ്രഷൻ വിശകലനം അഗ്രോണമിക് പ്രതീകങ്ങളും എള്ളിലെ ഓരോ ചെടിയുടെയും വിത്ത് വിളവും തമ്മിലുള്ള സുപ്രധാന ബന്ധത്തെ അടിവരയിടുന്നു. എഫ് 2, എഫ് 3 പോപ്പുലേഷനുകളിൽ, ഓരോ ചെടിയുടെയും കാപ്സ്യൂളുകളുടെ എണ്ണം വിത്ത് വിളവിനെ ബാധിക്കുന്ന ഏറ്റവും സ്വാധീനമുള്ള പ്രതീകമായി ഉയർന്നു.

TA5-32 കുടുംബത്തെ മികച്ചതായി കണക്കാക്കാം, കാരണം അത് വിളവുമായി ബന്ധപ്പെട്ട പ്രതീകങ്ങൾക്ക് കാര്യമായ വ്യത്യസ്ത മൂല്യങ്ങൾ രേഖപ്പെടുത്തിയിട്ടുണ്ട്, ഇത് അതിന്റെ സെഗ്രെഗേറ്റിംഗ് തലമുറകളിൽ നിന്ന് തിരഞ്ഞെടുക്കുന്നതിന് ധാരാളം സാധ്യതകൾ നിർദ്ദേശിക്കുന്നു. എഫ്3 ജനിതകരൂപങ്ങളുടെ പ്രകടനത്തെ അടിസ്ഥാനമാക്കി, **TA5-32-25, TA5-4-7, TA5-2-2, TA1-5-1, TA5-5-1** എന്നിങ്ങനെ അഞ്ച് മികച്ച ലൈനുകൾ തിരിച്ചറിഞ്ഞു. വിത്ത് വിളവ്, എണ്ണയുടെ അളവ് എന്നിവയിൽ, എള്ളിൽ അത്യുത്പാദനശേഷിയുള്ള ഇനങ്ങൾ വികസിപ്പിക്കുന്നതിന് ഈ ലൈനുകൾ അടുത്ത തലമുറകളിലേക്ക് കൊണ്ടുപോകാം.