EVALUATION OF SESAME (*Sesamum indicum* L.) GENOTYPES TO THE SHADED UPLANDS OF SOUTHERN REGION

by

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(2011-11-112)

THESIS

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DECLARATION

I hereby declare that this thesis entitled **"Evaluation of sesame (*Sesamum indicum* L.) genotypes to the shaded uplands of Southern region"** is a bonafide record of research work done by me during the course of research and that the thesis has not previously formed the basis for the award of any degree, diploma, fellowship or other similar title, of any other University or Society.

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Abhijatha A.

Dedicated to

My
Ma’m and Mom

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF ABREVIATIONS

%	-	per cent
CD	-	Critical difference
cm	-	centimetre
et al.	-	and others
Fig.	-	Figure
g	-	gram
GA	-	Genetic Advance
GCV	-	Genotypic Coefficient of Variation
h^2	-	Heritability
ha	-	hectare
I.U.	-	International Unit
KAU	-	Kerala Agricultural University
kg	-	Kilogram
m	-	metre
mg	-	milligram
mm	-	millimetre
^{o}C	-	Degree celsius
PCV	-	Phenotypic Coefficient of Variation
s	-	seconds

Introduction

1. INTRODUCTION

Sesame (*Sesamum indicum* L., 2n=2x=26) commonly known as *gingelly, til, tila* in Sanskrit and *ellu* in Malayalam, is a member of the order Tubiflorae and family Pedaliaceae. Sesame is known as the 'Queen of Oilseeds' owing to its innumerable uses.

India is considered to be the major centre of genetic diversity even though the crop originated in Africa (Maiti *et al.*, 2012). Among the oilseeds, sesame was the first to be cultivated (Sengupta and Das, 2003) and used by man. In India, sesame seeds are used for Hindu religious purposes (Banerjee and Kole, 2009).The Sanskrit derivation of the word *Taila- Tilasya jata taila* strengthens the view that perhaps the first vegetative oil was from Tila (Sengupta and Das, 2003). The anti-oxidant properties in sesame oil were recommended for management of ageing and obesity (Anon., 2012).

Sesame is an important annual oilseed crop in the tropics and warm subtropics, where it is usually grown in small patches (Bedigian, 2003). Sesame is highly valued for its cooking quality, medicinal value of its oil, high seed oil content (50-60 per cent), protein (18-25 per cent), calcium, phosphorous, oxalic acid and excellent qualities of the seed oil and oil cake (Prasad, 2002; Arslan *et al.,*2007). Sesame is highly nutritive and its oil contains an antioxidant called sesamol which imparts a high degree of resistance against oxidative rancidity (Davidson, 1999). The external use of sesame oil is suggested as a prevention method for reducing phlebitis complication of chemotherapy in cancer patients (Nekuzad *et al*., 2012). Sesame cake is a nutritious feed for dairy cattle and it can also be used as fertilizer (Ashri, 1989).

Sesame crop has many agricultural advantages. It is grown on residual soil moisture with low inputs, and is a good crop for rotations with an extensive tap root system (Ashri, 1998). In India, sesame is cultivated in an area of 1.94 m ha with 0.755 m ton production (Gayathri, 2011). However, the average productivity of sesame in India (453 kg ha^{-1}) is far below the average productivity in China (1127 kg ha^{-1}) and Egypt (1211 kg ha^{-1}) (Ashri, 1998). The mean seed yield obtained is low, which is mainly attributed to lack of improved cultivars, low harvest index, susceptibility to biotic and abiotic stresses, seed shattering, indeterminate growth habit and asynchronous capsule ripening (Gayathri, 2011).

The oilseed scenario in India has undergone a dramatic change in the last 27 years with the setting up of Technology Mission on Oilseeds (TMO) in May, 1986. India is the largest producer of sesame covering 42 per cent of world's sesame area and 27 per cent of the production. Nearly 7.4 per cent of the total area under oilseeds in India is under sesame (Anon., 2005).

The present sesame varieties under cultivation have limited yield potential. Most of the varieties evolved and released for cultivation are selections from local cultivars or closely related populations, which contributes to the low productivity potential of cultivars grown in India. This highlights the need to enhance the productivity of the crop by developing high yielding genotypes. A thorough screening of the available germplasm for genetic variability for yield and its component traits will help in identifying elite genotypes. Sesame has a wide range of genetic variability in its extensive germplasm collections (Ashri, 1998).

In Kerala, sesame is mainly cultivated in summer rice fallows. During 1990-91, 5.59 lakh hectares were under paddy; however during 2009-10 it was only 2.34 lakhs ha. Thus within two decades, there was a decline of 3.25 lakh hectares (Kumari, 2011). Shrinking lowlands, shortage of labour and unprecedented summer showers resulting in crop failure, are the major reasons for the dwindling sesame cultivation in the state. Upland sesame cultivation is gaining importance in this scenario. Coconut gardens are the potential areas where we can intervene for upland sesame cultivation in the state since there has been a 28 per cent increased area under coconut over a period of twenty years (Govt. of Kerala, 2006).

Sesame being an important oil seed crop of Kerala, suitable varieties have to be developed which can be successfully grown with the changing cropping situations and also the changing climatic factors especially drought. Hence, a thorough screening of the genotypes collected from diverse agro ecological conditions may identify cultivars which are suited for upland cultivation that tolerate shade.

In this context, the present study entitled ‘Evaluation of sesame (*Sesamum indicum* L.) genotypes to the shaded uplands of Southern region’ was initiated with the following objectives

- To collect and evaluate different cultivars of *S.indicum* for morphological traits and yield attributes.
- To estimate the nature and extent of variability for seed yield and its component traits.
- To analyse the degree and direction of association between various economic traits and to estimate the direct and indirect effects of various components on yield.
- To study the genetic divergence of sesame genotypes.
- To identify sesame genotypes for shaded upland conditions.

Review of Literature

2. REVIEW OF LITERATURE

2.1 Origin and distribution of sesame

Sesame (*Sesamum indicum* L.) is probably the most ancient oilseed known and used by man, so ancient that it is almost impossible to say with any degree of accuracy where and when this domestication took place (Sengupta and Das, 2003). Despite the fact that the majority of the wild species of the genus *Sesamum* are native to sub-Saharan Africa, sesame was first domesticated in India (Maiti *et al.,* 2012). The Sanskrit words for the seed and the oil are the same, 'tila' and in fact the Sanskrit word for oil in general was 'taila' which itself is derived from 'tila'. In India, seeds of sesamum are used in Hindu religious functions (Banerjee and Kole, 2009).

A variety of cytogenetic, botanical, archeological, biochemical and historical-linguistic criteria have been used to know the ancestry, origin and evolution of sesame by many workers (Bedigian, 2003 and Pham *et al*., 2010). Two alternative centers of origin have been proposed: East Africa (Ethiopia) and Asia (Indian sub-continent or central Asia). The African origin of sesame is supported by the fact that most wild *Sesamum* species are endemic there (Nyongesa *et al*., 2013). A centre of origin in the Indian sub-continent is revealed by morphological and cytogenetic affinities between domesticated sesame and the south Indian native *S. mulayanum* Nair., as well as archaeological evidence that it was cultivated at Harappa in the Indus Valley between 2250 and 1750 BC, and a more recent findings of charred sesame seeds in the Makran region of Pakistan (Maiti *et al.,* 2012).

The taxonomy and cytogenetics of the genus require more definitive investigations. Nayar and Mehra (1970) referred thirty four species and Kobayashi (1991) listed thirty seven species. New species, such as *S. mulayanum* (Mehetre *et al*., 1993) and *S. indicum* var s*encottai* and var. y*anamalai* (Devarathinam and Sundaresan, 1990) have been added since then. John *et al*. (2008) studied wild sesame species in southern districts of Kerala and reported that diversity of wild species was greatest in Alappuzha. However, many of the wild species remain unknown, their chromosome numbers have not been determined and their distribution areas have not been fully described (Ashri, 1998).

2.2 Intercropping

Intercropping is an age-old practice of growing simultaneously two or more crops on the same field such that the period of overlap is long enough to include a vegetative stage (Gomez and Gomez, 1983). Intercropping has been a regular practice followed by the farmers of India, Africa, Sri Lanka, Malaya and West Indies. Intercropping is mainly practiced to cover the risk of failure of one of the component crops due to vagaries of weather or pest and disease incidence. Best utilization of nutrients, moisture, space and solar energy can be derived through mixed/intercropping system. Sarkar *et al.*, (1995) reported that intercropping not only stabilizes crop production by reducing the impact of weather vagaries, but also increases cropping intensity considerably.

In Kerala, sesame is mainly cultivated in summer rice fallows. The area under rice cultivation is dwindling at an alarming rate. During 1960-61 the area was 7.90 lakh hectares which decreased to 2.34 lakh hectares in 2009-10 (Kumari, 2011). Upland sesame cultivation is gaining importance in this scenario.

In 1985-86 the area under coconut crop was 7.05 lakhs ha in Kerala, which increased to 9.0 lakhs ha in 2004-05. There is an increase of 28 per cent under the area of coconut over a period of twenty years (Government of Kerala, 2006). Intercropping in coconut gardens is a potential area where we can intervene for upland sesame cultivation in the state.

At Kasaragod, sesame was tried in intercropping experiments under coconut during the rainy season. Although the early growth of these intercrops was satisfactory, rainwater dripping from coconut leaves affected their growth at a later stage, and ultimately they performed very poorly (Hegde and Yusuf, 1992).

An experiment conducted during the rainy season to assess the performance of rice, maize, sesame, green gram and black gram grown in sole and intercropping systems on Gangetic alluvial upland (Entisol) in West Bengal revealed that only sesame + rice had higher total productivity in terms of rice equivalent yield and net returns than all the sole crops (Sarkar *et al*., 1995).

Sharma *et al.* (1998) recorded significantly higher plant height, capsules per plant and number of branches per plant of sole sesame than when intercropped.

In a field experiment conducted by Yadav *et al*. (2008) in Uttar Pradesh to determine productivity and economic feasibility of sesame - based intercropping system in rainfed uplands, sesame + urd gave higher seed yield, net return and return per rupee investment in comparison to sole sesame.

Field trials conducted to determine the productivity and compatibility of the cropping systems obtained from intercropping varieties of sesame and sunflower in the humid forest–savanna transition zone showed that intercropping did not affect the number of branches per plant, number and weight of capsules per plant, weight of seeds per plant, 1000-seed weight or seed production efficiency (SPE) of any of the varieties in both years (Olowe and Adeyemo, 2009).

A field experiment was carried out by Bhatt *et al*. (2010) to assess the economic performance of sesame, hybrid cotton and castor in sole and intercropping systems. All intercropping systems of sesame + cotton had higher total productivity in terms of sesame equivalent yield, net return, return per rupee invested and income equivalent ratio (IER) than all the sole crops and sesame + castor intercropping systems.

A study conducted by Ahirwar *et al.* (2011) revealed that intercropping of sesame with other crops like black gram, green gram, cluster bean and pearl millet significantly increased the plant height, number of branches, number of capsules and grain yield of sesame.

2.3 Weather and crop growth

In trials in Cheju Island, where sesame was grown, air temperatures and rate of plant development were compared. As air temperature increased, the duration of the development stages from sowing to emergence and from sowing or emergence to flowering or maturity decreased (Taek *et al.*, 1995).

A field experiment was conducted on a sandy loam soil in the summer season by Nath *et al*. (2001) to assess the effects of macro and microclimatic variations on yield of sesame. Ambient temperature above 30°C up to 100 per cent flowering had a direct positive effect on sesame yield. Crop exposure to sixty to eighty per cent relative humidity up to 100 per cent flowering had a direct negative effect. Temperature profile at fifty days after emergence, within the crop canopy, had direct positive effects on yield.

In an experiment conducted to study the effects of day length and air temperature on stem growth and flowering in sesame, Kumazaki *et al.* (2008) reported that the growth and flowering behavior were unaffected by a low temperature during the seedling stage whereas a low temperature during the flowering period decreased the flowering-node number.

2.4 Seed yield and component characters

The available literature on seed yield and selected component characters in sesame are reviewed under the following headings

1. Variability
2. Heritability and genetic advance

3. Correlation
4. Path analysis
5. Divergence studies
6. Selection index

2.4.1 Genetic variability

Genetic variability refers to the potential for a given characteristic or genotype to vary within a population when faced with a particular influence. Phenotypic variability in a population is of great importance as it reflects the existence of genetic diversity among the genotypes of such a population. Greater the genetic diversity wider is the scope for selection. The extent of variability of a character is measured by different statistical parameters such as phenotypic and genotypic variance and coefficient of variation. Knowledge of availability and extent to which the genetic diversity is heritable is essential for effective selection among individuals of crop population.

Sesame is known to possess greater genetic variability than most of the self-pollinated crops. Evidence for the presence of this wide range of variability in various characters of sesame plant has been extensively reported by many sesame investigators (Acevedo and Penso, 1998; Gebremichael and Parzies, 2011).

An analysis of variance for sixteen quantitative characters of sesame by John and Nair (1993), indicated that coefficients of variation were greatest for number of capsules on branches, seed yield per plant and number of capsules on main stem. Phenotypic coefficients of variability were greater than the respective genotypic coefficients for all sixteen characters. Genotypic coefficients of variability were greatest for number of capsules on branches, seed yield per plant, number of capsules on main stem, number of capsules per plant and number of branches.

Similarity between estimates of genotypic and phenotypic coefficients of variation for 100-seed weight, capsule length, capsule breadth, oil content, days to 50 per cent flowering, days to maturity and seed number per capsule was reported in sesame by Joel and Thangavelu (1997).

Genetic analysis of yield and yield components in sesame was studied by Zargar (2000), who reported that significant variation was observed for maturity, morphological and yield component traits which were also reflected in high genotypic coefficient of variation for seed yield per plant, capsules plant, capsule bearing nodes and branches per plant. Significant contribution from G x E variance was observed in days to flowering and maturity and seeds/ capsule. Significant G x E interaction was observed for most of the traits.

Krishnaiah *et al*. (2002) in a trial with sesame varieties reported a close resemblance between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation for days to 50 per cent flowering, days to maturity, plant height, number of primary branches, number of secondary branches, capsules on the main stem, capsules on primary branches, capsules on secondary branches, capsule length, seeds per capsule, 1000-seed weight, seed yield per plant and harvest index.

Studies of Shajan (2002) on the genetic basis of seed yield quality in sesame revealed that number of branches, number of capsules per plant and seed yield per plant had high phenotypic and genotypic coefficient of variation, while plant height, number of seeds per capsule and oil content had moderate values.

A study was conducted with different accessions of sesame by Singh and Singh (2004) to estimate variability parameters for quantitative characters such as days to 50 per cent flowering, days to maturity, plant height, number of primary branches, capsule per plant, capsule length, capsule width, seeds per capsule and grain yield. The study revealed a wide range of variation for all the characters except for capsule length. High heritability along with high magnitude of genetic advance was recorded for capsules per plant and grain yield. Days to maturity exhibited high heritability and low genetic advance. Phenotypic coefficients of variation were higher than the genotypic coefficients of variation for all the characters studied.

Variability in seed yield and its components (days to 50 per cent flowering, plant height, branches per plant, capsules per plant, seeds per capsules and 1000 seed weight) was assessed in approximately 136 determinate sesame germplasm lines at RRS, Vridhachalam. Analysis of data revealed significant differences among the genotypes for all traits studied. The genotypic and phenotypic coefficients of variation were low for most traits. Number of capsules per plant recorded the highest coefficient of variation (Ganesan, 2005).

High phenotypic and genotypic coefficient of variation were observed for number of branches per plant, seed yield per plant, number of capsules per plant and number of capsules bearing nodes in sesame (Gangarde *et al.*, 2009).

In an experiment conducted by Raghuwanshi (2005) the genetic variability for eight characters (days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, seed yield, 1000-seed weight and oil content) were assessed in 100 genotypes of sesame. A wide range of variability was observed for yield and its components in all environments. High variability was observed for all characters, except for 1000-seed weight which showed low to moderate variability. Genotype × environment interaction had significant effect on seed yield. The genotypic variance was lower than the phenotypic variance.

Velu and Shunmugavalli (2005) revealed that in sesame, high phenotypic and genotypic coefficient of variation was observed for plant height and number of capsules per plant.

Genetic variation was determined by Banerjee and Kole (2006) in sesame. They reported that phenotypic and genotypic coefficients of variation were high for plant height, branches per plant, capsules per plant, seeds per capsule and seed yield per plant and low for 1000-seed weight.

An experiment was conducted by Manjunatha *et al*. (2008) in five locations with sixty sesame entries to study the genetic variability parameters, phenotypic and genotypic variances, heritability and genetic advance, correlations and path coefficients. Based on above studies, a plant type with the characters long duration, tallness, more plant height upto first branch, more number of nodes upto first branch, high number of primary branches and capsules, long and wide capsules can be considered as essential in achieving improvement in seed yield under late kharif conditions.

In an investigation with sesame genotypes by Mandal *et al*. (2010) the highest values of phenotypic and genotypic variances were observed in number of capsules per plant. The genetic coefficient of variance was high in number of capsules per plant, number of secondary branches and plant height.

Mohan (2011) studied the genetic variability and character association in sesame. Seed yield per plot, capsules per plant and primary branches per plant showed high phenotypic and genotypic coefficients of variation coupled with high to moderate heritability and high genetic advance indicating the predominance of additive gene effects in controlling these traits.

Study of genetic variation in sesame using agro-morphological traits revealed a relatively high genotypic coefficient of variation for number of fruiting branches per plant, capsules per plant, plant height and seed yield per plant (Parsaeian *et al*., 2011).

Genetic parameters of variability and heritability of different characters were studied by Revathi *et al*. (2012) and high genotypic and phenotypic coefficient of variations were observed for number of branches per plant, number of capsules per plant and seed yield per plant.

In a research for estimating the genetic variability and association among characters in sesame, Gidey *et al*. (2013) reported high genotypic and phenotypic coefficient of variation for seed yield per ha, height to first capsule, biomass per hectare, number of capsules per ha, number of primary branches per ha, number of seeds per capsule and plant height.

2.4.2 Heritability and genetic advance

Heritability of a trait is the extent of variability for that trait transferred to the progeny. Genetic advance is the expected improvement of a trait under a selection process. Heritability coupled with genotypic coefficient of variation would give a more reliable index of selection value (Burton, 1952). The genetic advance as per cent of mean together with high heritability is advantageous for selection because of the nature of additive gene action for the trait. Findings of different workers on heritability and genetic advance in sesame are listed here.

Seed yield per plant is reported to have the highest genetic advance, followed by the number of capsules on the main stem as per the study conducted on genetic variability, heritability and genetic advance in sesame by John and Nair (1993).

Genetic variability, heritability and genetic advance studies in sesame by Patil and Sheriff (1996) reported that heritability estimates were high for seed yield per plant, oil yield per plant, oil content, days to maturity, harvest index, number of capsules, days to 50 per cent flowering and capsule length. It was observed that characters like number of capsules, seed yield per plant and oil yield per plant had high genotypic variance and high heritability values coupled with greater genetic gain.

Saravanan *et al*. (2000) reported high heritability coupled with moderate genetic advance for the biometric characters such as plant height, number of branches per plant, number of capsules per plant and seed yield per plant in sesame accessions.

High heritability coupled with high genetic advance was observed for capsules on secondary branches, number of secondary branches, capsules on primary branches, capsules on main stem and plant height in a study conducted with sesame genotypes (Krishnaiah *et al*., 2002).

Saravanan *et al*. (2003) reported in sesame that single plant yield, plant height, photosynthetic rate, leaf area index and harvest index had high heritability and genetic advance, whereas days to 50 per cent flowering exhibited high heritability, but low genetic advance.

In an experiment to study the genetic variability, heritability and genetic advance of seed yield and its components in sesame, the estimates of heritability and genetic advance as per cent of mean were high for seed yield per plant, number of seeds per capsule, number of primary branches, number of capsules per plant and 1000-seed weight. Medium genetic advance as per cent of mean was recorded by days to 50 per cent flowering and plant height. Oil content and days to maturity had a low genetic advance as per cent of mean (Babu *et al*., 2005).

Ganesan (2005) in a trial conducted with sesame germplasm reported high heritability coupled with high genetic advance as percentage of mean for number of capsules per plant. Plant height, number of seeds per capsule and 1000-seed weight also recorded high heritability estimates and moderate level of genetic advance as percentage of mean indicating the presence of additive genes in governing these traits.

In the study conducted by Banerjee and Kole (2006) on the genetic variability and yield analysis in sesame, high to moderate estimates of heritability accompanied by high to moderate genetic advance was noticed for plant height, branches per plant, capsules per plant, seeds per capsule and seed yield per plant indicating the predominance of additive gene action for the expression of these characters.

The analysis of genetic parameters of sesame genotypes by Mothilal (2006) revealed high heritability and genetic advance as per cent of mean for plant height, number of branches per plant and number of capsules per plant and low genetic advance for seed yield per plant.

Gawali *et al.* (2007) reported in sesame that high heritability coupled with high genetic advance as percentage of mean in seed yield per plant, number of capsules per plant, seeds per capsule and 1000-seed weight indicated the presence of additive gene action.

Iwo *et al.* (2007) reported that in sesame plant height, days to 50 per cent flowering, number of branches per plant, number of capsules per plant, seeds per capsule and dry grain yield showed high estimate of heritability except capsule length. The high heritability values recorded were coupled with corresponding high genetic advance for number of branches per plant, number of capsule per plant and seed yield. These were regarded as indicators for effective selection.

In an experiment carried out to estimate the variability, heritability and genetic advance in sesame, the capsule length, number of capsules per plant showed high heritability estimates accompanied with high genetic advance as a per cent of mean (Gangarde *et al*., 2009).

Kumhar and Solanki (2009) studied genetic variability by growing eighty two genotypes of sesame. The mean sums of squares were significant for all the characters studied except oil content, indicating the presence of variability. Characters like seed yield, primary branches per plant, capsules per plant and plant height to first capsule exhibited high heritability coupled with high genetic advance revealing that these characters were controlled by additive gene action.

Genetic variability and yield analysis in sesame was carried out by Parameswarappa *et al*. (2009) and the study revealed that plant height, number of branches per plant, number of capsules per plant and seed yield per plant had high heritability coupled with high genetic advance.

Mandal *et al*. (2010) reported that highest value of heritability was observed for oil content and plant height whereas genetic advance was highest in plant height, when they evaluated sesame accessions.

The analysis of genetic parameters for thirty genotypes of sesame revealed high GCV, PCV, heritability and genetic advance as per cent of mean for number of capsules per plant, number of capsules in main stem, number of primary branches per plant, height upto first capsule and seed yield per plant indicating that selection could be effective in these characters for improving seed yield and yield attributes (Nayak *et al*., 2011).

Jadhav and Mohrir (2012) evaluated sesame germplasm lines for heritability and genetic advance as per cent of mean for quantitative traits and reported that high heritability and genetic advance as per cent of mean were recorded for seed yield per plant, number of capsules on main stem, number of capsules per plant, number of nodes on main stem and plant height for first capsule.

An assessment of genetic advance for morphological traits in sesame genotypes revealed high heritability coupled with high genetic advance as per cent of mean for number of primary branches per plant, height to first capsule and harvest index (Gidey *et al*., 2013).

An experiment was carried out with sesame germplasm at Sudan, for two consecutive rainy seasons by Salah and Abubakri (2013). They reported high heritability coupled with low genetic advance for days to 50 per cent flowering, days to maturity and plant height while low to moderate heritability with high genetic advance was recorded for the yield and its components.

2.4.3 Correlation

Yield is a quantitative trait that is dependent upon a number of other traits. An understanding of association between yield and yield contributing characters will help to make simultaneous selection for more characters. Correlation studies help to know the association between highly heritable traits with the most economic trait, the yield. The review on correlation studies in sesame by many authors is given below.

Kumar and Sivaswamy (1996) reported significant positive correlation of seed yield per plant with number of capsules on main stem, plant height and number of capsules on main stem and negative significant correlation between oil content and 1000-seed weight.

Information on correlation derived from data on yield-related traits in twenty five promising genotypes of sesame, of diverse ecogeographic origin revealed that seed yield exhibited significant and positive correlation with capsules per plant, seeds per capsule and primary branches per plant. Plant height showed negative correlation with 1000-seed weight (Tak, 1997).

Character association and path coefficient analysis in sesame by Backiyarani *et al*. (1999) showed that oil content is negatively correlated with yield.

Mukhekar *et al*. (2002) conducted an experiment to study the genetic variability and correlation in sesame. They reported that number of days to flowering, plant height and 1000 seed weight were positively correlated with yield.

Studies on correlation, regression and path analysis carried out on 576 accessions of sesame showed that seed yield was positively correlated with plant height, number of capsules per plant and 100-seed weight. The number of days to 50 per cent flowering, number of days to maturity and number of branches per plant were negatively correlated with seed yield (Raghuwanshi *et al*., 2003).

. Association analysis by Sankar and Kumar (2003) in sesame revealed that seed yield per plant was positively and significantly correlated with plant height, number of primary branches per plant, capsule length, number of capsules per plant and 1000-seed weight.

Correlation studies between yield and its attributing characters in sesame indicated that the oil yield per plant was positively associated with number of primary branches per plant, number of capsules per plant, number of seeds per capsule, 1000-seed weight and seed yield per plant both at genotypic and phenotypic levels (Babu *et al*., 2004).

Plant height, branches per plant, capsules per plant and seeds per capsule exhibited positive and significant genotypic and phenotypic correlations with seed yield in a population of thirty advance breeding lines of sesame in Sriniketan, West Bengal, during the 2002 and 2003 summer seasons (Banerjee and Kole, 2006).

Mothilal and Manoharan (2006) in a study to find character association in sesame genotypes reported that seed yield was positively and significantly correlated with number of branches, number of capsules on main stem, number of capsules on branches, number of seeds per capsule and 1000-seed weight.

In a study on genetic variability and correlation studies in sesame, it was found that seed yield is positively and significantly correlated with all traits except 1000-seed weight and oil percent (Gawali *et al.*, 2007).

Genetic variability and correlation studies in sesame by Iwo *et al.* (2007) reported that seed yield was positively correlated to number of days to 50 per cent flowering, seeds per capsule and number of capsule per plant at genotypic level. On the other hand, plant height and number of branches per plant were significantly correlated with seed yield at phenotypic level.

Thiyagu *et al.* (2007) studied the genotypic correlation between oil yield per plant and other yield contributing characters in sesame. Oil yield had highly significant and positive genotypic association with seed yield, number of capsules per plant and plant height. The seed yield per plant exhibited highly significant and positive genotypic association with number of capsules per plant.

Correlation studies in sesame by (Gnanasekaran *et al*., 2008) revealed that seed yield per plant had highly positive significant association with the number of branches per plant, number of capsules per plant and number of seeds per capsule and positive and significant association with capsule length and 1000-seed weight.

Sumathi *et al*. (2009) studied the association of yield and yield contributing traits in sesame and reported positive correlation between yield and plant height, number of branches per plant and number of capsules per plant.

An experiment conducted by Gayathri (2011) revealed that number of days to flowering, plant height, number of capsules per plant and oil content showed a significant association with seed yield per plant.

An experiment conducted to determine relationships between single plant seed yield and some morphological traits in sesame, revealed positive and statistically significant relationships between single plant seed yield and leaf nodes per plant, number of pods per plant, number of pods per main stem, breadth of pod, number of seeds per pod, 1000-seed weight and number of seeds per plant (Azeez and Morakinyo, 2011).

In a study conducted with sesame accessions by Mohan (2011) to find the association between characters, plant height and capsules per plant had positive and significant association with seed yield and were important traits to be considered for realizing improvement in seed yield.

2.4.4 Path analysis

Path coefficient analysis is important for partitioning the genotypic correlation coefficient into direct and indirect effects of component characters. A path coefficient is simply a standardized partial regression coefficient and it measures the direct influence of one variable upon another (Dewey and Lu, 1959). An estimation of the actual contribution of a trait and its influence through other traits is done. Works done by various authors in this line is reviewed here.

In an experiment to study the character association and path analysis in sesame, Reddy *et al*. (1992) derived information on yield correlations from data on seed yield, seed oil content and yield components in thirty genotypes. The study revealed that number of capsules, 1000-seed weight and plant height were major components for improvement of seed yield.

Shajan (2002) reported that plant height, number of branches, 1000-seed weight, number of capsules per plant and number of seeds per capsule had positive direct effect on seed yield per plant.

Path coefficient analysis on eight important economic traits of sesame, namely days to 50 per cent flowering, plant height, number of primary branches per plant, capsule length, number of capsules per plant, 1000-seed weight, oil percentage and single plant yield was done by Sankar and Kumar (2003). Partitioning of total correlation coefficient into components of direct and indirect effects revealed that the number of capsules per plant was the only character which contributed to seed yield directly. The other traits contributed indirectly through number of capsules per plant.

Character association and path coefficient analysis in a set of white seeded genotypes of sesame revealed that seed yield per plant exerted the highest positive direct effect on oil yield per plant followed by number of primary branches per plant, oil content, leaf area index and harvest index. Also, the characters number of primary branches per plant, number of capsules per plant, number of seeds per capsule, 1000-seed weight and seed yield per plant had highly significant positive association with oil yield per plant and also had positive direct as well as indirect effects through many other characters (Babu *et al*., 2004).

Genetic studies to ascertain selection criteria for yield improvement in sesame by Sengupta and Datta (2004) using path analysis showed that the number of capsules per plant had the greatest positive direct effect on seed yield, followed by capsule length, number of seeds per capsule, and total number of branches per plant. The indirect contribution of these traits on seed yield was also very significant and positive. Plant height, number of primary branches per plant, and number of capsules on the main axis showed direct negative effects on seed yield, and the indirect effects on seed yield via these traits were generally negative.

Siddiqui *et al*. (2005) reported strong positive direct effects for plant height, days to 50 per cent flowering and weight of seed per capsule. The indirect negative effects on yield were observed for days to first flowering, days to maturity, number of branches per plant, number of capsules per plant and length of capsule.

According to Vidhyavati *et al*. (2005) among the metric characters, namely, days to 50 per cent flowering, days to maturity, plant height, number of primary branches, number of capsules per plant, 100-seed weight and oil content, high positive direct effects were exerted by number of capsules per plant and plant height on seed yield.

The results of path analysis in a population of thirty advance breeding lines of sesame indicated that number of branches per plant, capsules per plant and seeds per capsule were the important characters determining seed yield (Banerjee and Kole, 2006).

A study on character association and path analysis for yield and yield components in sesame by Mothilal and Manoharan (2006) reported that number of branches, number of capsules on branches and number of seeds per capsule had positive direct effects on seed yield.

An experiment conducted on path coefficient analysis for yield and yield attributing traits in sesame revealed that the character number of capsules per plant showed high positive direct effects on grain yield per plant. The indirect effect of number of capsules per plant on grain yield through plant height, number of branches per plant, oil content and days to maturity was high (Sumathi *et al*., 2007).

Path analysis for oil yield and its components in cultivated sesame by Thiyagu *et al.* (2007) reported that seed yield had maximum direct effect on oil yield followed by number of capsules per plant.

Path co-efficient analysis in sesame by Gnanasekaran *et al*. (2008) revealed that seed yield per plant had positive and highly significant association with the number of branches per plant, number of capsules per plant and number of seeds per capsule and positive and significant association with capsule length and 1000-seed weight. Also the indirect effects of the number of branches per plant through number of capsules per plant and vice-versa were also positive.

Studies on genetic variability and character association in germplasm collection of sesame by Parameshwarappa *et al*. (2009) reported that plant height, number of capsules per plant and 1000 seed weight had positive direct effect on yield.

Georgiev *et al.* (2012) reported direct effect of the number of capsules on the main stem and branches on seed yield of a plant. The indirect positive impact of the height of the main stem is expressed by the positive relationship between the latter and the number of capsules on the branches and stem.

2.4.5 Divergence studies

Genetic diversity plays an important role in plant breeding as selection of parents for breeding programme is crucial. Mahalanobis (1928) developed the concept of D^2 statistics for a measure of group distance with respect to multiple characters. A review of work done by many authors in clustering sesame genotypes is given here.

Plant height, number of branches, capsules per plant and seed yield were measured in fifty two sesame genotypes and cluster analysis grouped the genotypes into six groups. Plant height was the major contributor to genetic divergence among the genotypes, followed by number of branches, seed yield and capsules per plant (Manivannan and Nadarajan, 1996).

Analyses of data on thirteen quantitative characters in forty genotypes of sesame originating from different states of India grouped them into fourteen clusters using Mahalanobis D^2 statistic (Swain and Dikshit, 1997). No relationship between geographic origin and genetic diversity was observed. Seed oil content made the largest contribution to total divergence, followed by 1000-seed weight, capsule length and days to flowering.

In a multivariate analysis of divergence by Dikshit and Swain (2000) eleven parents were grouped into six clusters and seed oil content was found to contribute maximum towards total divergence.

Manivannan and Ganesan (2001) subjected sixty-seven sesame genotypes to D^2 analysis in a field experiment and observations were recorded for plant height, number of branches per plant, number of capsules per plant, seeds per capsule, 1000-seed weight and seed yield per plant. The genotypes were grouped into ten clusters. Among characters, plant height, followed by number of branches per plant and 1000- seed weight contributed more towards the total divergence.

Navale *et al*. (2001) clustered fifty indigenous and exotic lines of sesame into six sets and the study indicated that genetic diversity is not related to geographical origin.

A study on genetic divergence for seed yield and other characters in sesame by Solanki and Gupta (2001) showed that number of capsules per plant contributed maximum to genetic divergence, followed by seed yield per plant.

Sudhakar (2003) clustered sixty two sesame genotypes to thirteen groups and found that the major contributors to genetic divergence were number of capsules per plant, number of seeds per capsule, days to maturity and days to 50 per cent flowering. Least contributors included plant height and seed yield per plant.

Seventy one diverse germplasm lines of sesame originating from different parts of India were studied by Anuradha and Reddy (2005) and observations on quantitative characters were subjected to Mahalanobis D^2 statistics. Days to maturity had the maximum contribution towards genetic divergence, followed by 1000-seed weight, seeds per capsule and capsule length.

The genetic diversity of fortythree sesame germplasm lines was determined using the D^2 statistics in a field experiment conducted in the kharif season (Rao, 2006). Multivariate analysis grouped the lines into eight clusters and the genotypes with different geographical origin clustered together. Seed yield, initial flowering and number of capsules per plant contributed to maximum divergence of the lines studied.

Genetic divergence was studied by Kumhar and Solanki (2009) by growing eighty two genotypes of sesame. Hierarchical cluster analysis indicated the presence of considerable genetic divergence among the genotypes. Among the eight characters studied, seed yield contributed the most towards the divergence of genotypes.

In an experiment conducted by Kumar *et al*. (2010), data on days to 50 per cent flowering, days to 100 per cent flowering, days to maturity, plant height, pods on main shoot, pod length, seeds per pod, seed size, seed yield per plant and per cent oil content were subjected to D^2 analysis. Total number of pods per plant, plant height, main shoot length and seeds per pod had greater contribution towards the observed genetic divergence. Principal component analysis also supported the contribution of total number of pods per plant, main shoot length and plant height towards divergence.

Sesame genotypes were evaluated for nine yield and yield attributing characters to study the genetic diversity existing among them by using Mahalanobis D^2 statistics. Analysis of variance revealed significant difference among genotypes for all the nine character studied. Based on the D^2 values, the genotypes were grouped into nine different clusters. The genotypes grouped into various clusters revealed that there was no relationship between geographical distribution and genetic diversity. Among the nine characters studied, 1000-seed weight contributed highest towards genetic divergence followed by number of capsules per plant and seed yield per plant (Parameshwarappa *et al*., 2010).

To determine the level of diversity in relation to geographical origins and morphological characteristics, Bandila *et al.* (2011) analyzed sixty accessions from different parts of the India using D^2 analysis. Number of seeds per capsule contributed highest towards the divergence. The distribution pattern of genotypes in different clusters indicated that genetic divergence was not related to geographical differentiation.

The relative ranking of different component characters of D^2 analysis in sesame by Gayathri (2011) showed that maximum contribution towards total divergence was attributed to plant height followed by days to flowering and seed yield per plant.

Genetic divergence analysis in sesame was done by Jadhav and Mohrir (2013) using Mahalanobis D^2 analysis and it was found that oil content contributed maximum towards genetic divergence.

2.4.6 Selection index

In population improvement programmes, selection is based on the phenotypic evaluation of several traits that are frequently obtained from the means of several replications. Selection indices evaluate the total genotypic value of individuals or families for several traits. Selection based on indices permits maximizing the response to selection for one or a group of traits. In reality, selection based on indices reflects not only the response with direct selection, but also the correlated response as selection is practiced for other traits simultaneously.

In an experiment to study breeding methodology and selection index for yield in sesame, Krishnamurthy *et al*. (1964) reported that number of capsules per plant, number of branches per plant and number of seeds per capsule was found to be good selection criteria for the improvement of yield.

Analysis of seven traits in fifteen varieties with respect to the genetic coefficient of variation, heritability estimates, expected genetic gain and phenotypic correlations revealed that selection index based on earliness and capsule and branch number per plant will be effective for the production of tall varieties (Chaudhary *et al*. 1977).

Expected genetic advance from the use of selection indices involving different combinations of quantitative characters was calculated by Lee and Chang (1986) from data on eighty two cultivars of sesame. The best selection index involved number of days to flowering, length of stem, length of capsule and capsule number per plant.

Selection indices in sesame were determined by Chopade *et al.* (1998), who reported that the index comprising all eight traits exhibited an increase in efficiency over straight selection for yield alone.

Materials and Methods

3. MATERIALS AND METHODS

The materials used and the methods followed during the course of this investigation are described in this chapter.

3.1 Experimental site

The experiment was conducted in the field of Instructional Farm, College of Agriculture, Vellayani which is located at latitude 8^0 25'N, longitude of 76^0 59' E and situated at an altitude of 29 m above mean sea level.

3.2 Experimental design

The experiment was conducted during rabi season, 2012-13 in a Randomized Block Design in a coconut garden. The experimental field was prepared to a fine tilth by tilling followed by leveling. A spacing of 30 cm between rows and 15 cm between plants was adopted. Observations were recorded in five randomly selected plants in each genotype. All the crop production practices as per the package of practices recommendation of Kerala Agricultural University (2011) were followed to raise a successful crop.

3.3 Experimental materials

The material for study comprised of thirty three genotypes of sesame collected from various research stations including the varieties from Kerala Agricultural University, University of Agricultural Sciences, Dharwad and Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The list of genotypes used in the present study is given in Table 1.

3.4 Observations

The following observations were recorded on five random competitive plants in each

Table 1. List of *Sesamum indicum* genotypes used for evaluation

Sl No:	Name	Source	Accession No:
1.	Prachi	ORARS, Kayamkulam	*SI* 1
2.	TKG - 22	ORARS, Kayamkulam	*SI* 2
3.	Brijeshwari	ORARS, Kayamkulam	*SI* 3
4.	TKG - 306	ORARS, Kayamkulam	*SI* 4
5.	RT - 54	ORARS, Kayamkulam	*SI* 5
6.	Smarak	ORARS, Kayamkulam	*SI* 6
7.	RT - 351	ORARS, Kayamkulam	*SI* 7
8.	VRI - 2	ORARS, Kayamkulam	*SI* 8
9.	AKT - 101	ORARS, Kayamkulam	*SI* 9
10.	GT - 10	ORARS, Kayamkulam	*SI* 10
11.	DSS - 9	UAS, Dharwad	*SI* 11
12.	DS - 5	UAS, Dharwad	*SI* 12
13.	DS (1) - C	UAS, Dharwad	*SI* 13
14.	Kayamkulam 1	ORARS, Kayamkulam	*SI* 14
15.	Surya	ORARS, Kayamkulam	*SI* 15
16.	Thilak	ORARS, Kayamkulam	*SI* 16
17.	Thilathara	ORARS, Kayamkulam	*SI* 17
18.	AKT - 64	PDKV, Akola	*SI* 18
19.	RT - 354	ORARS, Kayamkulam	*SI* 19
20.	Nirmala	ORARS, Kayamkulam	*SI* 20
21.	AVTS 12-7	ORARS, Kayamkulam	*SI* 21
22.	OSC - 560	ORARS, Kayamkulam	*SI* 22
23.	OSC - 79	ORARS, Kayamkulam	*SI* 23
24.	MT 10-8-1	ORARS, Kayamkulam	*SI* 24
25.	TKG 412-1	ORARS, Kayamkulam	*SI* 25
26.	TKG - 22	ORARS, Kayamkulam	*SI* 26
27.	SSD - 22	ORARS, Kayamkulam	*SI* 27
28.	MT 10-13-1	ORARS, Kayamkulam	*SI* 28
29.	IVTS 12-5	ORARS, Kayamkulam	*SI* 29
30.	MT 10-27-1	ORARS, Kayamkulam	*SI* 30
31.	SSD - 23	ORARS, Kayamkulam	*SI* 31
32.	SSD - 1	ORARS, Kayamkulam	*SI* 32
33.	Palakkad local	Palakkad	*SI* 33

replication. The average values were computed as treatment mean in each replication. The characters studied and techniques adopted to record the observations are given below.

3.4.1 Days to 50 per cent flowering

Number of days taken to initiate flowering in 50 per cent of the plants in each entry was recorded.

3.4.2 Plant height

The distance from ground level upto the terminal bud on main axis of a plant at maturity was recorded in centimetres.

3.4.3 Days to maturity

Days taken to mature 75 per cent of capsules in 75 per cent of individuals within each entry were recorded as days to maturity.

3.4.4 Number of capsules per unit length

The number of capsules per centimetre length was counted and the average of five plants was expressed.

3.4.5 Number of primary branches per plant

Number of branches emerging from main stem was counted at harvest and average was expressed as number of primary branches per plant.

3.4.6 Number of capsules per plant

Total number of seed bearing capsules on each plant including those on main stem and primary branches was counted and recorded.

3.4.7 Length of the capsule

Five matured capsules taken at random from each plant were measured and their mean length recorded in centimetres.

3.4.8 Number of seeds per capsule

Seeds were extracted from five pods per plant selected at random and counted. The average number of seeds per capsule was recorded.

3.4.9 Seed yield per plant

All the matured capsules obtained from each single plant were dried uniformly, seeds extracted and seed weight per plant recorded in grams.

3.4.10 1000-seed weight

One thousand randomly selected seeds from each plant were weighed and expressed in grams.

3.4.11 Root length

Length of primary root was recorded in centimetre.

3.4.12 Oil content

Clean seeds with 10-12 per cent moisture were used for oil estimation by cold percolation method where oil is extracted by repeated washing with petroleum spirit and estimated after removing the solvent (Nagaraj, 2009). For this one gram seeds was weighed, crushed and powdered with one spoonful of anhydrous sodium sulphate and oil was extracted with petroleum spirit with three repeated washings at one hour interval.

3.4.13 Scoring of pests and diseases, if any

3.5 Statistical analysis

The data recorded were processed using the following statistical procedures.

3.5.1 Analysis of variance (ANOVA)

The biometric observations recorded were subjected to ANOVA (Panse and Sukhatme, 1985) for comparison among various treatments and to estimate variance components.

ANOVA for each character

Sources of variation	Degrees of freedom	Mean sum of squares	'F' value calculated
Replication	r-1	MSR	MSR/MSE
Treatment	t-1	MST	MST/MSE
Error	(r-1) (t-1)	MSE	
Total	rt-1		

where, r = number of replications

t = number of treatments

MSR = mean square of replication

MST = mean square of treatments

MSE = mean square of error

Critical difference (CD) = $t_{\alpha} \sqrt{\frac{2MSE}{r}}$

where, t_{α} = Student's 't' table value at error degrees of freedom at α level of significance

3.5.2 Estimation of genetic parameters

3.5.2.1 Genetic components of variance

The phenotypic and genotypic variances were calculated by utilizing the respective mean square values (Johnson *et al.*, 1955).

i) Genotypic variance (V_G)

$$V_G = \frac{MST-MSE}{r}$$

ii) Environmental variance (V_E)

$$V_E = MSE$$

iii) Genotypic variance (V_G)

$$V_P = V_G + V_E$$

3.5.2.2 Coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated by following Burton (1952).

i) Phenotypic coefficient of variation (PCV)

$$\mathrm{PCV} = \frac{\sqrt{V_P}}{\bar{X}} \times 100$$

ii) Genotypic coefficient of variation (GCV)

$$\mathrm{GCV} = \frac{\sqrt{V_G}}{\bar{X}} \times 100$$

$\bar{X}$ = General mean of characters

Categorization of the range of variation was effected as proposed by Sivasubramanian and Menon (1973).

Category	Range
Low	< 10%
Moderate	10 – 20%
High	> 20%

3.5.2.3 Heritability

Heritability percentage in broad sense was estimated for various characters as per the formulae suggested by Johnson et al. (1955).

Heritability (h^2) = $\frac{V_G}{V_P}$ x 100

As suggested by Johnson *et al.* (1955) heritability in broad sense estimates were categorized as,

Category	Range
Low	0 – 30%
Medium	30 – 60%
High	> 60%

3.5.2.4 Genetic advance

Genetic advance is the measure of genetic gain under selection which depends upon standardized selection differential, heritability and phenotypic standard deviation (Allard, 1960). The genetic advance was calculated in percent by the formulae suggested by Johnson *et al* (1955).

Genetic advance (GA) = $k \times h^2 \sqrt{V_P}$

GA as percentage of mean = $\frac{GA}{\bar{X}} \times 100$

where, k = standardized selection differential (2.06 at 5% selection intensity)

h^2 = heritability

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

Category	Range
Low	< 10%
Moderate	10 – 20%
High	> 20%

3.5.3 Correlation analysis

Phenotypic, genotypic and environmental correlation coefficients were calculated using the respective variance and covariance of the characters which showed significant variation in the ANOVA.

Phenotypic correlation coefficients, $r_{PXY} = \frac{C_O V_P (X,Y)}{\sqrt{V_P (X).V_P (Y)}}$

Genotypic correlation coefficients, $r_{GXY} = \frac{C_O V_G(X,Y)}{\sqrt{V_G(X).V_G(Y)}}$

where, $C_O V_P(X,Y)$ = phenotypic covariance between two traits X and Y

$C_O V_G(X,Y)$ = genotypic covariance between two traits X and Y

$V_P(X)$ and $V_P(Y)$ = phenotypic variance for X and Y respectively

$V_G(X)$ and $V_G(Y)$ = genotypic variance for X and Y respectively

3.5.4 Path coefficient analysis

To study the cause and effect relationship of yield and its component characters, direct and indirect effects were analyzed using path coefficient analysis as suggested by Wright (1954).

The genotypic correlation between yield and selected component characters were subjected to path analysis and the direct effect of the character on yield as well as the indirect effects through other characters were estimated.

3.5.5 Genetic divergence analysis

Genetic divergence was measured using the technique D^2 statistics developed by Mahalanobis in 1928. Grouping of genotypes into clusters was done based on the relative distance (D^2 values) from each other, and was based on the method suggested by Tocher (Rao, 1952).

Results

4. RESULTS

An experiment entitled "Evaluation of sesame (*Sesamum indicum* L.) genotypes to the shaded uplands of Southern region" was undertaken at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani. Thirty three genotypes of sesame were evaluated and data collected on twelve characters were subjected to statistical analysis. The results of the experiment are presented in this chapter.

4.1 Weather and crop growth

The total rainfall received during the crop period was 412 mm. The maximum temperature recorded during the cropping season was in the range of 29.9^0C to 31.2^0C and the minimum temperature was 21.1^0 to 23.8^0C. Relative humidity during the entire crop season ranged between 62.5 and 99 per cent. Light intensity in the experimental field varied from 24.7 k lux to 43.5 k lux. The weather parameters during crop growth period are given in Table 2 and Fig. 1

4.2 Analysis of variance

The analysis of variance (Table 3) revealed highly significant differences among the thirty three genotypes with respect to days to 50 per cent flowering, plant height, days to maturity, number of primary branches, number of capsules per plant, length of capsule, number of seeds per capsule, root length, number of capsules per unit length and seed yield per plant. The 1000-seed weight did not show any significant difference among the genotypes.

4.3 Performance of the sesame genotypes

The range, mean performances of thirty three sesame genotypes for twelve characters studied and overall mean for different characters are presented in Table 4.

Table 2. Weather data during crop growth (at 15-day intervals)

Days	Temperature (^0C)		Relative humidity (%)		Total rainfall (mm)	Light intensity (k lux)	Shade (%)
	Max.	Min.	Max.	Min.			
1 to 15 days	31.2	23.8	89.5	69.4	63	39.1	63.8
16 to 30 days	29.9	23.6	89.1	71.4	58	35.6	64.2
31 to 45 days	29.9	23.1	92.2	77.8	62	33.8	60.1
46 to 60 days	30.5	23.3	97.2	69.4	20	41.2	60.5
61 to 75 days	30.6	22.4	99	66.3	5	43.5	61.7
76 to 90 days	30.8	22.8	94.3	62.5	45	35.9	59.5
91 to 105 days	30.4	23.4	96.8	73.3	154	24.7	66.9
106 to 120 days	30.3	21.1	95.9	74.3	5	40.2	58.6
Mean	30.4	22.9	94.3	70.6	51.5	36.8	61.9
Total					412		

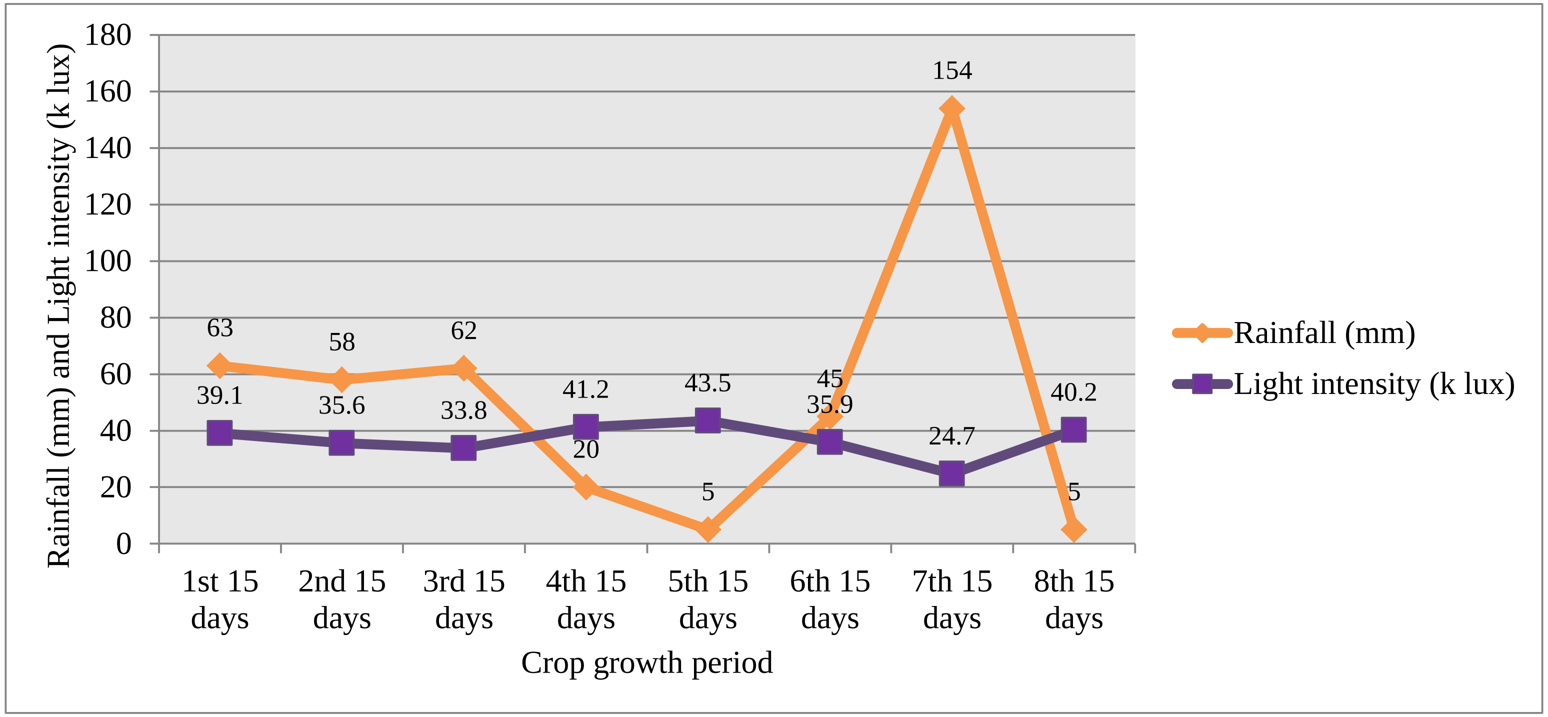


Fig. 1 Rainfall and light intensity distribution pattern during the crop growth period

Table 3. Analysis of variance for various characters of sesame genotypes

Characters	Mean sum of squares		
	Replication	Genotypes	Error
Days to 50% flowering	3.363	21.017**	0.645
Plant height (cm)	293.011	130.88 **	5.364
Days to maturity	26.250	57.332**	1.420
No. of primary branches	0.010	5.911**	0.020
No. of capsules/ plant	4.859	55.224**	0.120
No. of capsules/ unit length	0.007	0.041*	0.001
Length of capsule (cm)	0.023	0.185*	0.003
No. of seeds/ capsule	4.734	55.022**	0.977
Root length (cm)	1.149	13.704**	0.027
Oil content (%)	0.016	4.299**	0.001
1000-seed weight (g)	0.001	0.001	0.001
Seed yield/ plant (g)	0.207	1.449*	0.004

* significant at 5% level

** significant at 1% level

Table 4. Mean performance of sesame genotypes

Accession No.	Days to 50 % flowering	Plant height (cm)	Days to maturity	No. of primary branches	No. of capsules/ plant	Length of capsule (cm)	No. of seeds/ capsule	Root length (cm)	Oil content (%)	1000 seed weight (g)	Seed yield/ plant (g)	No. of capsules/ unit length
SI 1	28.33	28.33	115.33	3.67	19.00	1.97	51.33	8.93	49.73	3.16	3.08	0.19
SI 2	34.67	24.00	106.33	4.00	19.67	1.83	49.33	9.17	49.57	3.15	3.06	0.21
SI 3	33.00	32.00	103.67	2.00	19.67	2.00	52.00	12.57	49.95	3.15	3.22	0.31
SI 4	33.33	41.33	113.33	2.00	15.67	1.93	50.67	6.67	48.60	3.16	2.51	0.19
SI 5	31.67	32.00	109.00	2.00	18.00	1.83	48.67	6.30	49.67	3.18	2.78	0.28
SI 6	34.00	37.00	102.33	2.00	16.33	1.40	42.67	11.07	48.13	3.14	2.19	0.22
SI 7	31.67	52.00	111.33	2.00	26.00	2.07	53.33	9.23	48.31	3.16	4.38	0.25
SI 8	33.67	35.00	114.33	4.00	20.33	1.87	49.33	9.77	49.62	3.17	3.18	0.15
SI 9	28.00	43.00	113.00	2.00	17.00	2.20	56.00	9.00	49.23	3.14	2.99	0.20
SI 10	29.67	30.33	110.33	1.00	13.33	1.83	48.67	8.33	48.51	3.19	2.07	0.44
SI 11	34.67	39.33	106.00	4.00	23.33	1.63	43.33	5.90	46.75	3.15	3.19	0.15
SI 12	27.67	45.00	118.33	6.00	29.67	2.00	47.33	8.23	45.77	3.16	4.43	0.13
SI 13	27.67	38.33	106.00	6.00	23.33	1.43	42.67	8.37	48.63	3.16	3.15	0.09
SI 14	30.33	31.67	108.33	2.00	17.33	1.30	40.67	11.33	50.16	3.18	2.24	0.27
SI 15	26.33	38.33	102.00	4.00	11.33	1.53	42.00	5.90	49.00	3.15	1.50	0.07
SI 16	30.33	29.33	106.00	6.00	13.33	1.67	46.67	7.87	49.19	3.21	2.00	0.08
SI 17	32.67	29.33	110.67	4.00	13.67	2.03	53.33	9.13	49.68	3.16	2.30	0.12
SI 18	29.00	33.33	106.67	4.00	23.33	1.80	48.00	8.70	48.12	3.16	3.54	0.18
SI 19	28.33	35.00	106.00	2.00	19.67	1.43	42.67	5.57	48.50	3.14	2.63	0.29
SI 20	35.33	32.00	115.67	1.00	21.33	2.00	52.00	11.83	49.50	3.12	3.46	0.67
SI 21	29.00	37.00	109.33	4.00	19.33	1.50	44.00	10.80	45.52	3.17	2.69	0.13
SI 22	27.33	36.67	105.33	2.00	15.00	1.20	40.00	10.03	48.82	3.17	1.90	0.20
SI 23	33.67	28.67	104.33	1.67	14.33	1.67	45.33	6.97	47.68	3.17	2.06	0.34
SI 24	28.33	38.67	102.00	2.00	16.67	1.87	49.33	11.27	49.13	3.15	2.59	0.22
SI 25	28.67	40.67	111.00	4.00	18.33	1.60	44.00	5.47	48.67	3.12	2.52	0.11
SI 26	33.00	37.00	106.33	2.00	11.67	2.00	52.00	9.27	46.10	3.15	1.91	0.16

SI 27	29.33	49.00	107.67	2.00	13.67	2.07	54.67	10.93	48.33	3.17	2.37	0.14
SI 28	31.00	30.67	113.33	4.00	19.33	1.67	45.33	12.47	48.64	3.15	2.76	0.16
SI 29	33.00	51.67	107.67	4.00	21.00	1.97	51.33	10.33	49.97	3.16	3.40	0.10
SI 30	33.00	34.00	114.33	4.00	17.33	1.90	50.00	6.40	47.83	3.15	2.73	0.13
SI 31	34.33	37.00	105.33	2.00	12.33	1.47	43.33	5.77	48.62	3.19	1.71	0.17
SI 32	31.67	34.67	111.00	2.00	12.33	1.80	48.00	8.47	49.77	3.16	1.87	0.18
SI 33	27.33	31.00	114.67	4.00	19.00	1.90	50.00	5.87	47.57	3.12	2.96	0.15
CD	1.31	3.78	1.95	0.23	0.56	0.09	1.61	0.27	0.03	NS	0.11	0.06
Mean	30.78	36.16	109.00	3.07	17.93	1.76	47.82	8.72	48.59	3.16	2.71	0.20
Min.	26.33	24.00	102.00	1.00	11.33	1.20	40.00	5.47	45.52	3.12	1.50	0.07
Max.	35.33	52.00	118.33	6.00	29.67	2.20	56.00	12.57	50.16	3.20	4.43	0.67

4.3.1 Days to 50 per cent flowering

Significant difference was noticed among the genotypes for number of days to 50 per cent flowering. The genotype *SI* 15 (26.33 days) was the earliest to attain 50 per cent flowering with two genotypes (*SI* 22 and *SI* 33) on par with it. The genotype *SI* 20 (35.33 days) took the maximum days to flower. Of the thirty three genotypes, seventeen genotypes were having days to 50 per cent flowering less than the general mean of 30.78 days.

4.3.2 Plant height

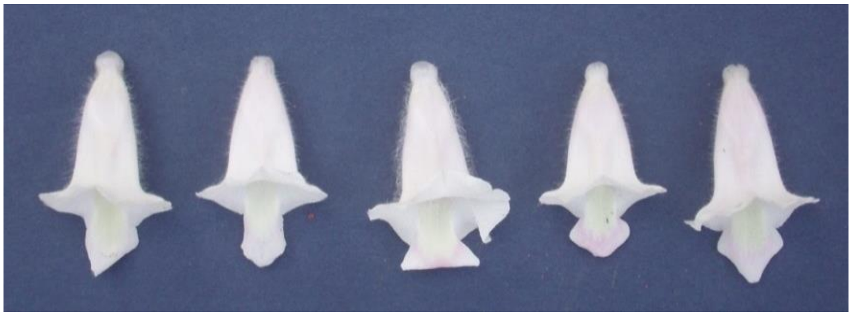
Significant difference was noticed among the accessions for plant height with an overall mean of 36.16 cm. The genotype *SI* 7 was the tallest (52 cm) and the genotype *SI* 2 (24 cm) recorded the minimum value for this trait. The genotypes *SI* 29 and *SI* 27 were on par with the tallest genotype.

4.3.3 Days to maturity

The maximum days to maturity was noticed in genotype *SI* 12 (118.33 days). The minimum duration of 102 days was recorded in genotypes *SI* 15 and *SI* 24. Two genotypes, viz., *SI* 3 (103.67) and *SI* 6 (102.33) were on par with the minimum duration. The average number of days to maturity was 109 days. Among the thirty three genotypes which differed significantly for this trait, seventeen genotypes had the mean number of days to maturity less than the general mean.

4.3.4 Number of primary branches

The genotypes *SI* 20 and *SI* 10 manifested the minimum number of primary branches (1) while genotypes *SI* 12, *SI* 13 and *SI* 16 registered maximum number of primary branches (6). Among the thirty three genotypes evaluated sixteen genotypes had more branches than the general mean and seventeen genotypes had fewer branches than the general mean (3.07)



(B)

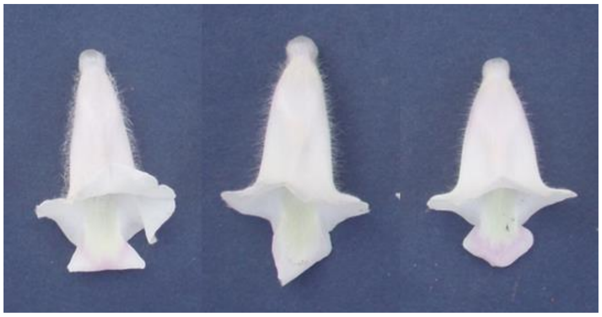


Plate 1. Variability in sesame flower: (A) Flower size & shape (B) Flower hairiness

4.3.5 Number of capsules per plant

The genotypes differed significantly for number of capsules per plant with a general mean of 17.93. The maximum number of capsules per plant was recorded for *SI* 12 (29.67) which was significantly superior to all the other genotypes. The minimum was recorded for *SI* 15 (11.33). Among the thirty three genotypes, seventeen genotypes had more capsules than the general mean.

4.3.6 Number of capsules per unit length

The different accessions differed significantly and the genotype *SI* 20 had the maximum number of capsules per unit length (0.67) while the genotype *SI* 15 had the minimum (0.07). The average number of capsules per unit length was 0.20 with twelve genotypes having more number of capsules per unit length than it.

4.3.7 Length of capsule

Significant difference was noticed among the accessions for capsule length with longest capsules being recorded by *SI* 9 (2.2 cm) and tiny capsules by *SI* 22 (1.2 cm). The general mean for length of capsules was 1.76 cm. None of the genotypes were statistically on par with either the minimum or maximum value for the character. Twenty genotypes had longer capsules than the average for this character.

4.3.8 Number of seeds per capsule

The genotypes differed significantly with respect to number of seeds per capsules having an average of 47.82 seeds per capsule. The genotype *SI* 9 produced the maximum number of seeds per capsule with 56 seeds with one genotype *SI* 27 on par with it while genotype *SI* 22 produced the minimum number of seeds per capsule (40).

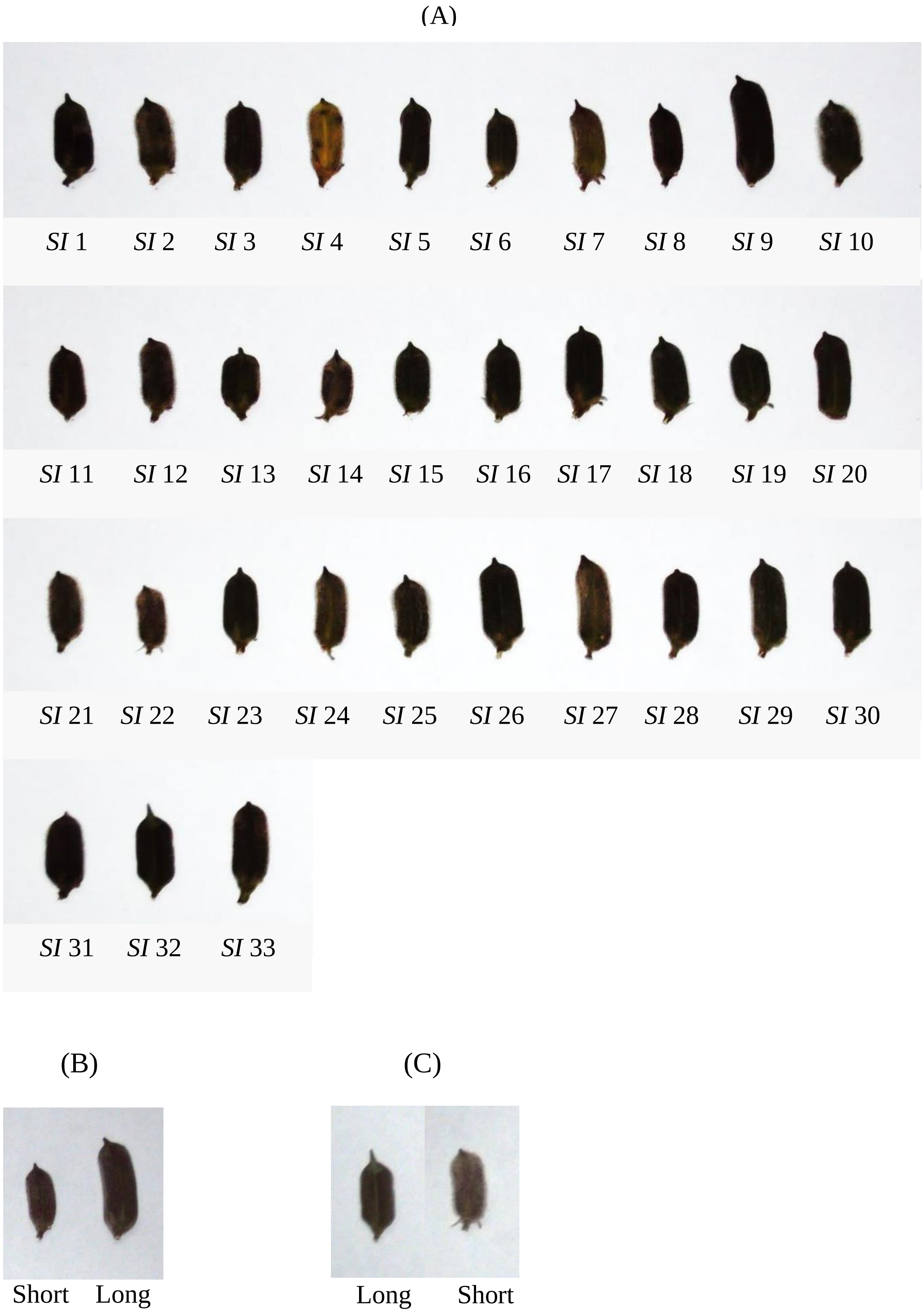


Plate 2. Variability in capsules of sesame (A) Capsules of thirty three genotypes (B) Capsule length (C) Capsule beak

4.3.9 Root length

The genotypes differed significantly for root length. The genotype *SI* 3 had the longest roots with 12.57 cm and the genotype *SI* 28 (12.47) was on par with it. The shortest root was possessed by the genotype *SI* 25 (5.47 cm) and the overall mean for root length was 8.72 cm.

4.3.10 Oil content

Oil content also recorded significant difference among the thirty three accessions studied with an overall mean of 48.59 per cent. The oil content ranged from 45.52 per cent (*SI* 21) to 50.16 per cent (*SI* 14).

4.3.11 1000-seed weight

There was no significant difference among the accessions for 1000-seed weight. The weight of 1000 seeds ranged between 3.21g (*SI* 16) and 3.12g (*SI* 20) with an average of 3.16g.

4.3.12 Seed yield per plant

The genotypes exhibited wide significant variation for seed yield per plant and the general mean for this character was 2.71g. The genotype *SI* 12 registered the maximum yield of 4.43g (70.88 g/m^2) and the genotype *SI* 7 was on par with it. The minimum yield was manifested by the genotype *SI* 15 which produced only 1.50g seeds per plant. Among the thirty three genotypes evaluated, fifteen genotypes recorded more yield and eighteen genotypes had less yield than the overall mean seed yield.

4.3.13 Pest and disease scoring

There was no incidence of pests and diseases during the crop growth period.

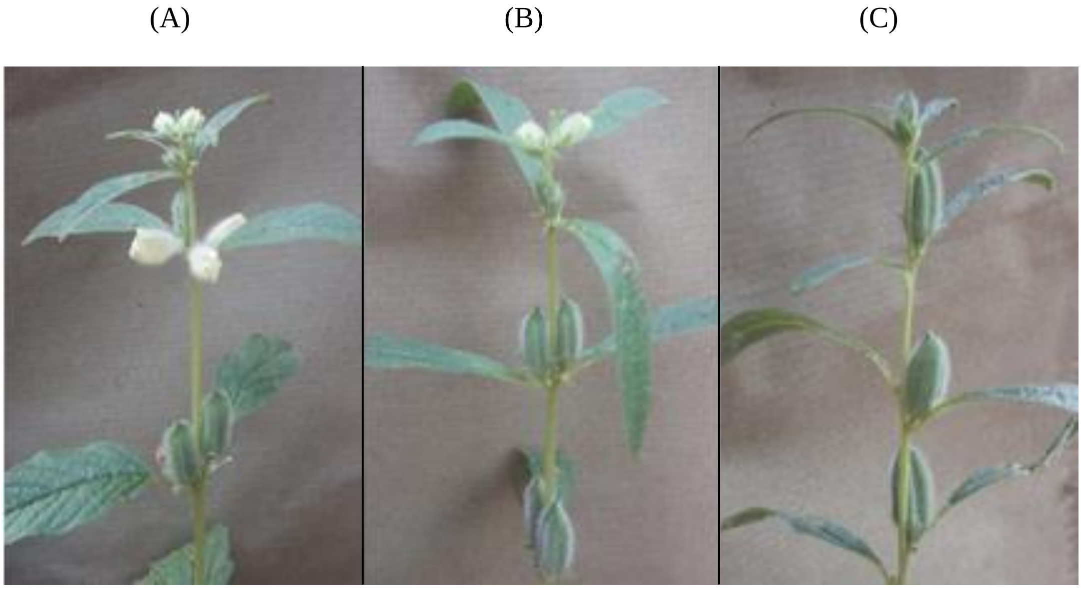


Plate 3. Variability in sesame genotypes for number of capsules per node

(A) Four capsules/node (B) Two capsules/node (C) One capsule/node

4.4 Genetic variability parameters

An attempt was made in the present investigation to study the genetic parameters such as PCV, GCV, heritability and genetic advance for thirty three sesame genotypes for twelve characters which will help in formulating breeding strategies for sesame improvement for various characters. As the genotypic and phenotypic variances are associated with units, the coefficients of variations were worked out for valid comparisons among the characters. The estimates of genetic variability parameters for the twelve characters are presented in Table 5 and Figs. 2 and 3.

4.4.1 Days to 50 per cent flowering

Low PCV and GCV values with narrow difference between them (8.86 per cent and 8.46 per cent respectively) coupled with high heritability (91.33 per cent) and a moderate genetic advance (16.60 per cent) was evident for days to 50 per cent flowering.

4.4.2 Plant height

A moderate estimate of PCV (19 per cent) and GCV (17.87 per cent) were recorded plant height. This trait also exhibited a high heritability (88.64 per cent) and a higher genetic advance (34.69 per cent).

4.4.3 Days to maturity

Days to maturity exhibited a low PCV (4.11 per cent) and GCV (3.96) with high heritability estimates (92.92 per cent) and low genetic advance (7.86).

Table 5. Estimates of variability parameters for various characters of sesame genotypes

Characters	PCV	GCV	Heritability (%)	GA as % mean
Days to 50% flowering	8.86	8.46	91.33	16.60
Plant height (cm)	19.00	17.87	88.64	34.69
Days to maturity	4.11	3.96	92.92	7.86
No. of primary branches	45.87	45.64	98.97	93.54
No. of capsules/ plant	23.98	23.90	99.36	49.08
No. of capsules/ unit length	59.19	56.68	91.69	95.80
Length of capsule (cm)	14.31	13.95	95.05	28.06
No. of seeds/ capsule	9.11	8.88	94.86	17.80
Root length (cm)	24.55	24.48	99.41	50.29
Oil content (%)	2.46	2.45	100.00	5.08
1000-seed weight (g)	0.63	0.62	100.00	1.27
Seed yield/ plant (g)	25.74	25.62	99.09	52.51

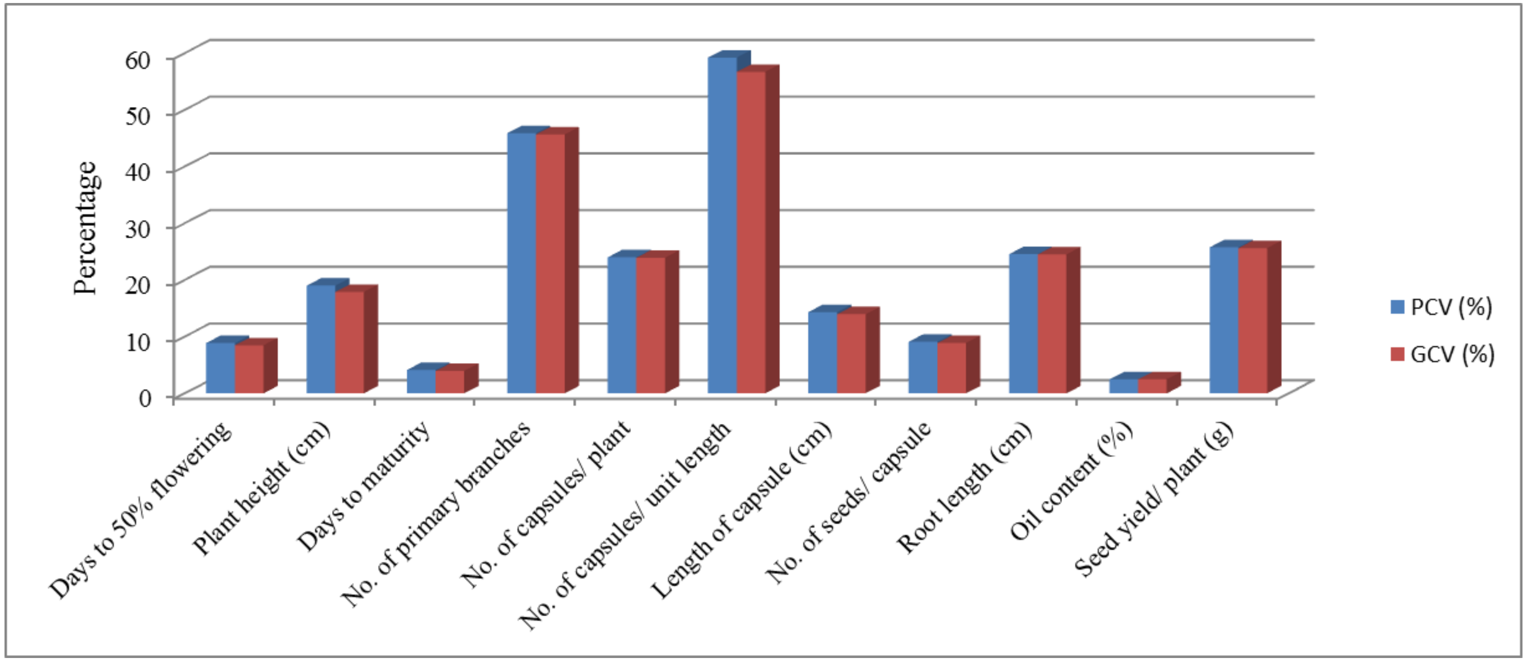


Fig. 2 PCV (%) and GCV (%) for various characters of sesame genotypes

PCV: Phenotypic coefficient of variation

GCV: Genotypic coefficient of variation

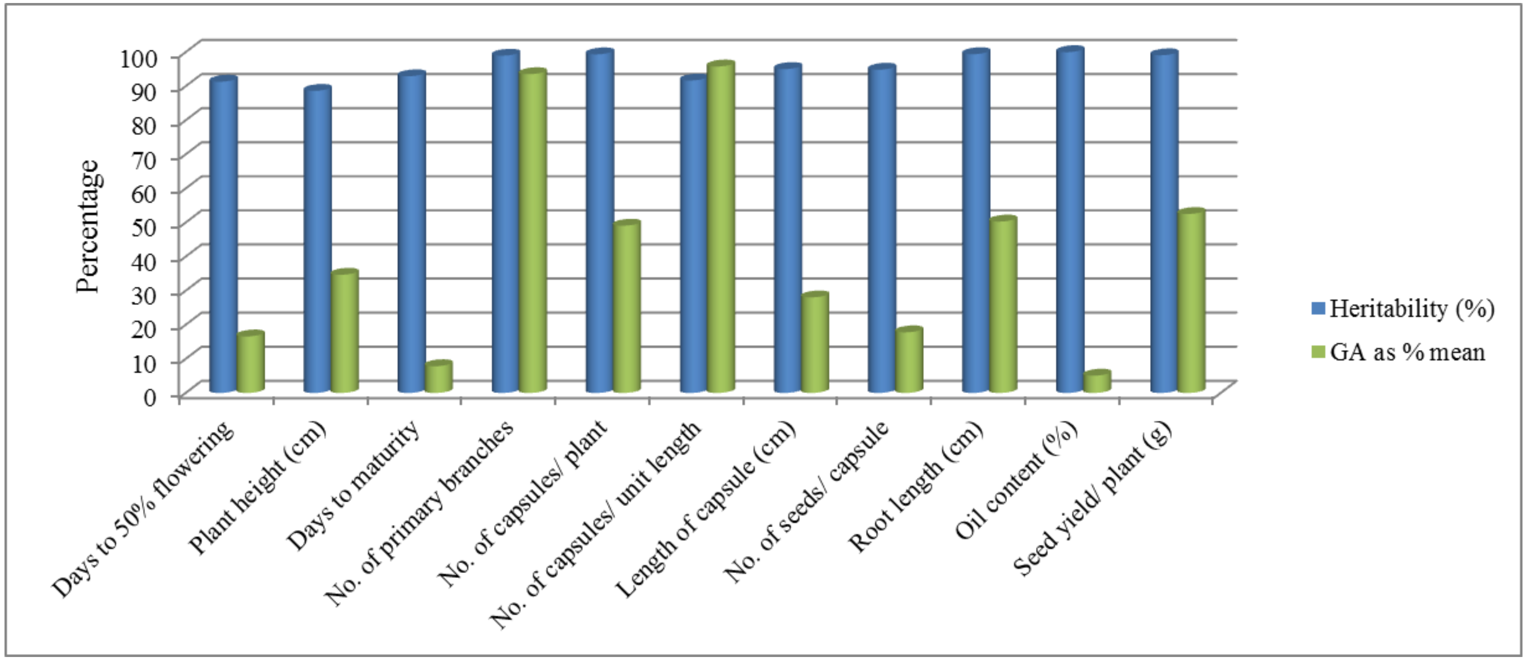


Fig. 3 Heritability (%) and Genetic advance (%) for various characters of sesame genotypes

GA: Genetic advance

4.4.4 Number of primary branches

A high PCV and GCV was noticed (45.87 per cent and 45.64 per cent, respectively) with high heritability (98.97 per cent) and higher genetic advance (93.54 per cent) for this trait.

4.4.5 Number of capsules per plant

The estimates of PCV (23.98 per cent) and GCV (23.90 per cent) were high. A high heritability (99.36 per cent) and a high genetic advance (49.08 per cent) were also recorded.

4.4.6 Number of capsules per unit length

Number of capsules per unit length showed high value for PCV (59.19 per cent) and GCV (56.68 per cent) along with high heritability estimates (91.69 per cent) and a higher genetic advance (95.80 per cent).

4.4.7 Length of capsule

A moderate PCV of 14.31 per cent and GCV of 13.95 per cent were recorded. The estimates of heritability and genetic advance (95.05 per cent and 28.06 per cent, respectively) were high for this character.

4.4.8 Number of seeds per capsule

A low PCV and GCV with 9.11 per cent and 8.88 per cent respectively were exhibited for number of seeds per capsule. The heritability estimates were higher (94.86 per cent) were as the genetic advance was moderate (17.80 per cent)

4.4.9 Root length

A comparatively higher PCV and GCV was noticed (24.55 per cent and 24.48 per cent, respectively) with high heritability (99.41 per cent) and a higher genetic advance as per cent of mean (50.29 per cent) for this character.

4.4.10 Oil content

The PCV and GCV estimates were low (2.46 per cent and 2.45 per cent, respectively). A high heritability of 100 per cent and low genetic advance as per cent of mean of 5.08 per cent was noticed for this trait.

4.4.11 1000-seed weight

Low PCV of 0.63 per cent and GCV of 0.62 per cent were recorded for 1000-seed weight. The heritability was high (100 per cent) with a low genetic advance (1.27 per cent). There was no significant difference among the accessions for 1000-seed weight.

4.4.12 Seed yield per plant

Greater variability was evident by a wide range for seed yield per plant. The estimates of PCV (25.74 per cent) and GCV (25.62 per cent) were high coupled with a higher estimate of heritability (99.09 per cent) and a high genetic advance as per cent of mean (52.51 per cent) for this trait.

4.5 Correlation analysis

The correlation coefficients were estimated for all possible combinations for twelve characters at phenotypic and genotypic levels and the results pertaining to character association is presented in Tables 6 and 7. In general, genotypic correlation coefficients were higher than phenotypic correlation coefficients for all characters.

Table 6. Phenotypic correlation among various characters of sesame

	DFF	PH	DM	NPB	NCP	LC	NSC	RL	OC	TSW	NCL	SYP
DFF	1.0000											
PH	-0.1100	1.0000										
DM	-0.0431	-0.0658	1.0000									
NPB	-0.2961*	-0.0066	0.1693	1.0000								
NCP	-0.0454	0.2263	0.3635**	0.3932**	1.0000							
LC	0.2090	0.1227	0.4259**	-0.1183	0.0863	1.0000						
NSC	0.2147	0.1317	0.4043**	-0.1707	0.0396	0.9693**	1.0000					
RL	0.1164	0.0229	-0.0334	-0.1892	0.1097	0.1404	0.2242	1.0000				
OC	0.1819	-0.1445	-0.0811	-0.2036	-0.2285	0.12	0.1565	0.2069	1.0000			
TSW	0.1016	-0.0906	-0.2348	0.0743	-0.3215**	-0.2196	-0.1817	-0.0535	0.0992	1.0000		
NCL	0.3526**	-0.2930*	0.0993	-0.6734**	0.0455	0.1306	0.1426	0.2536*	0.1845	-0.1775	1.0000	
SYP	0.0364	0.2566*	0.4675**	0.2932*	0.9385**	0.4050**	0.3730**	0.1795	-0.1357	-0.3355**	0.1013	1.0000

DFF – Days to first flowering

PH – Plant height (cm)

DM – Days to maturity

NPB – Number of primary branches / plant

NCP – Number of capsules/ plant

LC – Length of capsule (cm)

NSC – Number of seeds/ capsule

RL – Root length (cm)

OC – Oil content (%)

TSW – 1000 seed weight (g)

NCL – Number of capsules/ unit length

SYP – Seed yield/ plant (g)

* Significant at 5% level

** Significant at 1% level

Table 7. Genotypic correlation among various characters of sesame

	DFF	PH	DM	NPB	NCP	LC	NSC	RL	OC	TSW	NCL	SYP
DFF	1.0000											
PH	-0.1199	1.0000										
DM	-0.0331	-0.0478	1.0000									
NPB	-0.3086*	-0.0122	0.1760	1.0000								
NCP	-0.0482	0.2308	0.3809**	0.3953**	1.0000							
LC	0.2117	0.1329	0.4481**	-0.1191	0.0911	1.0000						
NSC	0.2258	0.1583	0.4208**	-0.1730	0.0444	0.9847**	1.0000					
RL	0.1239	0.0231	-0.0327	-0.1896	0.1109	0.1465	0.2310	1.0000				
OC	0.1899	-0.1529	-0.0838	-0.2048	-0.2293	0.1196	0.1613	0.2073	1.0000			
TSW	0.1061	-0.0958	-0.2436*	0.0741	-0.3220**	-0.2233	-0.1867	-0.0534	0.0985	1.0000		
NCL	0.3523**	-0.2855*	0.1052	-0.6837**	0.0499	0.1290	0.1414	0.2658*	0.1927	-0.1828	1.0000	
SYP	0.0357	0.2720*	0.4864**	0.2959*	0.9415**	0.4083**	0.3698**	0.1811	-0.1361	-0.3364**	0.1042	1.0000

DFF – Days to first flowering

PH – Plant height (cm)

DM – Days to maturity

NPB – Number of primary branches / plant

NCP – Number of capsules/ plant

LC – Length of capsule (cm)

NSC – Number of seeds/ capsule

RL – Root length (cm)

OC – Oil content (%)

TSW – 1000 seed weight (g)

NCL – Number of capsules/ unit length

SYP – Seed yield/ plant (g)

* Significant at 5% level

** Significant at 1% level

The results of correlation analysis are presented below.

4.5.1 Correlation between yield and other characters

Highly significant and positive phenotypic and genotypic correlation was recorded between yield and days to maturity (0.4675 and 0.4864), number of capsules per plant (0.9385 and 0.9415), length of capsule (0.4050 and 0.4083) and number of seeds per capsule (0.3730 and 0.3698).

Plant height (0.2566 and 0.2720) and number of primary branches per plant (0.2932 and 0.2959) was found to have significant positive phenotypic and genotypic correlation with yield. Thousand seed weight had highly significant and negative correlation with yield at phenotypic and genotypic levels (-0.3355 and -0.3364).

4.5.2 Correlation among the yield components

4.5.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering had highly significant positive correlation with number of capsules per unit length (0.3526 and 0.3523) and significant negative correlation with number of primary branches per plant (-0.2961 and -0.3086).

4.5.2.2 Plant height

Significant negative correlation was observed with number of capsules per unit length at both phenotypic (-0.2855) and genotypic (-0.2930) levels.

4.5.2.3 Days to maturity

The association of days to maturity at both phenotypic and genotypic level exhibited a highly significant positive correlation for number of capsules per plant (0.3635 and 0.3809), length of capsule (0.4259 and 0.4481) and number of seeds per capsule (0.4043 and 0.4208).

4.5.2.4 Number of primary branches

Highly significant positive correlation was recorded for number of primary branches with number of capsules per plant (0.3932 and 0.3953) while a highly significant negative correlation (-0.6734 and -0.6837) was noticed with number of capsules per unit length.

4.5.2.5 Number of capsules per plant

Number of capsules per plant showed highly significant positive correlation with seed yield (0.9415) but a significant negative correlation was associated with 1000 seed weight (-0.3215 and -0.3220).

4.5.2.6 Number of capsules per unit length

Number of capsules per unit length exhibited highly significant positive correlation with days to 50 per cent flowering (0.3256 and 0.3523) and significant positive correlation with root length (0.2536 and 0.2658). The correlation was significant and negative with number of primary branches per plant (-0.6734 and -0.6873 and plant height (-0.2930 and –0.2855).

4.5.2.7 Length of capsule

Length of capsule manifested a highly significant positive phenotypic (0.9693) and genotypic (0.9847) correlation with number of seeds per capsule.

4.5.2.8 Number of seeds per capsule

At both phenotypic and genotypic level, number of seeds per capsule had highly significant positive correlation with days to maturity (0.4043 and 0.4208) and length of capsule (0.9693 and 0.9847).

4.5.2.9 Root length

Root length was significantly and positively correlated with number of capsules per unit length (0.2536 and 0.2658).

4.5.2.10 Oil content

The phenotypic and genotypic correlation coefficients of oil content with all other characters were non-significant.

4.5.2.11 1000-seed weight

Highly significant negative correlation with number of capsules per plant (-0.3215 and -0.3220) was recorded for 1000-seed weight.

4.6 Path coefficient analysis

The genotypic correlation coefficients of seed yield per plant with yield contributing characters were partitioned into different components to find the direct and indirect contribution of each character to yield (Table 8 and Fig. 4). The characters viz., plant height, days to maturity, number of primary branches per plant, number of capsules per plant, length of capsule, number of seeds per capsule and oil content which manifested high genotypic correlation with yield were selected for path analysis.

4.6.1 Direct effects

Number of capsules per plant (0.9343) recorded the highest positive direct effect with seed yield per plant. Number of seeds per capsule (0.2526), length of capsule (0.0681), oil content (0.0277) and plant height (0.0114) also had positive direct effect on yield. Number of primary branches per plant (-0.0157) expressed negative direct effect on seed yield per plant.

Table 8. Direct and indirect effect of yield component characters on seed yield

Character	Plant height	Days to maturity	No. of primary branches	No. of capsules/ plant	Length of capsule	No. of seeds/ capsule	Oil content	Genotypic correlation
Plant height	**0.0114**	0.0001	0.0002	0.2156	0.0090	0.0400	-0.0042	0.2720
Days to maturity	-0.0005	**-0.0006**	-0.0028	0.3559	0.0305	0.1063	-0.0023	0.4864
No. of primary branches	-0.0001	-0.0001	**-0.0157**	0.3693	-0.0081	-0.0437	-0.0057	0.2959
No. of capsules/ plant	0.0026	-0.0002	-0.0062	**0.9343**	0.0062	0.0112	-0.0064	0.9415
Length of capsule	0.0015	-0.0003	0.0019	0.0851	**0.0681**	0.2487	0.0033	0.4083
No. of seeds/ capsule	0.0018	-0.0003	0.0027	0.0415	0.0670	**0.2526**	0.0045	0.3698
Oil content	-0.0017	0.0001	0.0032	-0.2142	0.0081	0.0407	**0.0277**	-0.1361

Residual effect = 0.0695

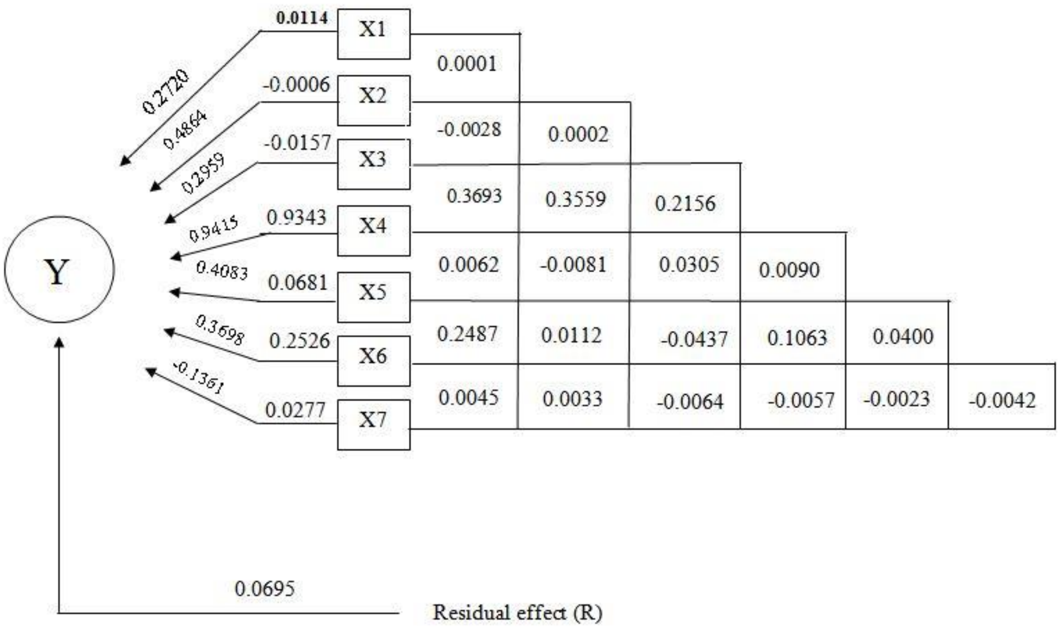


Fig. 4. Path diagram

Y: Seed yield per plant

X1: Plant height

X2: Days to maturity

X3: No. of primary branches

X4: No. of capsules per plant

X5: Length of capsule

X6: No. of seeds per capsule

X7: Oil content

4.6.2 Indirect effects

Plant height registered positive indirect effects mainly through number of capsules per plant (0.2156). Days to maturity exerted positive indirect effect through number of capsules per plant (0.3559). Number of primary branches per plant had positive indirect effect through number of capsules per plant (0.3693). Number of capsules per plant showed positive indirect effect through number of seeds per capsule (0.0112).

Length of capsule exhibited positive indirect effect through number of seeds per capsule (0.2487). Number of seeds per capsule presented positive indirect effect through length of capsule (0.0670). Oil content recorded positive indirect effect through number of seeds per capsule (0.0407).

The residual effect (R = 0.0695) indicates that the selected characters explain the total correlation well and the remaining characters have only minor contribution in the variability of seed yield.

4.7 Genetic divergence analysis

Following Mahalanobis statistics, the thirty three genotypes of sesame were subjected to D^2 analysis to identify the degree of divergence in biological population at genetic level. The present investigation was conducted for assessing the genetic diversity of thirty three sesame genotypes. The results of the analysis are presented below.

4.7.1 Contribution of each character towards total divergence

The relative contribution of different characters to genetic divergence is shown in Table 9 and depicted in Figure 5. The maximum contribution towards total divergence was attributed to root length (46.02 per cent) followed by number of

Table 9. Proportion of yield and yield contributing characters towards total divergence in sesame genotypes

Sl. No:	Character	Per cent contribution
1.	Days to 50% flowering	0.38
2.	Days to maturity	0.57
3.	Number of primary branches/plant	19.51
4.	Number of capsules/plant	29.17
5.	Length of capsule (cm)	2.84
6.	Root length (cm)	46.02
7.	Number of capsules/unit length	1.52

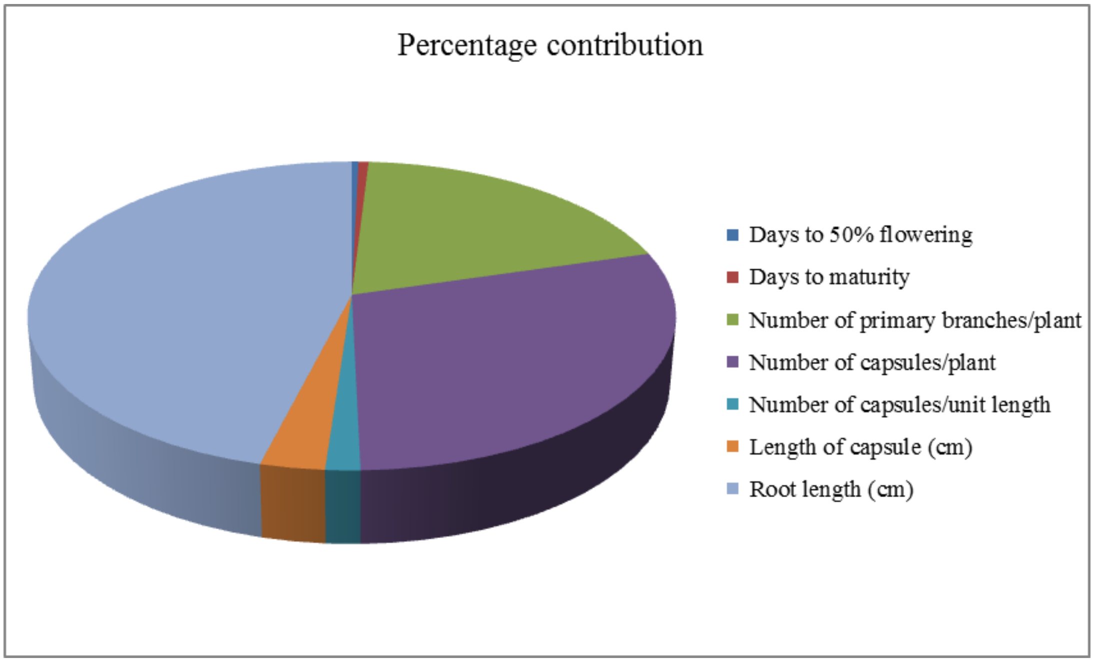


Fig. 5. Proportion of yield and yield contributing characters towards total divergence in sesame genotypes

capsules per plant (29.17 per cent) and number of primary branches per plant (19.51 per cent).

4.7.2 Group constellation: intra and intercluster D^2

The relative distance (D^2 values) of genotypes from each other was used to group the thirty three genotypes into six clusters following the method suggested by Tocher (Rao, 1952). The cluster composition of genotypes and the clustering pattern are presented in Table 10 and Fig 6. Cluster I was the largest with thirteen genotypes followed by Cluster II and Cluster III with ten and seven genotypes, respectively. Clusters IV, V and VI had only one genotype each.

The average intra and intercluster distances were estimated based on the total D^2 values (Table 11 and Fig 7). The intracluster distances varied from 140.34 to 211.46 whereas the intercluster distances ranged from 227.35 to 1973.78. The maximum intracluster distance was observed in Cluster III (211.46) and the minimum for solitary clusters IV, V and VI (0.00). The maximum intercluster distance was noticed between Clusters IV and VI (1973.78) while the closer proximity existed between Clusters V and VI (227.35).

For Cluster I, the maximum divergence distance was with cluster VI (1271.48) and minimum with Cluster IV (320.50). Intracluster D^2 value of Cluster I was 158.41. Cluster II had ten genotypes with an intracluster distance of 140.34. Maximum intercluster distance was recorded with Cluster IV (953.91) and minimum with Cluster V (356.60). The highest divergence of Cluster III was recorded with Cluster VI (967.94) and lowest with Cluster IV (349.65) with an intracluster distance of 211.46.

The Clusters IV, V and VI with single genotypes each recorded maximum and minimum values of 1973.78 (with Cluster VI) and 320.50 (with Cluster I); 1189.81

Table 10. Clustering pattern of sesame genotypes

Clusters	Number of genotypes	Accessions
I	13	SI 6, SI 14, SI 24, SI 22, SI 9, SI 27, SI 26, SI 32, SI 10, SI 4, SI 17, SI 23 and SI 5
II	10	SI 2, SI 8, SI 21, SI 29, SI 1, SI 18,SI 28, SI 7, SI 3 and SI 20
III	7	SI 30, SI 33, SI 25, SI 11, SI 19, SI 16 and SI 15
IV	1	SI 31
V	1	SI 13
VI	1	SI 12

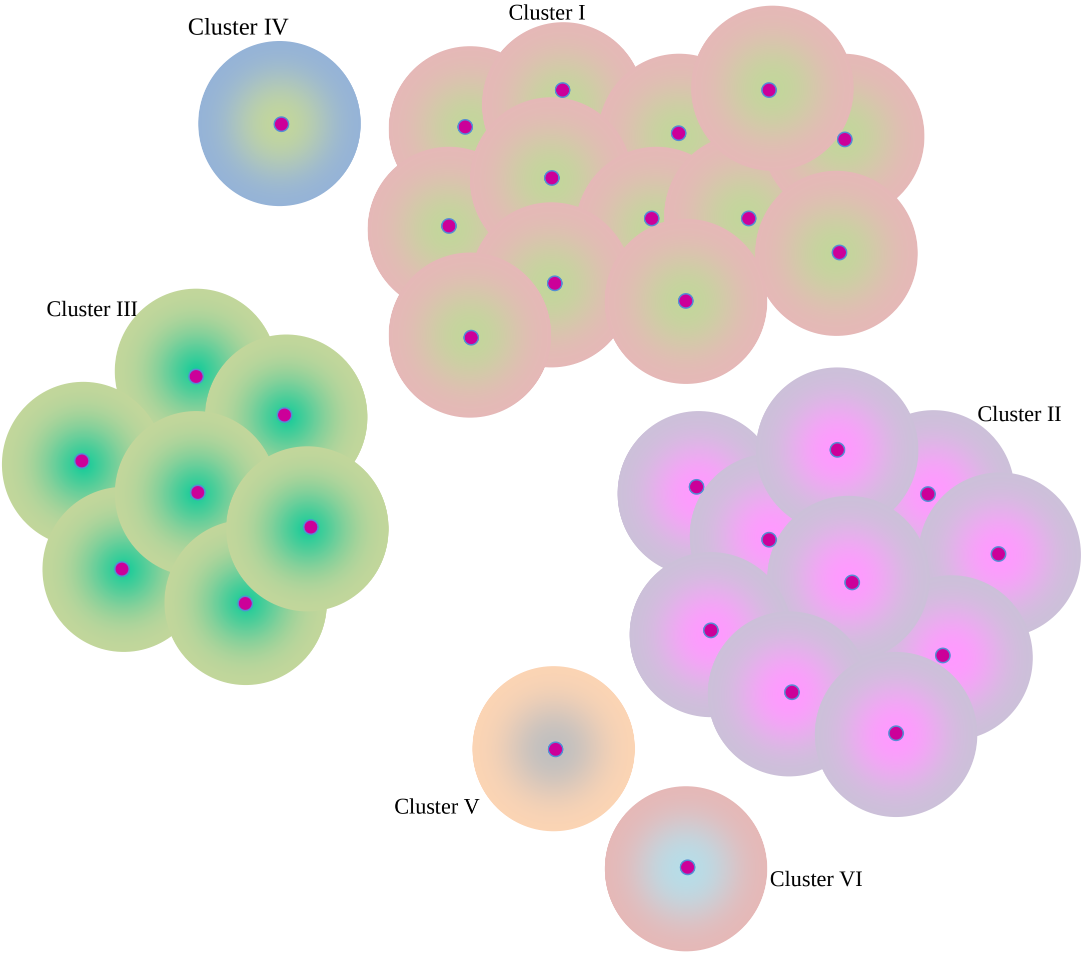


Fig. 6. Clustering pattern of sesame genotypes

Table 11. Average intra and intercluster distances for the six clusters

Clusters	I	II	III	IV	V	VI
I	**158.41**	389.34	365.54	320.50	762.77	1271.48
II	389.34	**140.34**	536.10	953.91	356.60	512.61
III	365.54	536.10	**211.46**	349.65	476.61	967.94
IV	320.50	953.91	349.65	**0.00**	1189.81	1973.78
V	762.77	356.60	476.61	1189.81	**0.00**	227.35
VI	1271.48	512.61	967.94	1973.78	227.35	**0.00**

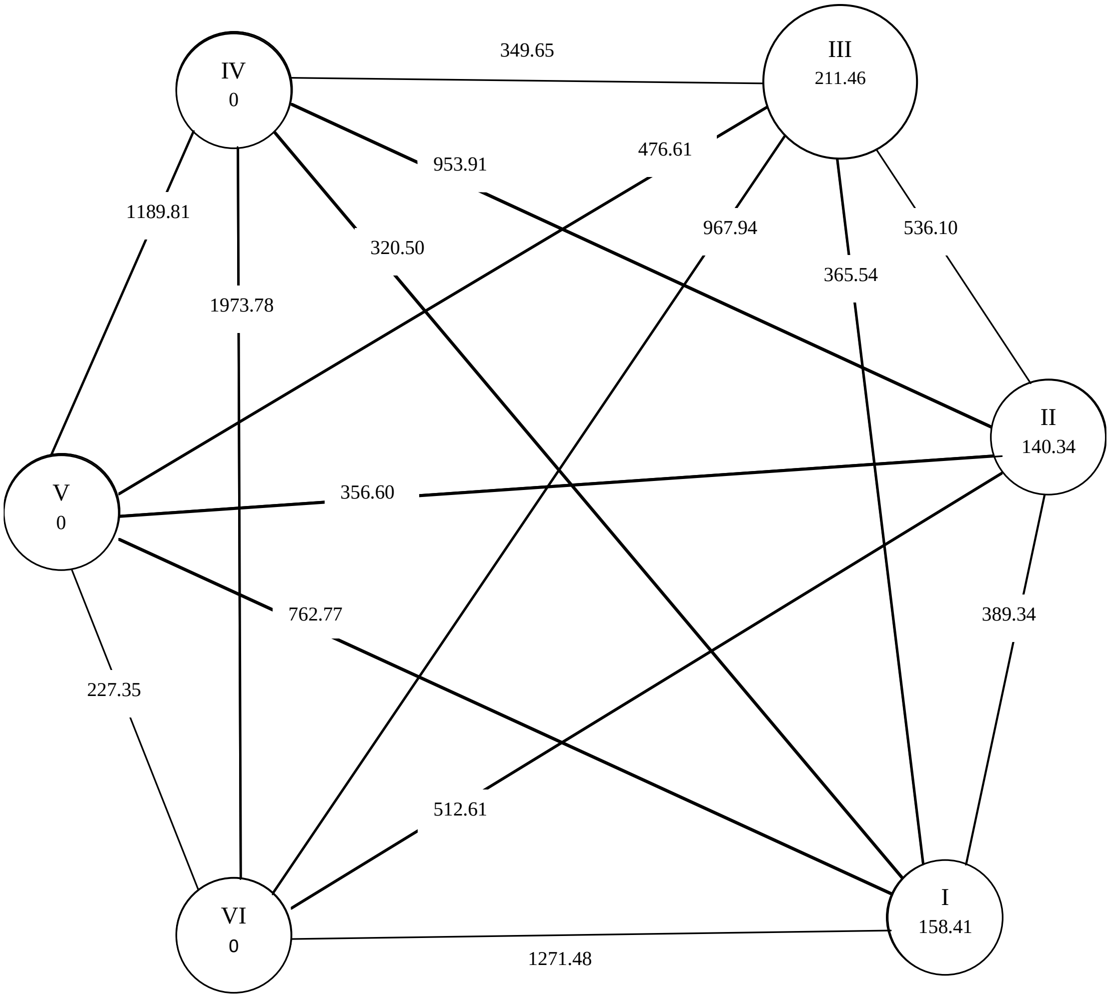


Fig. 7. Average intra and intercluster distances among the six clusters

(A)

(with Cluster IV) and 356.60 (with Cluster II); 1973.78 (with Cluster IV) and 227.35 (with Cluster V), respectively.

4.7.3 Cluster means

The cluster means obtained for the ten characters in each cluster are presented in Table 12. Cluster II showed the highest cluster mean for length of capsule (1.87), number of seeds per capsule (49.66), root length (10.38) and number of capsules per unit length (0.23). The maximum value of cluster mean for plant height (45.00), number of primary branches per plant (6.00) and number of capsules per plant (29.67) was recorded in Cluster V. The highest cluster mean for days to maturity (118.33) and seed yield per plant (4.43) was manifested in Cluster VI. Cluster IV exhibited the highest cluster mean for days to 50 per cent flowering (34.33).

Days to 50 per cent flowering had lowest mean in Cluster V (27.67) and highest in Cluster IV (34.33). In general, Cluster V had tall plants (45.00) and Cluster III had short plants (35.38). Days to maturity ranged from 105.33 (Cluster IV) to 118.33 (Cluster VI). Cluster V had plants with more primary branches (6.00) while plants in Cluster IV had fewer primary branches (2.00). Highest number of capsules per plant was recorded by Cluster V (29.67) and the lowest was recorded by Cluster IV (12.33). On an average, Cluster II had longer capsules (1.87) while Cluster V had smaller capsules (1.43). Among the clusters, number of seeds per capsule varied from 49.60 (Cluster II) to 42.60 (Cluster V). Root length ranged from 10.38 (Cluster II) to 5.77 (Cluster IV). Highest seed yield was recorded by Cluster VI (4.43) and lowest by Cluster IV (1.71). Cluster means for number of capsules per unit length recorded maximum in Cluster II (0.23) and minimum in Cluster V (0.09).

4.8 Selection index

Discriminant function technique was adopted for the construction of selection index for yield using seed yield per plant and the component characters *viz*. days to

Table 12. Cluster means for various characters

Character	Clusters					
	I	II	III	IV	V	VI
Days to 50% flowering	31.00	31.50	29.76	34.33	27.67	27.67
Plant height (cm)	36.10	35.60	35.38	37.00	45.00	38.33
Days to maturity	107.97	110.37	108.57	105.33	106.00	118.33
Number of primary branches/ plant	2.05	3.27	4.00	2.00	6.00	6.00
Number of capsules/plant	15.00	20.90	17.48	12.33	23.33	29.67
Length of capsule (cm)	1.78	1.87	1.67	1.47	1.43	1.80
Number of seeds/capsule	48.46	49.60	45.52	43.33	42.67	47.33
Root length (cm)	9.14	10.38	6.14	5.77	8.37	8.23
Seed yield/plant (g)	2.29	3.27	2.49	1.71	3.15	4.43
Number of capsules/unit length	0.23	0.23	0.14	0.17	0.09	0.13

50 per cent flowering, plant height, days to maturity, number of primary branches per plant, number of capsules per plant, number of seeds per capsule, length of capsule, root length, seed yield per plant and number of capsules per unit length. The index value for each genotype was determined and the genotypes were ranked accordingly.

The selection indices are presented in Table 13 according to the rank of each genotype. The highest index value (225.66) was recorded by the genotype *SI* 7 (RT-351 from ORARS, Kayamkulam) followed by *SI* 12 (DS-5 from Dharwad) (217.52). These genotypes were identified to be genotypically superior in terms of plant height, number of seeds per capsule and seed yield per plant.

Table 13. Selection indices of the sesame genotypes arranged in descending order

Rank	Accession No	**Genotypes**	**Selection index**
1.	*SI* 7	RT - 351	225.659
2.	*SI* 12	DS - 5	217.520
3.	*SI* 29	IVTS 12-5	214.414
4.	*SI* 20	Nirmala	210.073
5.	*SI* 8	VRI - 2	207.725
6.	*SI* 9	AKT - 101	207.337
7.	*SI* 27	SSD - 22	205.999
8.	*SI* 4	TKG - 306	200.792
9.	*SI* 1	Prachi	198.938
10.	*SI* 3	Brijeshwari	198.787
11.	*SI* 30	MT 10-13-1	197.658
12.	*SI* 28	MT 10-27-1	197.570
13.	*SI* 18	AKT - 64	196.547
14.	*SI* 11	DSS - 9	195.615
15.	*SI* 13	DS (1) - C	195.420
16.	*SI* 33	Palakkad local	193.945
17.	*SI* 21	AVTS 12-7	193.552
18.	*SI* 17	Thilathara	193.315
19.	*SI* 2	TKG - 22	191.072
20.	*SI* 24	MT 10-8-1	190.475
21.	*SI* 25	TKG 421-1	189.984
22.	*SI* 5	RT - 54	189.5550
23.	*SI* 32	SSD - 1	188.256
24.	*SI* 26	TKG - 22	186.256
25.	*SI* 6	Smarak	184.773
26.	*SI* 14	Kayamkulam 1	183.311
27.	*SI* 10	GT - 10	182.941
28.	*SI* 16	Thilak	180.051
29.	*SI* 19	RT - 354	179.099
30.	*SI* 31	IVTS 12-7	178.645
31.	*SI* 23	OSC - 79	176.741
32.	*SI* 22	OSC -560	176.555
33.	*SI* 15	Surya	170.374

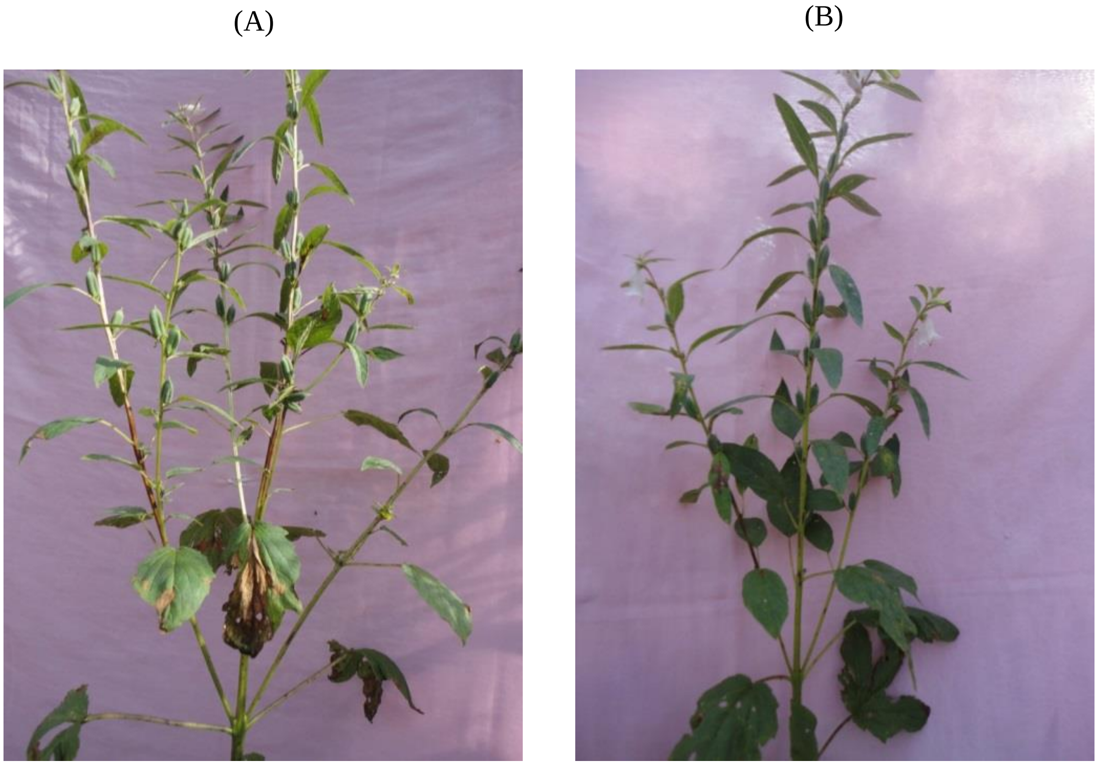


Plate 4. Superior genotypes (A) RT – 351 (B) DS – 5

Discussion

5. DISCUSSION

Evolution and domestication created improved plant species that are important for human survival. Selection plays a vital role in crop improvement. The improvement of any crop depends on the available variability, heritability of the character, genetic advance under selection and the association among the characters.

Sesame is an essentially self-pollinated annual oil seed crop of the warm tropics. There exists great diversity among the sesame genotypes with respect to various traits. Higher seed yield in sesame is a major goal of the plant breeders and several works have been done to increase the seed yield by many scientists. The importance and genetic control of different yield components namely number of primary branches per plant, number of capsules per plant, capsule length *etc.* have been stressed by many breeders for yield increase.

The present study was envisaged to evaluate different cultivars of sesame to estimate the variability, to analyze the association between various economic traits, to find the direct and indirect effect of different characters on yield, to study the genetic divergence and to identify sesame genotypes for shaded upland conditions. The results of the experiment conducted are discussed here.

5.1 Weather and crop growth

Crop growth is mainly dependent on the environmental factors. Fluctuations in weather conditions greatly influence the growth, development and thereby yielding ability of the crop. The rainfall was well distributed during the crop growth period as a result the crops did not suffer from moisture stress throughout the crop cycle. Since the temperature recorded during the experimental period is in the required optimum range, it helped in good vegetative and reproductive stage growth.

5.2 Variability studies

Analysis of variance revealed significant differences for all the characters studied except 1000-seed weight, indicating the presence of substantial amount of variability and selection could be effective for improvement of those characters. Similar results have also been reported by John and Nair (1993), Solanki and Gupta (2001), Valarmathi *et al.,* (2004) and Raghuwanshi (2005).

Wide range of variability was shown by plant height, number of branches per plant, number of capsules per plant and seed yield per plant, which has been reported by Banerjee and Kole (2006), Parameswarappa *et al.* (2009) and Mandal *et al.* (2010).

Coefficients of variation (GCV and PCV) are better indices of comparison of characters with different units of measurements. The GCV provides a valid basis for comparing and assessing the range of genetic variability for quantitative characters and PCV measures the extent of total variation. Even though phenotypic coefficient variation (PCV) was found to be higher than genotypic coefficient of variation (GCV) for all the characters, only a slight difference was observed between PCV and GCV for the characters days to 50 per cent flowering, days to maturity, number of primary branches, number of capsules per plant, root length, oil content, 1000-seed weight and seed yield per plant, indicating that these characters were less affected by environment and selection could be effective for further improvement of these traits. This similarity between PCV and GCV was reported earlier by Joel and Thangavelu (1997) and Krishnaiah *et al.* (2002).

High GCV was shown by characters number of capsules per unit length, number of primary branches, seed yield per plant, root length and number of capsules per plant, clearly indicating that selection will be rewarding. These results are in agreement with those of Solanki and Gupta (2001) and Valarmathi *et al.,* (2004). Mohan (2011), Jadhav and Mohrir (2012) and Gidey *et al*. (2013) also reported high GCV for number of primary branches per plant.

The estimates of PCV and GCV were high for the characters number of primary branches per plant, number of capsules per plant and seed yield per plant. Banerjee and Kole (2006), Parameswarappa *et al*. (2009), Mandal *et al*. (2010) and Gayathri (2011) reported similar results.

Moderate PCV and GCV were recorded for plant height and number of capsules per plant. This result is in confirmation with that of Sudhakar *et al.* (2007).

Low estimates of GCV for days to 50 per cent flowering, days to maturity, number of seeds per capsule, oil content and 1000-seed weight indicated limited scope for improvement of these characters through selection due to low magnitude of heritable variation. Shadakshari *et al.* (1995) and Thangavel *et al.* (2000) published comparable results on estimates of GCV and PCV.

The genotypes exhibited significant variation for oil content. The highest oil content noticed was 50.16 per cent and the lowest was 45.52 per cent with a mean of 48.59 per cent. Similar results were earlier reported by Shadakshri *et al.* (1995).

5.2 Heritability and genetic advance

Magnitude of heritability indicates the effectiveness with which selection of genotypes can be made based on phenotypic performance. High value of heritability indicates that phenotype of the trait strongly reflects the genotype and suggests the major role of genotypic constitution in the expression of the character. Such traits are considered dependable from breeding point of view.

In the present investigation high heritability was observed for all the characters studied. This is in agreement with the findings of Patil and Sheriff (1996) and Solanki and Gupta (2001).

High heritability combined with high genetic advance (as per cent of mean) was observed for number of capsules per unit length, seed yield per plant, number of primary branches, plant height, root length and number of capsules per plant. The result showed that these characters were controlled by additive gene effects and phenotypic selection for these characters is likely to be effective. Similar results were reported by Reddy *et al.* (2001), Krishnaiah *et al.* (2002), Ganesan (2005) and Sumathi *et al*. (2009).

The improvement of the characters days to fifty per cent flowering and number of seeds per capsule is also possible since these characters had high heritability and moderate genetic advance as per cent of mean. Reports of Shajan (2002) Banerjee and Kole (2006) and Salah *et al.* (2013) support this outcome.

Days to maturity, 1000-seed weight and oil content showed high heritability with low genetic advance. These results are in conformity with the findings of Reddy *et al.* (2001), Saravanan *et al.* (2003), Babu *et al.* (2005) and Sudhakar *et al.*, 2007.

5.3 Correlation studies

Yield is a complex quantitative trait, greatly influenced by environmental fluctuations. Hence, selection based on yield performance alone may give a biased result and leads to ambiguity. A study of the nature and degree of association of component characters with yield assumes greater importance for fixing up characters that play a decisive role in influencing yield. Selection would, therefore, be more effective, if it is based on component characters rather than directly on yield. Correlation coefficient analysis measures the mutual relationship between various characters and is used to determine the component character on which selection can be done for improvement in yield.

In the present study significant and positive phenotypic and genotypic correlation was recorded between seed yield and days to maturity, number of capsules per plant, length of capsule, plant height, number of primary branches per plant and number of seeds per capsule. The earlier reports of positive association of yield with these traits by Tak (1997), Sankar and Kumar (2003), Babu *et al.* (2004), Gnanasekaran *et al.* (2008), Sumathi *et al.* (2009) and Mohan (2011) corroborate the present findings.

1000-seed weight showed significantly negative association with seed yield per plant. Similar results were reported by Pawar *et al.* (2002), Ramireddy and Sundaram (2002) and Sankar and Kumar (2003).

Days to maturity showed significantly positive correlation with number of capsules per plant, length of capsule and number of seeds per capsule. Earlier reports of Ramireddy and Sundaram (2002) and Sankar and Kumar (2003) supported this positive association.

Positive and significant phenotypic and genotypic correlation was recorded between yield and days to maturity, number of capsules per plant, length of capsule and number of seeds per capsule. Similar results were recorded by Das *et al*. (2010), Sarwar and Hussain (2010) and Gayathri (2011) for number of capsules per plant.

Thousand seed weight had highly significant and negative correlation with yield at phenotypic and genotypic levels. The reports of Rong and Wu (1989), Begum and Dasgupta (2003) and Parimala and Mathur (2006) are in agreement with this result.

5.4 Path analysis

As with other crops, seed yield is a complex trait in sesame. Path coefficient analysis can provide a more realistic picture of relationships between these traits, as it takes into consideration direct as well as indirect effects of the different yield components. Determination of interrelationships between and among yield components and seed yield helps a plant breeder to easily identify selected traits that make the most significant contribution to yield.

In this study, a path coefficient analysis was used to separate the genotypic correlation coefficients of seed yield per plant with plant height, days to maturity, number of capsules per plant, number of primary branches per plant, number of seeds per capsule and oil content into direct and indirect effects. The path analysis revealed that seed yield per plant was positively and directly affected by the number of capsules per plant followed by number of seeds per capsule. All these had positive genotypic correlations with seed yield. The greater influence of these traits reflects their importance as seed yield components. Similar results were reported by Tomar *et al.* (1999), Mothilal (2005). Ganesh and Sakila (1999), Shajan (2002) and Kurdistani *et al.* (2011) reported that number of capsules per plant had the highest positive direct effect on seed yield which is in conformity with the present observation.

Plant height, number of capsules per plant, length of capsule, number of seeds per capsule and oil content showed positive direct effect on yield similar to the earlier report by Vidhyavati *et al.* (2005) and Mohan (2011). The direct negative effect of days to maturity and number of primary branches per plant were in analogous to the reports of Siddiqui *et al.* (2005).

The indirect effect of number of capsules per plant on seed yield through plant height, days to maturity, number of primary branches, length of capsule and number of seeds per capsule. Sumathi *et al.* (2007) and Georgiev *et al.* (2012) confirmed equivalent outcomes for plant height, days to maturity and number of primary branches and Gnanasekaran *et al.* (2008) for number of primary branches.

Path analysis revealed that number of capsules per plant recorded the highest positive direct effect with seed yield per plant followed by number of seeds per capsule and plant height. However, number of primary branches per plant and days to maturity expressed negative direct effect. Similar reports have been given by Manjunatha *et al.* (2008), Parameswarappa *et al.* (2009) and Gayathri (2011).

Based on the correlation and path coefficient analysis number of capsules per plant, length of capsule and number of seeds per capsule can be identified as the major characters contributing towards seed yield and selection based on these characters can be effective for developing high yielding varieties of sesame.

5.5 Genetic divergence

Genetic improvement primarily depends upon the amount of genetic variability present in a population. Information on genetic divergence among the different genotypes is important as the crosses between genetically divergent parents produce high heterosis and broad spectrum of variability in segregating populations. D^2 statistics is one of the potent techniques of measuring genetic divergence (Mahalanobis, 1936). This technique measures the force of differentiation at intra and intercluster levels and provides a rational basis for selection of genetically divergent parents in breeding programmes.

5.5.1 Clustering

D^2 statistics employing a combined classificatory approach revealed that the thirty three genotypes studied could be grouped into six clusters. The distribution pattern of genotypes in different clusters indicated that genetic divergence was not related to geographical differentiation.

The intercluster distances were greater in magnitude than the intracluster distances, indicating the presence of diversity among the clusters and that the genotypes included in the same cluster are less divergent than those in different clusters. Crosses are suggested between genotypes of the divergent clusters to generate heterosis and wide range of segregants. Similar results were reported by Bandila *et al*. (2011).

The Cluster II showed the highest cluster mean for length of capsule, number of seeds per capsule, root length and number of capsules per unit length. Varieties in a cluster with high order of divergence among themselves would be the best breeding material for achieving maximum genetic advance with regard to yield. It has been well established by researchers like Roy and Panwar (1993), Gayathri (2011) and Gidey *et al*. (2012).

5.6 Selection index

Selection index is calculated considering the yield related traits and is more efficient in identifying superior genotypes. Selection based on indices permits maximizing the response to selection for one or a group of traits. In reality, selection based on indices reflects the response with direct selection and the correlated response, as selection is practiced simultaneously for other traits also. Application of selection index enables more efficient selection for yield improvement than straight selection for yield alone.

Selection index for yield was constructed using seed yield per plant and the component characters days to 50 per cent flowering, plant height, days to maturity, number of primary branches per plant, number of capsules per plant, number of capsules per unit length, number of seeds per capsule, length of capsule and root length. The genotype *SI* 7 was having the maximum index score and it is identified to be the best genotype for the shaded uplands. The good criteria for selection in sesame for yield was identified to be based on number of days to flowering, plant height, number of branches, number of capsules per plant and number of seeds per capsule by several earlier workers like Krishnamurthy *et al.* (1964), Chaudhary *et al.* (1977), Lee and Chang (1986) and Chopade *et al.* (1998).

Future line of work

The present programme was conducted only for one season. Hence confirmation of these studies for more seasons and locations has to be done to arrive at more valid on conclusions.

At present there is no variety specifically for upland or shaded situations. Hence the cultivars identified by the selection index and cluster analysis may be utilized in hybridization programmes to evolve varieties or hybrids suitable for upland shaded conditions.

Summary

6. SUMMARY

Evaluation of sesame (*Sesamum indicum* L.) genotypes suitable for shaded uplands of southern Kerala was conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2012-2013.The germplasm was evaluated for morphological traits and yield attributes, genetic variability, degree and direction of association, direct and indirect effects of various components on yield and genetic divergence analysis

The sesame germplasm consisting of thirty three accessions collected from different parts of Kerala, Karnataka and Maharashtra were assessed for the extent of variability, heritability and genetic advance. The relationship among the yield and associated traits was also worked out. The population was analyzed for the degree and direction of association between various economic traits and the direct and indirect effects of various components on yield. Analysis of genetic divergence of the genotypes to identify the degree of divergence in the population at genetic level was also carried out.

The salient results of the investigation are summarized below:

- Analysis of variance revealed significant differences among the thirty three genotypes for all the characters studied except 1000-seed weight.
- The assessed germplasm contained sufficient variability and offered scope for selection based on characters like plant height, number of primary branches, number of capsules per plant, number of capsules per unit length, length of capsule, root length and seed yield per plant.
- The genotypic variance made up the major portion of phenotypic variance for all the characters studied. High values of phenotypic coefficient of variation with correspondingly high values of genotypic coefficient of variation were observed in the present study for number of primary branches, number of capsules per plant, number of capsules per unit

length, root length and seed yield per plant whereas moderate values for both PCV and GCV were recorded for plant height and length of capsule.

- High PCV and GCV indicated the presence of high degree of genetic variation and ample scope for improvement of these characters through selection. Narrow difference between GCV and PCV suggests that environmental influence is minimal for the traits studied.
- The heritability estimates were high for all the twelve characters. High estimates of heritability coupled with high genetic advance as per cent mean was recorded for plant height, number of primary branches, number of capsules per plant, number of capsules per unit length, length of capsule, root length and seed yield per plant suggesting additive gene action for these traits and hence simple and early selection will be effective.
- In the character association studies, yield had positive and significant association with plant height, days to maturity, number of primary branches, number of capsules per plant, length of capsule and number of seeds per capsule indicating that selection for these characters may improve yield.
- The inter correlations suggested that selection for length of capsule and days to maturity would improve yield by their direct influence and also their indirect influence through number of seeds per capsule.
- Path coefficient analysis revealed number of capsules per plant as the character with high direct effect and number of primary branches, days to maturity and number of seeds per capsule as the characters with high indirect effect. Selection based on these characters would be effective for developing high yielding varieties of sesame.
- Genetic divergence analysis showed appreciable divergence among the thirty three genotypes of sesame. The clustering pattern indicated that

Cluster I had the maximum number of genotypes (thirteen) followed by vCluster II and III with ten and seven genotypes respectively. Clusters IV, V and VI were had one genotype each. The maximum divergence was noticed between Clusters IV and VI (1973.78) while the closer proximity existed between Clusters V and VI (227.35).

- The cluster mean values obtained suggest that highest cluster mean for seed yield per plant was manifested in Cluster VI having the single variety *SI* 12. Cluster II showed the highest cluster mean for length of capsule, number of seeds per capsule, root length and number of capsules per unit length and included the high yielding genotypes *SI* 7. The characters such as number of primary branches, number of capsules per plant and root length contributed maximum towards total divergence.
- Selection index was constructed based on ten characters studied and the genotypes were ranked. The genotype *SI* 7 (RT – 351 from Kayamkulam) from cluster II recorded the highest index value followed by *SI* 12 from cluster VI (DS – 5 from Dharwad) which was comparable with the state average yield of sesame (582 kg/ha). As yield and other yield contributing traits are high for these genotypes under shaded conditions they may utilized in crossing programs to get effective hybrids/recombinants suitable for intercropping in shaded uplands.

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* original not seen

Abstract

ABSTRACT

The present investigation on ‘Evaluation of sesame (*Sesamum indicum* L.) genotypes to the shaded uplands of Southern region’, with an objective to identify sesame genotypes suitable for shaded uplands, was conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2011-2013. The germplasm was evaluated for morphological traits and yield attributes, genetic variability, degree and direction of association, direct and indirect effects of various components on yield and genetic divergence analysis.

The sesame germplasm consisting of thirty three accessions collected from different parts of Kerala, Karnataka and Maharashtra were assessed for the extent of variability, heritability and genetic advance, the relationship among the yield and associated traits, the direct and indirect effects of characters towards yield and divergence of different genotypes.Analysis of variance showed significant differences among the genotypes for almost all the characters studied. High and moderate phenotypic and genotypic coefficients of variation (PCV and GCV) were noticed for most of the yield contributing characters. Highest and lowest PCV and GCV were recorded for number of capsules per unit length and 1000-seed weight respectively.

High estimates of heritability coupled with high to moderate genetic advance as per cent over mean was recorded for all the yield associated traits except for days to maturity, oil content and 1000-seed weight, which exhibited high heritability with low genetic advance indicating non-additive gene action.

Yield had positive and significant association with the yield contributing characters such as plant height, number of primary branches, number of capsules per plant, length of capsule and number of seeds per capsule, signifying that selection based on these characters may improve yield. The highest genotypic and phenotypic correlation with yield was observed for number of capsules per plant.

Path analysis revealed that number of capsules per plant had the highest positive direct effect on seed yield per plant followed by number of seeds per capsule. Number of primary branches per plant and days to maturity had the maximum positive indirect effect on seed yield per plant through number of capsules per plant.

The thirty three genotypes were grouped into six clusters among which cluster IV, V and VI had only one genotype each. Maximum number of genotypes were grouped in cluster I with thirteen genotypes. The intercluster distance was maximum between clusters IV and VI whereas it was minimum between clusters V and VI.

The selection indices were worked out for thirty three genotypes based on yield and yield attributing characters. Based on the ranks obtained, the genotypes SI 7 (RT - 351 from ORARS, Kayamkulam) and SI 12 (DS - 5 from Dharwad) were the superior genotypes identified which are suitable for the shaded uplands. These genotypes possessed maximum number of capsules per plant, length of capsule and number of seeds per capsule and seed yield.