DEVELOPMENT OF SUPERIOR VARIETIES IN WHITE SEEDED SESAME FOR SEED YIELD AND OIL CONTENT

by

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THESIS

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DECLARATION

I, hereby declare that this thesis entitled **"DEVELOPMENT OF SUPERIOR VARIETIES IN WHITE SEEDED SESAME FOR SEED YIELD AND OIL CONTENT"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title of any other University or Society.

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LIST OF ABBREVIATIONS

^{o}C	Degree Celsius
et al	And others
cm	Centimetre
cm^2	Square centimeters
CD	Critical Difference
d.f.	Degrees of freedom
Fig.	Figure
GA	Genetic advance
GAM	Genetic advance as per cent of mean
g	Gram
GCV	Genotypic coefficient of variation
KAU	Kerala Agricultural University
viz.	Namely
No	Number
%	Per cent
PCV	Phenotypic coefficient of variation
Sl.	Serial
SE	Standard Error
i.e.	That is
via	Through
AN	After Noon
FN	Fore Noon
R.H.	Relative Humidity
Temp.	Temperature
RBD	Randomised Block Design
%	Per cent
F$_1$	First filial generation
F$_2$	Second filial generation
F$_3$	Third filial generation

LxT	Line x Tester
Plant^{-1}	Per plant
Capsule^{-1}	Per capsule
GCA/*gca*	General Combining Ability
SCA/*sca*	Specific Combining Ability
RH	Relative heterosis
HB	Heterobeltiosis
SH	Standard heterosis
mm	millimeter
Km/h	Kilometer per hour
h	hours

Introduction

1. INTRODUCTION

Sesamum (*Sesamum indicum* L., 2n=2x=26) belonging to the family Pedaliaceae is an annual herbaceous species cultivated for its edible seed and oil. Although originated in Africa, its cultivation is mainly in the tropical and subtropical parts of Africa, Southern America, and Asia. It began its journey from West Asia to Japan, India, and China which then became the secondary centres of distribution of the crop (Weiss, 1983). It is commonly known by the names *viz.*, sesame, til, gingelly, simsim, benniseed, gergelim to name a few, while in Kerala, Tamil Nadu and Karnataka it is popularly known as "ellu".

Sesame is considered as 'Queen of Oilseeds' due to its stable keeping quality attributed to high degree of resistance to rancidity and oxidation (Bedigian and Harlan, 1986). The seed oil content of sesame varies from 41 to 60 per cent, the highest value compared to other oil seed crops (Wei *et al.* 2015; Dossa *et al*. 2018). The major fatty acids present in the sesame oil include oleic acid (29.3–41.4%), linoleic acid (40.7–49.3%), palmitic acid (8.0–10.3 %), and stearic acid (2.1–4.8%) (Uzun *et al*. 2002). The seed of sesame is rich in vitamins (e.g., A and E), proteins (≈24%), policosanols (Tetracosanol, docosanol, octacosanol, and hexacosanol), lignans (sesamin and sesamolin), phytosterols (β-sitosterol and campesterol), γ-tocopherol, and lipids (Anastasi *et al*. 2017; Gharby *et al*. 2017; Dossa *et al*. 2018). The favourable fatty acid and nutrient profile of sesame oil is favoured by the pharmaceutical industry. Sesame seed is a reservoir of nutritional components such as phosphorus, iron, magnesium, calcium, manganese, copper and zinc. It has antioxidant, anticancer, antihypertensive, antiaging, cholesterol-lowering, and antimutagenic properties (Anilakumar, 2010). Sesame serves diverse value chains. It is useful in the food, feed, confectionery and baking industry. Sesame seed is industrially processed to supply cooking oil, tahini, halvah and cosmetic oils, while the seed cake is used for livestock feed.

Sudan (981,000 tons) is the world's largest producer followed by Myanmar. India is the third largest sesame-producing country in the world with total annual production of 746,000 tons. In India, sesame has a productivity of 431 kg/ha and its cultivated area is 17.30 lakh ha. India shares 12.4 per cent of world sesame production (FAO STAT, 2020). Madhya Pradesh ranks first in production (195.04 tonnes) followed by West Bengal and Rajasthan while Meghalaya is leading in productivity with 937 kg/ha followed by Karnataka and Arunachal Pradesh (Indiastat, 2021). However, in Kerala, the crop provides only a small contribution to the total area of oil seeds. Sesame occupied only 378 ha of area in Kerala during the year 2018-19 with a production of 158 MT (GOK, 2020). In Kerala, sesame is cultivated in summer rice fallows and rabi uplands. Onattukara region in Kerala has a sandy loam belt which is regarded as the home of sesame. In summer, the farmers in this area cultivate sesame as a 3rd crop during rice fallows after two crops of paddy. What makes sesame an ideal crop in this region is its short duration and relatively less water requirement.

In the international market, the superior quality of sesame oil and the confectionary value of its seed have helped it to emerge as a prominent commodity. Generally, sesame seeds are of three main colours: Brown, Black and White. The development of white seeded sesame varieties that possess durable lustre has gained a lot of recognition in most of the prominent sesame cultivating nations including India (Pandey *et al*. 2013). Physical outlook of the seed colour is an important marketing criterion and cultural preferences also play a key role in the acceptability of sesame type. White coloured sesame is mostly preferred for making confectionary and bakery products. Also, it is known to possess higher oil, protein, linoleic acid and moisture ratios when compared with black seeded sesame (Kanu, 2011; Dossa *et al.* 2018). The white varieties of sesame elicit better antioxidant activity than the black ones (Vishwanath *et al*., 2012). The uniform, lustrous, white and bold seed, free from insect pests and pesticide residue, with low free fatty acid per cent (<2), low oxalic acid per cent (<1) and high lignan content (>830 mg/100 g seed), is preferred for export (Kumaraswamy *et al*., 2015). Even though the white seeded sesame is getting an ameliorating demand recently, high yielding varieties with sufficient oil content are very scarce in Kerala compared to black seeded varieties.

Although it is an ancient crop with high economic value, sesame is listed as a neglected and underutilized crop by the International Plant Genetic Resources

Institute (IPGRI) due to its limited cultivation and expansion in the world. Despite its significance, sesame has neither received the required support from the scientific community, nor from the industries and policy makers. Hence it is often considered as an orphan crop. As a result, it lags behind other major oilseed crops in genetic improvement (Dossa, 2016). The seed yield of cultivated sesame is very low (300–400 kg/ha) owing to some wild characters like indeterminate growth habit, asynchronous capsule ripening, and seed shattering (Islam *et al*., 2016). Thus, it is very crucial to develop sesame cultivars for better seed quality and enhanced productivity to successfully cope up with the growing demand of its oil. Augmenting its productivity by exploiting heterosis is an easy and fast way of identifying and combining desirable traits from diversified parents. Selection of suitable parents and combining ability analysis to identify the parents with good *gca* and crosses with good *sca* effects is an important step in developing good varieties.

Easy manual emasculation, pollination, high multiplication ratio for manual seed production, high number of seeds produced flower^{-1}, and low seed rate favours hybrid production in sesame (Jadhav and Mohir, 2013). Most of the high yielding varieties in sesame were developed through hybridization followed by selection. Hence, heterosis breeding appears to be promising in achieving the yield breakthrough. A crucial step in heterosis breeding is effective selection of parents for identifying heterotic crosses.

Keeping these aspects in view, the current investigation entitled “Development of superior varieties in white seeded sesame for seed yield and oil content” was envisioned and the following objectives were formulated.

- To identify high yielding and high oil yielding genotypes
- To study genetic variability for traits that contribute to the yield of the crop
- To estimate heritability, genetic advance and to determine correlation coefficients
- To understand the direct as well as indirect effects of characters that contribute to yield

- To estimate the extent of heterosis
- Selection of superior segregants in F_2 and F_3 segregating generation for high yield and oil content
- To estimate the protein and oil content in sesame seeds

Review of Literature

2. REVIEW OF LITERATURE

The literature on crop improvement relevant to the present study aimed in developing superior varieties in white seeded sesame for seed yield and oil content is reviewed under different headings.

2.1 GENETIC VARIABILITY

The information regarding genetic variability in the available germplasm is a crucial step in any crop improvement programme. When the genetic variability is more, greater will be the chances for selection of better genotypes. The genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) provides an idea regarding the degree of variability existing in a population. Therefore, the information of these parameters helps in the manipulation of available genetic heterogeniety in the desired direction through suitable selection criteria.

Gangadhara *et al.* (2012) conducted genetic variability studies in eighty-one local accessions and elite varieties of sesame. The traits, seed yield plant^{-1}, capsules plant^{-1} and height of the plant showed high GCV and PCV estimates. While, the branches plant^{-1}, capsule length, 1000 seed weight and seeds capsule^{-1} recorded moderate values. Among the eleven traits studied, the traits; oil content, maturity days and days for 50 per cent blooming recorded low PCV and GCV values.

In an evaluation with thirty-one germplasm lines of sesame for genetic variability, Jadhav and Mohrir (2012) noticed very little difference between GCV and PCV values for the characters seed yield plant^{-1}, number of capsules plant^{-1} and number of primary branches. High GCV and PCV values were reported for seed yield plant^{-1} and number of capsules plant^{-1}. Moderate GCV values were found for the characters *viz.*, number of primary branches, 1000 seed weight, height of the plant and days for 50 per cent blooming, whereas characters like maturity days, capsule length, oil content and seeds capsule^{-1} showed low GCV values.

In an experiment performed by Teklu *et al.* (2014), wide genetic variability was observed among sixty-four accessions of sesame for all fourteen characters under investigation with number of capsules plant^{-1} recording the highest GCV and PCV estimate.

Bamrotiya *et al.* (2016) assessed the information on genetic variability among forty genotypes of sesame. High values of PCV and GCV were obtained for number of capsules per leaf axil, seed yield plant^{-1} and number of capsules plant^{-1}. The values of GCV and PCV obtained for number of branches plant^{-1}, number of seeds capsule^{-1}, height of the plant and capsule length were moderate. Low values of GCV and PCV were obtained for 1000 seed weight, maturity days and days to flowering.

Thirty-three accessions of sesame were studied by Abhijatha *et al.* (2017) and recorded high PCV and GCV estimates for number of primary branches, seed yield plant^{-1} and number of capsules plant^{-1}. Days for 50 per cent blooming, maturity days, number of seeds capsule^{-1}, oil content and 1000 seed weight showed low vales of PCV and GCV.

According to the study conducted by Virani *et al.* (2017), analysis of variance showed highly significant variations among the genotypes for all the characters suggesting that the sesame genotypes showed significant variations for all the investigated characters. Among the parents, except for the characters days for 50 per cent blooming and oil content, all other characters exhibited highly significant variations. All the investigated characters of the hybrids also showed significant variations which indicate the existence of adequate diversity among the hybrids for all the characters studied. The differences between the parents *vs* hybrids were seen to be significant for characters *viz*., days for 50 per cent blooming, maturity days, capsule length, number of capsules plant^{-1} and seed yield plant^{-1}.

A study was done by Agrawal *et al.*, (2018) to reveal the importance of genetic variability using forty sesame germplasm accessions and observed higher estimates of GCV for number of capsules plant^{-1}, number of branches plant^{-1} and seed yield plant^{-1}, while, it was moderate for capsule length and number of seeds capsule^{-1}. The GCV values for the characters *viz.*, maturity days, days for 50 per cent blooming, 1000 seed weight, height of the plant, protein content, and oil content were low.

Abd-Elsaber *et al*. (2019) studied the inheritance of yield and its component traits in sesame. All the investigated traits associated with the genotypes, parents, crosses and parents *vs*. crosses, exhibited highly significant differences.

The evaluation of thirteen sesame genotypes by Kalaiyarasi *et al.* (2019a) revealed highest phenotypic and genotypic variances for the trait, number of branches plant^{-1} followed by seed yield plant^{-1}. The traits, days to fifty per cent flowering have exhibited lowest phenotypic and genotypic variances. High GCV and PCV estimates were observed for seed yield plant^{-1}, number of capsules plant^{-1} and number of branches plant^{-1}. The characters, 1000 seed weight and maturity days recorded moderate and low GCV and PCV estimates respectively.

Umamaheswari *et al*. (2019) observed that difference between PCV and GCV was high for length of the capsule, 1000 seed weight followed by seed yield plant^{-1} suggesting the effect of environment on sesame genotypes. The result revealed high estimates of PCV for number of branches plant^{-1}, seed yield plant^{-1} and height of the plant. Moderate PCV and GCV was observed in number of capsules plant^{-1}, 1000 seed weight, length of the capsule and number of seeds capsule^{-1}.

The investigation on genetic variability for seed yield and its attributing traits in forty-five genotypes of sesame depicted the values of PCV were slightly higher than that of GCV for all the traits studied (Kadvani *et al.* 2020). The high estimates of GCV and PCV were recorded for seed yield plant^{-1}, leaf area plant^{-1} and number of branches plant^{-1} indicated the presence of wide genetic variation for these characters.

Kehie *et al*. (2020) conducted a study on twenty-five genotypes of sesame that reported highest GCV for seed yield plant^{-1}. For all the investigated characters, the GCV was lower than the PCV denoting the influence of environment variance.

Genetic variability in respect of eleven quantitative characters was studied by Kumari *et al*. (2020) on twenty-eight genotypes of sesame. Among the genotypes, all the eleven characters investigated showed highly significant differences in analysis of variance. High GCV and PCV were recorded for seed yield plant^{-1} followed by number of capsules plant^{-1}, test weight and number of primary branches plant^{-1} indicating greater scope for selection of these characters for further improvement programme. While moderate GCV and PCV were observed for days for 50 per cent blooming, oil content, height of the plant and protein content.

Manjeet *et al.* (2020) estimated the magnitude of variability in twenty-four sesame genotypes. The PCV was greater than GCV for all the investigated characters which showed the effect of the environment on them and observed high PCV for seed yield plant^{-1}.

An experiment done by Mohanty *et al*. (2020) with thirty genotypes of sesame found highly significant variation among the genotypes for all characters under investigation. High phenotypic and genotypic variance was exhibited by the traits *viz*., number of capsules plant^{-1}, height of the plant, number of seeds capsule^{-1} and oil content. High magnitude of PCV and GCV were visible for the traits *viz.*, productive capsules plant^{-1}, seed yield plant^{-1} and productive branches plant^{-1}. The results showed the greater scope for selection of these traits for further breeding programmes. Moderate values of GCV and PCV were noticed for characters *viz.*, height of the plant, number of seeds capsule^{-1}, oil content and 1000 seed weight. Low values of GCV and PCV were noticed for days for 50 per cent blooming and maturity days.

In an investigation conducted by Oza Hely *et al*. (2020), analysis of variance exhibited considerable variations among the sesame genotypes for all characters, suggesting the presence of adequate variability in the experimental material for all the characters evaluated. Differences among the parents were highly significant for the traits *viz.*, days for 50 per cent blooming, number of capsules per leaf axil, number of seeds capsule^{-1} and seed yield plant^{-1}. Differences among the hybrids were also seen to be significant for all the characters indicating the presence of adequate diversity among them. The differences among the parents *vs* hybrids were noted to be significant for seven characters *viz.*, maturity days, days for 50 per cent blooming, height to first capsule, height of the plant, number of capsules per leaf axil, number of capsules plant^{-1} and 1000 seed weight.

A study was undertaken by Pavani *et al.* (2020) to estimate genetic variability in respect of ten quantitative characters using thirty sesame genotypes. High PCV and GCV were noted for number of capsules plant^{-1} while it was moderate for days for 50 per cent blooming and the number of branches plant^{-1}. The traits *viz.*, height of the plant, capsule length, 1000 seed weight, maturity days, oil content, and seed yield plant^{-1} showed low GCV and PCV.

Saravanan *et al.* (2020) carried out genetic variability studies in F_2 population of the cross OMT 21 A x JLSC 96 and recorded high GCV and PCV values for the traits *viz.* seed yield plant^{-1}, number of branches plant^{-1} and the number of capsules plant^{-1}.

Sirohi *et al.* (2020) noticed significant differences for most of the characters, except oil content in mean sum of squares due to parents while studying heterosis and combining ability analysis in sesame. The mean squares due to hybrids were seen to be significant for almost all the traits under consideration.

Significant variations were visible among evaluated sesame genotypes for all traits studied (Aboelkassem *et al.,* 2021). The maximum mean values of 1000 seed weight and seed yield plant^{-1} were obtained from the genotype M2A23, while the minimum mean value was obtained from the genotype B-42. The high estimates of PCV and GCV were on traits *viz.*, number of branches plant^{-1}, number of capsules plant^{-1}, and seed yield plant^{-1}.

Rathod *et al.* (2021) conducted experiments comprising of a full diallel set of eight diverse parental lines in sesame and their 56 F_1 s that included reciprocals. Mean performance of the parents showed a significant difference for all the investigated traits except seed yield and days for 50 per cent blooming. The hybrids exhibited high yield, 1000 seed weight, and oil content.

An investigation was performed by Vamshi *et al*. (2021) to assess variability for twelve different traits in twenty-seven breeding lines in sesame along with three checks. High PCV and GCV were noted for seed yield per plot and number of capsules plant^{-1}. High PCV and moderate GCV was recorded for number of primary branches plant^{-1}. Further, moderate PCV and GCV were noted for height of the plant, oil content and days for 50 per cent blooming. Low PCV and GCV were noted for the traits *viz.*, maturity days, capsule length and test weight.

Kumar *et al.* (2022) revealed that in sesame, larger magnitude of GCV and PCV was seen for seed yield and number of productive branches.

Variability in seed yield and yield component traits were assessed in 500 sesame accessions at Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur. PCV values were found to be higher than GCV values under the study. High PCV and GCV were observed for seed yield plant^{-1}. Moderate GCV and PCV values were observed for number of primary branches plant^{-1}, number of capsules plant^{-1}, 1000 seed weight, number of seeds capsule^{-1} and capsule length whereas low GCV and PCV values were recorded for maturity days, days to fifty per cent flowering, oil content and height of the plant (Ranjithkumar *et al*. 2022).

Roy *et al*. (2022) found higher PCV and GCV for number of branches plant^{-1} and number of capsules plant^{-1} while studying genetic variation of twenty-nine sesame genotypes based on morphological traits.

Analysis of variance for eight biometric characters in sesame was studied by Sasipriya *et al*. (2022) and noted high GCV and PCV estimate in the trait 1000 seed weight. Moderate estimates of GCV and PCV were observed for the traits *viz.*, days for 50 per cent blooming, number of branches plant^{-1}, height of the plant, number of capsules plant^{-1}, number of seeds capsule^{-1} and seed yield plant^{-1}.

An experiment was done by Srikanth and Ghodke (2022) to assess the sesame genotypes using eleven traits to provide the indication of the degree of variability in yield and with traits that attribute to yield. The maximum GCV was recorded for seed yield plant^{-1}, whereas maturity days showed for low GCV values.

2.2 HERITABILITY AND GENETIC ADVANCE

The estimates of genetic parameters like heritability and genetic advance help the plant breeder to select elite genotypes from a heterogenous genetic population. Even though the estimates of heritability denote the relative efficacy of selection based on the phenotypic expression of a trait, a more beneficial tool for anticipating the actual value of selection is genetic advance (Johnson *et al.* 1995). The available literature on genetic advance and heritability for seed yield and yield associated traits in sesame is reviewed here under.

Gangadhara *et al.* (2012) observed high heritability combined with high genetic advance for the traits *viz.*, seed yield plant^{-1}, capsules plant^{-1}, height of the plant, number of branches plant^{-1}, capsule length, seeds capsule^{-1} and 1000 seed weight in sesame. High heritability coupled with moderate genetic advance was estimated for the traits *viz.*, days for 50 per cent blooming, maturity days and oil content.

An investigation conducted by Jadhav and Mohrir (2012) revealed high heritability estimates for the traits *viz.*, number of capsules plant^{-1}, seed yield plant^{-1} and oil content in sesame. However, lower estimate of heritability was noticed in characters maturity days and capsule length. The high genetic advance was recorded in characters *viz.*, height of the plant and number of capsules plant^{-1} while capsule length showed low genetic advance. High heritability along with high genetic advance as per cent of mean were shown by seed yield plant^{-1}, number of capsules plant^{-1}, 1000 seed weight, number of primary branches and height of the plant indicated that selection could be effective for these characters. Oil content showed high heritability accompanied by low genetic advance as per cent of mean (GAM).

Gidey *et al*. (2013) conducted an experiment with eighty-one sesame genotypes for fifteen characters and observed high values of heritability combined with high values of genetic advance as per cent of mean for number of primary branches plant^{-1}.

An investigation carried out by Bindhu *et al.* (2014) with thirty-one sesame genotypes during summer 2011 at Onattukara Regional Agricultural Research Station, Kerala Agricultural University, Kayamkulam revealed high heritability combined with high genetic advance as per cent of mean for height of the plant, number of branches, number of capsules plant^{-1}, oil content and days for 50 per cent blooming and 1000 seed weight showed moderate heritability and low genetic advance as per cent mean.

According to Teklu *et al*. (2014) heritability was highest for days for 50 per cent blooming. High genetic advance as per cent mean was recorded for number of primary branches plant^{-1}, number of capsules plant^{-1} and 1000 seed weight. Oil content and maturity days recorded low genetic advance as per cent mean.

Hika *et al*. (2015) assessed heritability and genetic advance for eleven traits in sixty-four sesame populations and reported high estimates for heritability values for days for 50 per cent blooming, height of the plant, number of primary branches and number of capsules plant^{-1}. The character 1000 seed weight showed only moderate heritability.

Kumari and Ganesamurthy (2015) evaluated forty-five hybrids developed by using fourteen genotypes of sesame. High heritability along with high genetic advance over mean was reported for number of primary branches.

High heritability estimates were reported for number of capsules per leaf axil, capsule length, seed yield plant^{-1}, number of seeds capsule^{-1} and number of capsules plant^{-1} in sesame (Bamrotiya *et al.* 2016). Moderate heritability estimates were observed for height of the plant, number of branches plant^{-1} and maturity days, while it was lower for 1000 seed weight. The genetic advance expressed as per centage of mean was recorded maximum for number of capsules per leaf axil followed by seed yield plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, capsule length, number of branches plant^{-1} and height of the plant. High estimates of heritability combined with high genetic advance expressed as per centage of mean were estimated for seed yield plant^{-1}, number of seeds capsule^{-1}, number of capsules plant^{-1}, capsule length, number of capsules per leaf axil, number of primary branches and height of the plant.

Abhijatha *et al.* (2017) revealed high heritability combined with high genetic advance (as per cent of mean) for seed yield plant^{-1}, number of primary branches, height of the plant, and number of capsules plant^{-1} in sesame.

According to the study conducted by Agrawal *et al.,* (2018), the characters *viz.*, capsule length, number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1} and seed yield plant^{-1} exhibited high genetic advance coupled with high heritability in sesame.

Gogoi and Sarma (2019) conducted a study using thirty-three sesame genotypes and found high heritability combined with high genetic advance as per cent of mean for seed yield plant^{-1} and 1000 grains weight suggesting that these characters are guided by additive gene effect.

Kalaiyarasi *et al.* (2019a) found high heritability for the characters *viz.,* seed yield plant^{-1}, number of branches plant^{-1}, height of the plant, number of capsules plant^{-1} and number of seeds capsule^{-1}. High genetic advance as per centage of mean was recorded in seed yield plant^{-1} and number of branches plant^{-1}, however, low genetic advance as per centage of mean was observed in the case of days for fifty per cent flowering. High heritability along with high genetic advance was seen for the characters *viz.*, seed yield plant^{-1}, number of seeds capsule^{-1}, number of capsules plant^{-1}, number of branches plant^{-1} and height of the plant.

A study was conducted by Mourad *et al*., (2019) in eleven sesame line and reported high broad-sense heritability followed by high genetic advance for number of branches plant^{-1} and seed yield plant^{-1}.

Umamaheswari *et al*. (2019) estimated high heritability combined with high genetic advance as per cent of mean for height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1} in sesame.

Kadvani *et al.* (2020) noticed high estimates of heritability for 1000 seed weight followed by leaf area plant^{-1}, oil content, capsule length, number of capsules plant^{-1}, maturity days and seed yield plant^{-1} in sesame. The traits *viz.,* height of the plant and number of seeds capsule^{-1} exhibited moderate estimates of heritability. The genetic advance as per cent of mean was found maximum for leaf area plant^{-1}, seed yield plant^{-1}, number of capsules plant^{-1} and 1000 seed weight. Moderate estimates of genetic advance as per cent of mean were recorded for capsule length, oil content, height of the plant and number of seeds capsule^{-1}, while the value was low for maturity days. High estimates of heritability accompanied by high genetic advance as per cent of mean was seen for leaf area plant^{-1}, seed yield plant^{-1}, number of capsules plant^{-1} and 1000 seed weight. High heritability combined with moderate genetic advance was seen for capsule length and oil content. High estimates of heritability with low genetic advance were observed for maturity days, while moderate heritability along with moderate genetic advance was seen for the traits *viz.,* height of the plant and number of seeds capsule^{-1}.

Kehie *et al*. (2020) recorded the highest genetic advance as per cent of mean for seed yield plant^{-1} in sesame. High heritability along with high genetic advance as per cent mean was reported for number of capsules plant^{-1}, seeds capsule^{-1}, 1000 seed weight, days for 50 per cent blooming and oil content.

After estimating heritability and genetic advance, Kumari *et al*. (2020) reported high values for 1000 seed weight, number of capsules plant^{-1}, seed yield plant^{-1}, days for 50 per cent blooming, oil content, protein content, number of primary branches plant^{-1} and height of the plant. Low heritability combined with low genetic advance as per cent of mean was observed for the characters *viz.*, maturity days and capsule length.

Manjeet *et al.* (2020) carried out genetic analysis in twenty-four sesame genotypes and reported high heritability combined with high genetic advance for number of branches plant^{-1} and seed yield plant^{-1}.

In another study in sesame, Pavani *et al*. (2020) observed high heritability and genetic advance as per cent mean for days for 50 per cent blooming, number of branches plant^{-1} where as high heritability with moderate genetic advance as per cent over mean was observed for height of the plant. Low heritability and low genetic advance as per cent over mean observed capsule length, 1000 seed weight, maturity days, oil content, and seed yield plant^{-1}.

Saravanan *et al*. (2020) reported that the traits; number of branches plant^{-1} and 1000 seed weight showed a high heritability combined with a high genetic advance as per cent of mean.

Aboelkassem *et al.* (2021) conducted an investigation to determine the genetic behaviour of fourteen genetically diverse genotypes of sesame and recorded high heritability coupled with the high genetic advance as a per cent of mean in number of branches plant^{-1}, number of capsules plant^{-1}, and seed yield plant^{-1}.

In a study carried out on heritability and genetic advance as per cent of mean, Mohanty *et al*. (2020) reported high heritability estimates for oil content, number of capsules plant^{-1}, days for 50 per cent blooming, seed yield plant^{-1}, number of branches plant^{-1}, height of the plant, and number of seeds capsule^{-1}. Moderate heritability was recorded for maturity days and 1000 seed weight. High heritability combined with high genetic advance was exhibited by oil content, and number of capsules plant^{-1}, seed yield plant^{-1} and height of the plant. High heritability combined with moderate genetic advance was recorded for days for 50 per cent blooming and number of seeds capsule^{-1}.

The findings of Teklu *et al.* (2021) revealed higher heritability, and genetic advance of the traits *viz.*, number of primary branches and thousand seed weight.

In an experiment carried out to estimate heritability and genetic advance as per cent mean in sesame, Vamshi *et al.* (2021) noticed high heritability combined with high genetic advance as per cent of mean for the characters *viz.,* oil content and height of the plant. High heritability values combined with moderate genetic advance was manifested in the traits *viz.,* days for 50 per cent blooming and 1000 seed weight in sesame. Further, number of primary branches plant^{-1} and number of capsules plant^{-1} exhibited moderate heritability coupled with high genetic advance.

A study was undertaken by Ranjithkumar *et al.* (2022) for the genetic analysis of dark brown sesame in twelve traits. High heritability was recorded for the traits *viz.,* capsule length, 1000 seed weight, number of seeds capsule^{-1}, maturity days, oil content, days to fifty per cent flowering, number of primary branches, height of the plant, seed yield plant^{-1} and number of capsules plant^{-1}. Genetic advance as per centage of mean was seen to be high for seed yield plant^{-1}, number of primary branches, number of capsules plant^{-1}, 1000 seed weight, capsule length and number of seeds capsule^{-1}. High heritability coupled with high genetic advance was recorded for 1000 seed weight, seed yield plant^{-1}, number of primary branches plant^{-1}, capsule length, number of seeds capsule^{-1} and number of capsules plant^{-1}. High heritability combined with moderate genetic advance as per centage of mean recorded for height of the plant and oil content, while the traits maturity days and days for 50 per cent blooming showed as high heritability combined with low genetic advance per cent as mean.

On evaluating twenty-nine sesame genotypes based on morphological traits, Roy *et al.* (2022) reported that high heritability combined with high genetic advance for seed yield plant^{-1}, number of branches plant^{-1} and number of capsules plant^{-1}.

Sasipriya *et al.* (2022) recorded that the characters *viz.,* days for 50 per cent blooming, height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight, seed yield plant^{-1} showed high heritability along with high genetic advance as per cent of mean. High heritability accompanied by moderate genetic advance as per cent of mean was seen for capsule length.

Srikanth and Ghodke (2022) investigated the estimates of heritability and genetic advance as per cent mean in sesame and reported that the traits *viz.*, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight, and seed yield plant^{-1} exhibited high heritability accompanied by high genetic advance as per cent mean.

2.4 CORRELATION STUDIES

Correlation studies measure the degree and direction of relationship between variables such as yield and its different components. The association may be in either positive or negative directions. Some of the research works done in sesame to bring out correlation is briefly reviewed hereunder.

Goudappagoudra *et al.* (2011) studied correlation analysis of seed yield and its component traits in F_4 families of sesame. Ten quantitative traits were investigated on a total of 120 families. The magnitude of correlation with seed yield plant^{-1} was significant, positive and highest in the case of number of capsules plant^{-1} followed by number of seeds capsule^{-1}, number of branches plant^{-1}, height of the plant and 1000 seed weight. Considering correlation among the yield components number of capsules plant^{-1} had significant and positive correlation with days for 50 per cent blooming, height of the plant and number of branches plant^{-1}.

Vanishree *et al.*, (2011) estimated correlation coefficient among traits in one hundred and twenty-four F_4 families of a cross E8 x Tamil Nadu Local in sesame. The traits *viz.,* days for 50 per cent blooming, maturity days, height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, capsule length and number of seeds capsule^{-1} had positive and significant association with seed yield plant^{-1}. Number of capsules plant^{-1} showed highest significant positive correlation with seed yield plant^{-1}.

Gangadhara *et al.* (2012) conducted correlation analysis on eighty-one genotypes of sesame for eleven characters and noticed the significant positive association of seed yield plant^{-1} with number of capsules plant^{-1}, capsule length, height of the plant, maturity days, number of branches plant^{-1} and number of seeds capsule^{-1}.

Ibrahim and Khidir, (2012) evaluated 220 F_5 families which were derived from ten crosses of sesame and advanced by the single seed descent method to determine the effects of various traits on seed yield among themselves. Highly significant and positive genotypic correlations were obtained for seed yield plant^{-1} with height of the plant, number of capsules plant^{-1}, number of primary branches plant^{-1}, days for 50 per cent blooming and maturity days. Negative and significant correlation was found for number of capsules plant^{-1} with number of seeds capsule^{-1} and 1000 seed weight.

Rao *et al.* (2013) analysed character association between yield and its contributing traits in 48 sesame genotypes. Seed yield had significant positively correlated with capsule length, 1000 seed weight, number of capsules plant^{-1}, number of branches plant^{-1} and days for 50 per cent blooming. Among the inter correlations, days for 50 per cent blooming had significant positive connection with maturity days and number of branches plant^{-1} while it had significant negative association with capsule length. Maturity days showed significant negative connection with capsule length whereas number of capsules plant^{-1} recorded significant positive connection with capsule length. Height of the plant exhibited significant positive association with number of capsules plant^{-1}.

Teklu *et al.* (2014) observed that seed yield plant^{-1} had positive and significant genotypic correlation with days for 50 per cent blooming, height of the plant, number of capsules plant^{-1}, number of primary branches plant^{-1} and number of seeds capsule^{-1}.

Meenakumari and Ganesamurthy, (2015) found that the traits *viz.*, number of seeds capsule^{-1}, number of capsules plant^{-1} and number of seeds capsule^{-1} showed a significant positive correlation with seed yield plant^{-1} in sesame. A significant positive correlation was observed by the traits *viz.*, maturity days, number of primary branches and number of capsules plant^{-1} with days to first flowering. Maturity days were also positively associated with number of primary branches, and number of capsules plant^{-1}. Height of the plant demonstrated a significant positive correlation with number of capsules plant^{-1} and 100 seed weight. Similarly, number of primary branches exhibited significant positive correlation with number of capsules plant^{-1}, number of seeds capsule^{-1} and 100 seed weight. The trait, number of capsules plant^{-1} also demonstrated a significant positive association with number of seeds capsule^{-1} and 100 seed weight.

According to Bamrotiya *et al*. (2016), seed yield plant^{-1} showed significant and positive correlation with maturity days, height of the plant and number of seeds capsule^{-1} at both genotypic and phenotypic levels in sesame.

Abhijatha *et al.* (2017) observed positive and significant association of the contributing characters *viz.*, height of the plant, number of primary branches, number of capsules plant^{-1}, length of capsule and number of seeds capsule^{-1} with seed yield plant^{-1} in sesame. The highest genotypic and phenotypic correlation with seed yield plant^{-1} was observed for the trait number of capsules plant^{-1}.

Kindeya, (2017) carried out an experiment with seventeen white seeded sesame genotypes at six environments in northern Ethiopia and obtained significant and positive correlation of seed yield with number of branches and number of capsules plant^{-1}. However, seed yield had negative and significant correlation with maturity days and flowering time.

Abate (2018) investigated genetic association of seed yield and its components in 81 sesame accessions based on morphological traits. At phenotypic and genotypic level number of capsules plant^{-1} and 1000 seed weight exhibited highly significant and high positive association with seed yield plant^{-1}.

A study was undertaken by Lalpantluangi and Shah (2018) to study the character association among twenty-one genotypes of sesame. Number of capsules plant^{-1} showed highest positive and significant correlation with seed yield plant^{-1} at both genotypic and phenotypic level. The trait, days for 50 per cent blooming manifested significant positive correlation with number of seeds capsule^{-1}, height of the plant and number of primary branches plant^{-1}. Capsule length showed significant positive correlation with number of seeds capsule^{-1}.

Sasipriya *et al.* (2018) stated positive significant correlation of the traits *viz.*, number of branches plant^{-1}, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1} and 1000 seed weight with seed yield both at phenotypic as well as genotypic levels in sesame.

A study was carried out by Aye and Htwe (2019) to determine interrelationship among the traits in forty Myanmar sesame germplasm. At the genotypic level, days for 50 per cent blooming, height of the plant, number of primary branches plant^{-1}, number of capsules plant^{-1} and capsule length showed significant positive correlation with seed yield plant^{-1}. Days for 50 per cent blooming, number of primary branches plant^{-1} and capsule length showed significant negative correlation with 1000 seed weight. Height of the plant exhibited significant positive correlation with days for 50 per cent blooming and maturity days.

Disowja *et al.* (2020) noticed significant and positive association seed yield plant^{-1} in sesame with number of capsules plant^{-1}, height of the plant and 1000 seed weight at both genotypic and phenotypic level. The trait, 1000 seed weight expressed positively significant association with capsule length at both genotypic and phenotypic levels and negatively significant with days to fifty per cent flowering at genotypic level. Maturity days registered a negative and non-significant correlation with seed yield plant^{-1}.

Gogoi and Sarma (2019) reported that none of the characters showed significant association with seed yield plant^{-1} in sesame which might be due to difference of the genotype used and environmental effect masking the true genetic correlation.

In a study carried out on correlation analysis to understand the relationships existing between yield and yield components in sesame, Kalaiyarasi *et al.* (2019b) revealed positive significant correlation of number of seeds capsule^{-1} and height of the plant and significant negative correlation of days to fifty per cent flowering with seed yield plant^{-1} at both genotypic and phenotypic level. Days to fifty per cent flowering was significant and negative correlation with height of the plant and significant positive correlation with number of branches plant^{-1}. Significant positive correlation was noticed between height of the plant and number of capsules plant^{-1}.

Manjeet *et al.* (2019) revealed that seed yield per seed yield plant^{-1} showed significant and positive correlation with number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1} and 1000-seeds weight at both the genotypic and phenotypic levels in sesame. While, seed yield plant^{-1} showed negative and significant correlation with days for 50 per cent blooming at genotypic level and height of the plant at both genotypic and phenotypic levels respectively. Out of the studied characters, days for 50 per cent blooming was significantly and positively correlated with maturity days at both genotypic and phenotypic level and with 1000 seed weight at genotypic level only. However, it had significant and negative genotypic correlation with height of the plant and number of capsules plant^{-1}. Height of the plant exhibited significant and negative correlation with number of branches plant^{-1} and number of capsules plant^{-1} at genotypic level only. Maturity days showed no significant association with seed yield plant^{-1}.

Navaneetha *et al.*, (2019) reported highest significant positive correlation coefficient of number of capsules plant^{-1} with seed yield plant^{-1} followed by height of the plant, number of seeds capsule^{-1} and number of primary branches plant^{-1} in sesame.

Umamaheswari *et al.* (2019) determined positive association of seed yield plant^{-1} with number of capsules plant^{-1}, number of seeds capsule^{-1}, number of branches plant^{-1} and 1000 seed weight of sesame.

Correlation studies conducted by Kehie *et al*. (2020) revealed that days for 50 per cent blooming exhibited significant positive correlation with height of the plant at the genotypic level. The traits,1000 seed weight and oil content in sesame exerted positive but nonsignificant correlation association with seed yield.

Patidar *et al.* (2020) evaluated twenty-seven elite lines of sesame for correlation studies in twelve characters. Seed yield showed highly significant and positive association with number of seeds capsule^{-1}, while significant and negative correlation was exerted with height of the plant. The trait, oil content showed significant and positive correlation with day to maturity and height of the plant at genotypic level. Maturity days exhibited highly significant and positive correlation with days for 50 per cent blooming at both genotypic and phenotypic level.

Correlation studies between yield and its attributing traits in sesame indicated that the traits *viz.*, number of capsules plant^{-1}, 1000 seed weight, height of the plant and the number of branches plant^{-1} had significant positive correlation with seed yield plant^{-1} (Saravanan *et al*., 2020).

Association analysis by Aboelkassem *et al*. (2021) also revealed the positive and significant correlation of the traits; number of capsules plant^{-1} and 1000 seed weight with seed yield plant^{-1} in sesame.

According to the study conducted by Kumar *et al.* (2022) in sesame, seed yield exhibited significant and high positive correlation with the traits *viz.*, number of branches, number of capsules plant^{-1}, number of seeds capsule^{-1} and maturity days.

2.5 PATH COEFFICIENT ANALYSIS

The total correlation coefficient is partitioned into direct and indirect effects of component variables such as yield related variables on seed yield by path coefficient analysis. Since seed yield is a dependent trait influenced by several other traits, selection based on only seed yield without considering the component traits will be not effective. The knowledge of path analysis facilitates indirect selection for the genetic improvement of yield. A brief review of works related to path analysis in sesame is presented here under.

Goudappagoudra *et al.* (2011) stated that number of capsules plant^{-1}, number of seeds capsule^{-1} and 1000 seed weight exhibited high and positive direct effect on seed yield plant^{-1} in sesame. High and positive direct effect of number of capsules plant^{-1} on seed yield plant^{-1} was observed *via* the traits *viz.*, days for 50 per cent blooming, height of the plant, and number of branches plant^{-1}.

An experiment conducted on path analysis for yield and yield attributing traits in sesame revealed that the character number of capsules plant^{-1} had maximum direct impact on seed yield plant^{-1} followed by number of seeds capsule^{-1} and 1000 seed weight. Number of capsules plant^{-1} had highest direct influence on seed yield plant^{-1} through indirect effects of maturity days, number of branches plant^{-1}, days for 50 per cent blooming and height of the plant (Vanishree *et al*. 2011).

According to Gangadhara *et al.* (2012), path coefficient analysis revealed maximum positive direct impact of number of capsules plant^{-1} on seed yield. Number of capsules plant^{-1} had indirect influence through height of the plant, number seeds capsule $^{-1}$, capsule length, and 1000 seed weight.1000 seed weight exhibited a positive direct effect on seed yield by the positive indirect effect through height of the plant, number of capsules plant^{-1} and number of seeds capsule^{-1}. Height of the plant exhibited positive direct effect on seed yield *via* number of capsules plant^{-1}, capsule length, days for 50 per cent blooming and branches plant^{-1}. Number of seeds capsule^{-1} exerted positive direct effect on seed yield through positive indirect effects of height of the plant, branches plant^{-1}, number of capsules plant^{-1} and 1000 seed weight. Days for 50 per cent blooming exhibited positive direct effect on seed yield plant^{-1} *via* positive indirect effect through height of the plant, capsule length, seeds capsule^{-1}, and 1000 seed weight. However, the characters *viz.*, maturity days and capsule length exerted negative direct effect on seed yield.

Path coefficient analysis of the direct and indirect effects of five yield components in sesame *viz.*, height of the plant, number of capsules plant^{-1}, number of primary branches plant^{-1}, number of seeds capsule^{-1} and 1000seed weight was done by Ibrahim and Khidir (2012). Dividing the total correlation coefficient into various components of direct and indirect influences showed that, the number of capsules plant^{-1}, 1000 seed weight and number of seeds capsule^{-1} had high positive direct effects on seed yield plant^{-1} in sesame. The trait, 1000 seed weight had the highest negative indirect effect on seed yield plant^{-1}, through the number of capsules plant^{-1}. Number of primary branches plant^{-1} showed the highest positive indirect effect on seed yield plant^{-1} through the number of capsules plant^{-1}.

After conducting path coefficient analysis, Rao *et al.* (2013) reported number of capsules plant^{-1} and 1000 seed weight as the major traits to be included for realizing the improvement of yield in sesame.

Teklu *et al.* (2014) observed highest positive direct effects of height of the plant on seed yield in sesame followed by number of primary branches plant^{-1} whereas capsule length showed negative direct effect on seed yield.

Meenakumari and Ganesamurthy, (2015) noticed the positive direct effect of the trait number of seeds capsule^{-1} on seed yield plant^{-1}, while maturity days, number of capsules plant^{-1} and 100 seed weight had negative direct effect.

Bamrotiya *et al*. (2016) reported that number of seeds capsule^{-1} followed by number of branches plant^{-1} and number of capsules plant^{-1} had high and positive direct effect on seed yield plant^{-1} in sesame.

Abhijatha *et al.* (2017) reported the highest positive direct influence of number of capsules plant^{-1} with seed yield plant^{-1} followed by number of seeds capsule^{-1} and height of the plant. However, number of primary branches plant^{-1} and maturity days expressed negative direct effect. The indirect effect of number of capsules plant^{-1} was more on seed yield plant^{-1} through height of the plant, maturity days, number of primary branches, length of capsule and number of seeds capsule^{-1}.

According to the investigation conducted by Abate (2018), number of capsules plant^{-1} imposed highest direct impact on seed yield plant^{-1} and also emphasized the indirect contribution of 1000 seed weight and number of capsules plant^{-1} on seed yield plant^{-1}.

Lalpantluangi and Shah (2018) conducted path coefficient analysis to study different yield contributing characters on seed yield and found the maximum direct effect of number of seeds capsule^{-1} on seed yield plant^{-1}.

Sasipriya *et al.* (2018) found positive direct effect on seed yield in sesame by number of capsules plant^{-1}, 1000 seed weight, number of branches plant^{-1} and number of seeds capsule^{-1} whereas negative direct effect was exhibited by days for 50 per cent blooming. The indirect effect of number of seeds capsule^{-1} on seed yield plant^{-1} was exerted by the traits *viz.*, height of the plant, number of branches plant^{-1} and capsule length. The trait number of capsules plant^{-1} exhibited positive direct effect on seed yield through 1000 seed weight. Number of branches plant^{-1} showed positive direct effect on seed yield through indirect effects of height of the plant, capsule length and number of seeds capsule^{-1}.

Path coefficient analysis in sesame by Aye and Htwe (2019) revealed that seed yield plant^{-1} had positive direct effect with 1000 seed weight, number of capsules plant^{-1}, number of primary branches and capsule length. Primary branches plant^{-1} positive direct effect on seed yield *via* number of capsules plant^{-1}, height of the plant, capsule length and days for 50 per cent blooming. The number of capsules plant^{-1} manifested positive direct effect on seed yield *via* indirect effects of height of the plant, days for 50 per cent blooming, capsule length, primary branches and maturity days.

Disowja *et al.* (2020) determined path coefficient analysis and reported maximum direct effect on seed yield plant^{-1} was contributed by number of capsules plant^{-1} followed by 1000 seed weight and capsule length in sesame.

Gogoi and Sarma (2019) studied path coefficient analysis of yield attributing traits in sesame and revealed that days for 50 per cent blooming and

1000 seed weight had high direct effect on seed yield plant^{-1}. The direct effect of branches plant^{-1} and maturity days *via* indirect effect of days for 50 per cent blooming was high. Number of seeds capsule^{-1} showed a high positive direct effect through 1000 seed weight and number of branches plant^{-1} on seed yield plant^{-1}.

Kalaiyarasi *et al.* (2019b) recorded the positive direct effect of the traits *viz.*, number of seeds capsule^{-1}, height of the plant and 1000 seed weight on seed yield plant^{-1} by carrying out path coefficient analysis for yield attributing traits in sesame. Days for 50 per cent blooming showed negative direct effect on seed yield plant^{-1}. The highest positive indirect effect *via* number of capsules plant^{-1} was expressed by height of the plant and 1000 seed weight.

After studying path coefficient analysis, Manjeet *et al.* (2019) observed low direct effect of number of seeds capsule^{-1} and number of capsules plant^{-1}. However, its association with seed yield was positive. Height of the plant exhibited negative direct effect on seed yield plant^{-1}.

Navaneetha *et al.*, (2019) reported low positive direct effect of number of primary branches plant^{-1}, number of seeds capsule^{-1} and 1000 seed weight on seed yield plant^{-1} in sesame, while capsule length showed moderate and positive direct effect.

A study undertaken on path coefficient analysis for seed yield and its components revealed that height of the plant, number of capsules plant^{-1} and number seeds capsule^{-1} were directly influencing the seed yield plant^{-1}. The trait 1000 seed weight had negligible positive indirect effect on seed yield through 50 per cent flowering, height of the plant at maturity, number of capsules plant^{-1} and number of seeds capsule^{-1} (Umamaheswari *et al.* 2019).

In an investigation conducted on path coefficient analysis, Kehie *et al.* (2020) reported positive direct effect of capsule length, number of seeds capsule^{-1} and number of capsules plant^{-1} on seed yield, while height of the plant, 1000 seed weight and days for 50 per cent blooming had negative direct effect on seed yield. The maximum direct effect on seed yield was contributed by capsule length.

Patidar *et al.* (2020) estimated path coefficient analysis on twenty-seven elite lines of sesame and revealed that the positive direct effect on seed yield was exhibited by the traits *viz*., number of seeds capsule^{-1}, number of capsules plant^{-1} and 1000 seed weight.

Saravanan *et al*. (2020) investigated path coefficient analysis of yield and yield related traits in sesame and recorded that the number of capsules plant^{-1} had a high positive direct effect on yield plant^{-1}. The traits *viz.*, height of the plant, number of branches plant^{-1}, number of seeds capsule^{-1} and 1000 seed weight also exerted positive direct effect on seed yield plant^{-1}.

According to the study conducted by Aboelkassem *et al*. (2021), number of capsules plant^{-1} and 1000 seed weight had high positive and direct effect on seed yield plant^{-1} in sesame. However, number of branches plant^{-1} showed negative direct effect on seed yield plant^{-1}. But it showed the greatest positive indirect effect on seed yield plant^{-1} through the number of capsules plant^{-1}.

By studying path coefficient analysis of in sesame, Kumar *et al.* (2022) suggested that the traits number of branches plant^{-1}, number of capsules plant^{-1} had high positive direct effect seed yield. The direct effect on height of the plant through number of branches plant^{-1} and number of capsules plant^{-1} was positive and high. Thousand seed weight had negative indirect effects through number of branches plant^{-1}.

2.5 COMBINING ABILITY AND GENE ACTION

Certain combinations of parents produce superior hybrids while performance of certain combinations of parents involving equally promising parents produce disappointing hybrids as the combining ability depends upon complex interaction among genes. Therefore, combining ability studies provide useful information for the selection of parents in terms of performance of hybrids and the nature and magnitude of gene actions involved in the expression of quantitative traits can be elucidated. Heterosis also depends upon both general and specific combining ability. The available reports pertaining to the combining ability studies in sesame using different biometrical methods have been reviewed here under.

Azeez and Morakinyo (2014) studied combining ability through five distinct accessions of sesame which were employed in a diallel mating design. The predominance of non-additive gene action was shown by the traits *viz*., height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, capsule length and number of seeds capsule $^{-1}$. The trait, 1000 seed weight exhibited additive gene action. Two cross combinations, had highly significant *sca* effect for seed yield and its attributing traits. The parents involved in the promising crosses were low x high, medium x low and medium x high general combiners for seed yield and other characters.

Combining ability for eleven characters in sesame was studied by Joshi *et al.* (2015) using ten lines and four testers which were crossed in line x tester mating design. Combining ability analysis revealed preponderance of non- additive gene action for all the characters *viz.*, days for 50 per cent blooming, height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, capsule length, maturity days, number of seeds capsule $^{-1}$, 1000 seed weight and seed yield plant^{-1}.

The general and specific combining ability in sesame using five lines and nine testers through line x tester analysis were estimated by Kumari *et al.* (2015). Since the characters like seed yield plant^{-1}, 100 seed weight, number of capsules plant^{-1} and number of primary branches had significant and positive *sca* effects in hybrid combinations these can be utilized for yield improvement through heterosis and pedigree breeding.

Subashini *et al.* (2015) carried out line x tester analysis involving seven lines and five testers to study gene action for seed yield and yield components in sesamum. Dominance variance was found to be more than additive variance. The characters like days for 50 per cent blooming, height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight and single plant yield indicating predominance of non-additive gene action.

Based on mean performance, *sca* effects and standard heterosis some of the hybrids were identified to be suitable for heterosis breeding while some other hybrids had non-significant *sca* effects and the corresponding parents with significant *gca* effects were considered as suitable for recombination breeding.

Pawar *et al*. (2016) assessed combining ability through 8 x 8 half diallel set in sesame at the Agricultural Research Station, Junagadh Agricultural University. Significant *sca* effects was found for the traits *viz*., seed yield plant^{-1}, days for 50 per cent blooming, maturity days, height of the plant, number of primary branches plant^{-1}, capsule length, number of seed capsule^{-1}and 1000 seed weight. Significant *sca* effects was observed for seed yield plant^{-1}, days for 50 per cent blooming, number of branches, capsule length, number of seeds capsule^{-1} and 1000 seed weight. The cross AT 192 x G.Til 1 exerted the highest, significant positive *sca* effect which involved average x good general combining parents for seed yield plant^{-1} was found to be best hybrid for seed yield plant^{-1}.

Priya *et al*. (2016) made an attempt to study the general and specific combining ability in sesame through line x tester analysis with four lines and eleven testers. The results revealed significant *gca* effects for the traits *viz*., days for 50 per cent blooming, maturity days, height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1}. Among the hybrids, the best hybrid showed significant *sca* effects for maturity days, number of branches plant^{-1}, number of capsules plant^{-1} and seed yield plant^{-1}.

Tripathy *et al.* (2016) performed a diallel analysis with twelve diverse parental genotypes of sesame to study gene action and select appropriate parents or crosses using combining ability analysis. The magnitude of *gca* effects were invariably higher than *sca* effects for the characters *viz*., days to initial flowering, days to cessation of flowering, maturity days, height of the plant, number of primary branches plant^{-1}, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 500-seed weight, and seed yield plant^{-1} indicating preponderance of additive gene action for inheritance of the traits.

El-Kader *et al.* (2017) conducted an experiment to determine combining ability and gene action in a half diallel set involving six parental sesame genotypes and 15 F_1 crosses. Additive gene action was governed in most studied traits like days for 50 per cent blooming, maturity days, height of the plant, number of capsules plant^{-1} and seed yield plant^{-1}. Valuable positive *sca* effects were detected for number of branches plant^{-1}, number of capsules plant^{-1}, thousand seed weight and seed yield plant^{-1}.

The combining ability studies in sesame were carried out by Manapure *et al.* (2017) using line x tester mating design involving fifteen lines and three testers. The results showed that the lines *viz.,* SI-11, JCSC-8, SP-1102-B, NIC-16207, Tarun, RT-46, Hima, SI-7-2 and testers JLT-7 and AKT-64 were good general combiners for seed yield and yield associated traits. The cross combinations *viz.*, Phule Til-1 × NIC-16207, AKT-64 × NIC-16207, JLT-7 × RT-46 and JLT-7 × GT-L exhibited high mean values with involvement of either parent with significant general combining ability effects and high positive significant specific combining ability.

Raikwar (2018) analysed combining ability through 8 x 8 diallel cross mating design with parents and F_1s to estimate gene action and combining ability for yield and yield associated traits in sesame. The ratio of *sca* to *gca* variance was greater than one for the traits *viz*., height of the plant, number of primary branches plant^{-1}, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, days for 50 per cent blooming, maturity days and seed yield plant^{-1} indicating the preponderance of non-additive gene action in the expression of these traits.

Virani *et al.* (2018) generated fifty crosses generated in line x tester design by mating ten lines and three testers to estimate combining ability for fourteen characters in sesame. Analysis of variance for combining ability revealed that the mean squares due to lines, testers and line x testers were significant for the traits *viz.*, days for 50 per cent blooming, height of the plant, number of branches plant^{-1}, capsule length, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1} except mean squares due to lines for maturity days.

The combining ability analysis revealed that non-additive gene action was predominant in the genetic control of all the characters studied except height of the plant.

Combining ability analysis for yield and yield contributing traits *viz.*, days for 50 per cent blooming, height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1} in sesame was studied through line × tester mating design with seven lines and three testers. The variance due to *sca* was higher than the corresponding variance due to *gca* for all the traits evaluated (Amarnath *et al.* 2019).

Bhalodiya *et al*. (2019) investigated general and specific combining ability through line × tester mating design using five lines and seven testers. The parents, GJT-5 and G. Til-4 displayed high *gca* effects and good *per se* performance for seed yield plant^{-1} and might be utilised in multiple crossing programmes. Among the eight hybrids which manifested significant and positive *sca* effects for seed yield plant^{-1}, the best three specific combiners were Keriya-7 × G. Til-2, AT-319 × GJT-5 and ABT-33 × G. Til-1.

Dela *et al.* (2019) evaluated thirty-seven test entries comprising of twenty-eight hybrids developed from eight diverse parental lines and one standard check to study combining ability for seed yield and its component traits in sesame using diallel mating design. The magnitude of *gca* and *sca* variances revealed that the *sca* variances were higher than their respective *gca* variances for all the characters studied which confirmed the preponderance of non-additive gene action for all the traits *viz.*, days for 50 per cent blooming, height of the plant, number of branches plant^{-1}, capsule length, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1}.

Deshmukh *et al.* (2019) reported general and specific combining ability for eleven quantitative traits in sesame through line x tester analysis by using five lines and ten testers. The best general combiner among the lines had significant *gca* effects for days for 50 per cent blooming, maturity days, number of capsules plant^{-1}, number of seed capsule $^{-1}$, 1000 seed weight and seed yield plant^{-1}. The tester exhibited highly positive *gca* effects for seed yield plant^{-1} and 1000 seed weight. The best cross exhibited significantly high *sca* effects for the characters *viz*., number of capsules plant^{-1}, 1000 seed weight and seed yield plant^{-1}.

Ismail *et al.* (2020) conducted an experiment in sesame to estimate combining ability for yield and its component character using line x tester design with seven lines and 3 testers. Variances due to *gca* and *sca* indicated the non-additive gene action for all the traits *viz.,* height of the plant, number of primary branches plant^{-1}, number of capsules plant^{-1}, seed yield plant^{-1} and 100-seed weight.

With a view to produce elite hybrids, Jeeva *et al.* (2020) conducted combining ability analysis through diallel analysis by using five sesame genotypes. The combining ability variance revealed the preponderance of additive gene action for all the characters studied *viz.,* days for 50 per cent blooming, height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1}.

A study was undertaken by Pramitha *et al.* (2020) to estimate the combining ability for eleven yield attributing traits in sesame using line x tester analysis (100 testers and 2 lines). The preponderance of non-additive gene action was observed for all the traits *viz.,* days to fifty per cent flowering, height of the plant, number of primary branches, number of capsules in main stem, number of capsules in branches, capsule length, number of seeds capsule^{-1}, maturity days, seed yield plant^{-1} and thousand seed weight.

Sirohi *et al.* (2020) conducted an investigation on line x tester analysis of three lines and nine testers in sesame and reported the predominance of non-additive gene action for height of the plant, days for 50 per cent blooming, maturity days, number of effective branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1} and seed yield plant^{-1}.

Disowja *et al*. (2021) studied the general and specific combining ability in sesame through line x tester analysis using four lines and six testers. The estimates of σ^2 SCA were greater than the corresponding σ^2 GCA for all the characters, *viz.*, days for 50 per cent blooming, height of the plant, the number of primary branches, number of capsules plant^{-1}, capsule length, maturity days, 1000 seed weight and seed yield plant^{-1}; which indicated the presence of non-additive gene action.

Parameshwarappa *et al*. (2021) conducted a study to estimate combining ability for yield and yield attributing traits using line x tester mating design with four lines and three testers. GCA and SCA variances showed major contribution of additive gene action for the characters *viz.,* maturity days, height of the plant, number of primary branches plant^{-1}, number of capsules plant^{-1}, capsule length, 1000 seed weight and seed yield plant^{-1}. while, for number of seeds capsule^{-1}, the estimate of *sca* was higher than the *gca* indicating the predominance of non-additive gene action for this trait.

Combining ability estimates were done for yield and yield attributing traits in eight parents and 28 F_1 hybrids produced through half diallel mating design by Sikarwar *et al*. (2021). The parents, TKG-22 was identified as the best general combiners for high seed yield, number of seeds capsule^{-1} and capsule length. The cross combination which involved low x high, low x low, medium x high, medium x low were identified as general combining parental combination for seed yield plant^{-1}.

Ghule *et al.* (2022) carried out line x tester analysis in sesame with four lines and six testers to estimate the combining ability effects for thirteen characters. Among the parents, AT-255 and GT-3 were found as good general combiners for seed yield plant^{-1}. The cross combination, GT-3 x AT-255 showed the maximum positive and significant *sca* for seed yield plant^{-1} and hence recommended for heterosis breeding.

2.6 HETEROSIS

Successful exploitation of heterosis require two basic prerequisites namely significant heterotic effect must be present and production of large-scale hybrid seed should be possible. The information on the magnitude of heterosis is very essential in the development of hybrids. It is easy for hand emasculation and pollination in sesame; and also, single crossed capsule gives a greater number of seeds. So, in sesame heterosis breeding can be largely exploited. The exploitation of hybrid vigour as a mean of maximizing the yield of agricultural crops has become one of the outstanding ways to increase productivity of it. For the present study, the literature pertaining to heterosis in sesame is reviewed here under.

A study of heterosis was undertaken by Jadhav and Mohrir (2013) with the aim to assess the extent of the heterosis for sixteen quantitative traits including seed yield plant^{-1} in 48 F_1 hybrids generated through line x tester method (8 lines and 6 testers). Heterosis for seed yield plant^{-1} was ranged from -55.79 to 84.09 per cent, -58.06 to 65.31 per cent and -28.62 to 193.10 per cent over mid parent, better parent and standard variety respectively.

Parimala *et al*. (2013) revealed that all characters showed in variable crosses depicted heterosis in both positive and negative directions indicating that genes with negative as well as positive effects were dominant. Standard heterosis was found to be highly significant for the traits *viz*., height of the plant, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1}. The hybrid, Chandana x Swetha (39.63%) exhibited highest standard heterosis for seed yield plant^{-1}.

Vavdiya *et al.* (2013) assessed the extent of heterosis for fifteen quantitative traits using twelve lines and three testers which were crossed in a line x tester fashion. The standard heterosis for seed yield plant^{-1} ranged from -12.32 per cent to 137.39 per cent. The highest value of standard heterosis was displayed by the cross NIC-75 x G. Til 10. The crosses which showed high heterosis for seed yield plant^{-1} also had high heterosis for number of capsules plant^{-1}, number of branches plant^{-}

^{1}, height of the plant, number of internodes plant^{-1}, length of capsule and number of seeds capsule^{-1} which confirmed the association of heterosis exhibited by the component to the heterosis for seed yield plant^{-1}.

Azeez and Morakinyo (2014) observed that the cross, 65-8B x PACH had the highest significant positive mid and better parent heterosis for primary branches, height of the plant while cross S530 x PACH for 1000 seed weight.

Chaudhari *et al.* (2015) computed the extent of heterosis for eleven quantitative traits using five lines and ten testers which were crossed in line x tester mating design. Heterobeltiosis for seed yield plant^{-1} ranged from -38.12 to 89.65 per cent. The cross Patan-64 x JL408 showed highest relative heterosis (89.65%). The range of standard heterosis over Gujarat Til-4 and TKG-22 was -38.89 to 85.81 per cent and -34.87 to 98.08 per cent, respectively.

Rani *et al.* (2015) studied the extent of heterosis in sesame using thirty-eight hybrids and reported 22, 35 and 10 hybrids which recorded positive standard heterosis for seed yield plant^{-1} over checks, TKG 22, Pragathi and Swetha respectively. Among these, the cross Swetha x VS 07-023 (32.8%) exhibited highest standard heterosis for seed yield plant^{-1}.

Patel *et al.* (2016) evaluated heterosis over mid parent and better parent for days to flowering, maturity days, height of the plant, number of primary branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1} and seed yield plant^{-1} in 36 crosses derived from a 9 x 9 diallel mating design in sesame. The cross combinations, Priya x Vinanak, PBTil-1 x TMV-6 and TC-25 x Vinayak showed a highly significant relative heterosis and heterobeltiosis for seed yield plant^{-1} and some of its yield components and hence could be exploited for developing superior varieties in sesame.

According to El-Kader *et al.*, (2017), significant relative heterosis and heterobeltiosis was found for the traits *viz.,* days for 50 per cent blooming, height of the plant, number of branches plant^{-1}, number of capsules plant^{-1}, 1000 seed weight and seed yield plant^{-1}. The highest heterotic effects over better parent were detected in the F_1 hybrid NA.80 x NA.35 (28.56 %) for seed yield plant^{-1}.

Heterosis for yield and its attributes in fifteen selected crosses belonging to fifteen parental lines were studied by Imran *et al.* (2017). Highest degree of relative heterosis and heterobeltiosis was observed for seed yield plant^{-1} and the lowest degree was observed for capsule length. Among the 15 hybrids, the cross RT-346/ VRI-2 showed the highest heterosis (271.08%) for seed yield plant^{-1} followed by AKT-64/ Kanak (46.69%). The hybrids *viz.*, RT-346/ VRI-2 (38.74%), Kanak/ Smarak (26.58%) and RT-346/ Amrit (16.89%) had high standard heterosis for seed yield over the high yielding commercial check variety Amrit.

Kumari and Ganesamurthy (2017) conducted an experiment to study the expression of heterosis for ten characters in forty-five crosses of sesame developed by crossing five lines with nine testers in line x tester mating design. The relative heterosis and heterobeltiosis for seed yield plant^{-1} ranged from -69.57 to 124.18 and from -71.54 to 104.13 per cent, respectively where as the standard heterosis ranged from -74.12 to 64.51 per cent and from -68.75 to 98.66 per cent over standard varieties *viz.*, CO 1 and TMV 7 respectively. The cross TMV 5 x ORM 7 (98.66%) expressed highest standard heterosis for seed yield plant^{-1}.

An investigation was undertaken by Patil *et al*. (2017) involving two female (JLT-7 and JLS-302-11) and 100 diverse male parents to estimate extent of heterosis for yield and its components. The study revealed that the heterosis in seed yield was influenced by high heterotic manifestation in the traits *viz.*, number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1} and 1000 seed weight. Standard heterosis ranged from 8.50 to 50.10 per cent for seed yield plant^{-1}. The hybrids *viz.*, JLS-302-11 × Usha, and JLT-7 × N-32 for seed yield, number of capsules plant^{-1} and higher number of branches, while the cross *viz.*, JLS-302-11 × TKG-306 for seed yield, 1000 seed weight and number of capsules manifested desirable heterosis.

According to the study conducted by Virani *et al*. (2017), the highly significant heterosis was observed for days for 50 per cent blooming, maturity days, number of branches plant^{-1}, capsule length, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1}. The heterobeltiosis for seed yield plant^{-1} ranged from -44.14 to 50.90 per cent, while the standard heterosis ranged from 42.01 to 54.90 per cent. The crosses which showed high heterosis for seed yield plant^{-1} also exhibited high heterosis for height of the plant, number of branches plant^{-1}, 1000 seed weight and number of capsules plant^{-1} which revealed that the heterosis for seed yield plant^{-1} was associated with the heterosis expressed by its component characters.

Karande *et al*. (2018) worked out heterosis for seed yield and yield contributing traits in twenty-one hybrids in sesame generated from line x tester analysis (seven lines and three testers). The highest magnitude for relative heterosis (90.44%) and heterobeltiosis (68.07%) and standard heterosis (over check Phule til) (125.19%) was displayed by the cross BSG-5 x LT-8. The cross, BSG-5 x LT-5 (109.36%) showed the highest magnitude of standard heterosis over the standard check JLT-7.

Raikwar, (2018) reported twenty hybrids that showed standard heterosis for seed yield plant^{-1}. The maximum significant and positive heterosis over standard check TKG22 for seed yield plant^{-1} was observed in hybrid TKG22 x SI-205-1(65.3%) while the maximum heterobeltiosis for seed yield plant^{-1} was shown by the hybrid RMT-187 x SI205-61(108.2%).

A study was conducted by Vekariya and Dhaduk (2018) in sesame to assess the extent of heterosis for fourteen quantitative traits by using two lines and ten testers which were crossed in a line x tester fashion. The standard heterosis for seed yield plant^{-1} ranged from -35.34 to 17.71 per cent. The cross, G. Til-3 x DS 21 showed desirable standard heterosis over the check GJT-5, for seed yield plant^{-1} along with other trait *viz.*, height of the plant, number of capsules plant^{-1}, number of seeds capsule^{-1} and 1000- seed weight and the cross, G. Til-3 x RT 127 showed significant standard heterosis for seed yield plant^{-1} and 1000 seed weight.

According to the experiment conducted by Bhalodiya *et al.* (2019), the heterobeltiosis for seed yield plant^{-1} ranged from −39.76 (AT-379 x G. Til-1) to 68.28 per cent (Keriya-7 x G. Til-2), while the standard heterosis ranged from −61.82 to 1.57 per cent over the check variety G. Til 10.

Dela and Sharma (2019) conducted a study to know the nature and magnitude of heterosis for seed yield plant^{-1} and its eleven yield attributing components. The estimates of heterobeltiosis ranged from -35.63 per cent (AT 396 x G.TIL 4) to 31.26 per cent (AT 377 x AT 396). The spectrum of variation for standard heterosis was from -21.19 per cent (AT 345 x AT 347) to 22.86 per cent (AT 347 x G.TIL 4) over the standard parent G.TIL 4.

According to the investigation of Jeeva *et al.*, 2020, the hybrids *viz.* TMV 3 / TMV 5, TMV 5 / TMV 3, TMV 6 / SVPR 1 and TMV 5 / SVPR 1 exhibited highly significant standard heterosis for seed yield plant^{-1}. Among that the hybrid TMV 3 / TMV 5 recorded significant and positive standard heterosis for all the traits except days to fifty per cent flowering.

Oza Hely *et al.* (2020) estimated heterosis for seed yield and its components in a set of line × tester crosses (nine lines and five testers) of sesame. The standard heterosis for seed yield plant^{-1} ranged from -60.61 to 42.60 per cent. The highest value for standard heterosis for seed yield plant^{-1} was displayed by the cross AT-471 × GT-2 (42.60%) followed by AT-472 × GT-3 (33.06%) and AT-483 × GT-3 (17.96%). The result also revealed that the crosses which showed high heterosis for seed yield plant^{-1} also had high heterosis for days for 50 per cent blooming, maturity days, number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1} and 1000 seed weight.

Ghule *et al.* (2021) carried out an investigation to study the extent of heterosis in thirty-two hybrids obtained by crossing in ‘L x T’ fashion using four lines and eight testers. The highest significant heterosis effects was recorded by the cross GT-3 x AT-255 for seed yield plant^{-1} over both the standard check JLT-408 (23.00%) and Phule Til-1 (21.72%). The results showed that the cross GT-3 x AT-

255 (22.79%) also exhibited highest magnitude of significantly positive heterosis over better parent for seed yield plant^{-1}.

Disowja *et al*. (2021) performed line x tester analysis with four lines and six testers and twenty-four hybrids and estimated the heterosis for seed yield and yield contributing traits in sesame. The hybrid, TMV 6 x Thilathara showed the highest positive significant standard heterosis for seed yield plant^{-1} and for some of the yield contributing characters *viz.*, days for 50 per cent blooming, height of the plant, maturity days and 1000 seed weight with standard heterosis in the desirable direction. The hybrid VRI 3 x Thilottama also showed the positive significant standard heterosis for yield along with height of the plant and maturity days in desirable direction. The standard heterosis over the standard parent VRI 3 ranged from -56.13 to 39.32 per cent. The results also revealed that the heterosis for seed yield plant^{-1} cognate with component traits.

Heterosis for seed yield and yield attributes was studied in 10 x 10 half diallel set of ten diverse sesame genotypes in Rajasthan. The crosses *viz*., RT-346 x TKG-22, RT-346 x RT-46, RT-346 x GT-10, TKG-22 x TC-25, RT372 x TC-25, RT-372 x RT-103, PRAGATI x RT-351, RT-46 x GT-10 and RT-125 x RT-103 exhibited positive significant relative heterosis and heterobeltiosis which were found to be the promising combinations for seed yield plant^{-1} (Nehra *et al*. 2021).

Parameshwarappa *et al*. 2021 investigated heterosis for yield and yield attributing traits in 12 F_1 hybrids generated through line x tester mating design (4 lines and 3 testers). The magnitude of heterobeltiosis for seed yield plant^{-1} ranged from -16.51 to 24.57 per cent, while the standard heterosis over standard check variety DS-5 ranged from -12.74 to 33.58 per cent. The maximum significant and positive heterobeltiosis and standard heterosis was observed in the cross AT 238 x DS-5 which also had significant heterotic effect on the the traits *viz.*, height of the plant, number of capsules plant^{-1} and number of primary branches plant^{-1}.

Rathod *et al*. (2021) found that among the 56 F_1's evaluated, TBS-105 x R-09 (148.42 % and 114.87 %), TBS-105 x V-29 (141.61 % and 108.97 %) and TBS-

7 x V-29 (140.41 % and 106.78 %) were in the top-ranking crosses which manifested highly significant and desirable heterosis for seed yield over better parent and standard check (JLT-408), respectively. The hybrid TBS-105 x R-09 also showed significant heterosis for yield component characters *viz.*, number of branches plant^{-1}, the number of capsules plant^{-1} and number of seeds capsule^{-1} and TBS-105 x V-29 and TBS-7 x V-29 for the number of capsules plant^{-1} and capsule length

The extent of heterosis for eleven traits, including seed yield plant^{-1}, was investigated in sesame by Kumar *et al*. (2022). The estimate of standard heterosis for seed yield plant^{-1} ranged from -38.90 per cent (SKT 1501 x AT 413) to 42.18 per cent (SKT 1501 x AT 307). While heterobeltiosis for seed yield plant^{-1} ranged from -35.80 (AT 338 x AT 307) to 35.23 (GT 03 x SKT 1501). The cross GT 03 x SKT 1501 also registered significant and desirable standard heterosis and heterobeltiosis for the component traits *viz.*, days to flowering, maturity days, number of primary branches plant^{-1}, height of the plant, number of capsules plant^{-1} and 1000 seed weight and the cross SKT 1501 x AT 307 for number of primary branches plant^{-1}, number of capsules plant^{-1} and 1000 seed weight.

Materials and Methods

3. MATERIALS AND METHODS

The present study entitled “Development of superior varieties in white seeded sesame for seed yield and oil content” was aimed at developing superior combinations of white seeded sesame genotypes having high yield and oil content necessary for transgressive and heterosis breeding. The information on the utilized materials and adopted techniques during the course of the research are presented hereunder.

3.1 EXPERIMENT I - EVALUATION OF WHITE SEEDED SESAME GENOTYPES

3.1.1 Materials

The materials in the first experiment comprised of thirty white seeded sesame genotypes which were collected from different institutions. The varieties were denoted by treatment numbers T_1 to T_{30}. The list and source of white seeded sesame genotypes used for the study are given in Table 1.

3.1.2 Layout and Conduct of Experiment I

The experimental crop was raised in September 2019 at Onattukara Regional Agricultural Research Station, Kayamkulam using randomized block design with three replications. It was located at 9^0 30' N and 76^o 20' E longitude at an altitude of 3.05 m above mean sea level at the Onattukara Agro-ecological Zone. The experimental field was divided into three blocks of thirty plots each and the treatments were allotted to each block at random. The plot size was 3x1.5m. A spacing of 30 cm was allocated between the rows and a spacing of 15 cm was allotted between the plants in each row. Recommended agronomic practices were ensured to be followed during the period of growth of the crop, as per the “Package of Practices recommendations” of Kerala Agricultural University (KAU, 2016).

3.1.3 Biometric Observation

Five plants were randomly selected from each experimental unit in all the three replications and those were used for obtaining the observations on yield and

Table 1. List and source of white seeded sesame genotypes used for the study

No.	Genotype	Source	No.	Genotype	Source
T_1	Gu. Til 2	Junagadh Agricultural University	T_{16}	PCU-39	Jawaharlal Nehru Krishi Vishwavidyalaya
T_2	Gu. Til 4	Junagadh Agricultural University	T_{17}	PCU-40	Jawaharlal Nehru Krishi Vishwavidyalaya
T_3	VRI-3	Tamil Nadu Agricultural university	T_{18}	PCU-41	Jawaharlal Nehru Krishi Vishwavidyalaya
T_4	Punjab Til No.2	Punjab Agricultural University	T_{19}	PCU-42	Jawaharlal Nehru Krishi Vishwavidyalaya
T_5	RT-346	Punjab Agricultural University	T_{20}	PCU-43	Jawaharlal Nehru Krishi Vishwavidyalaya
T_6	SI-44	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{21}	NIC-8322	Jawaharlal Nehru Krishi Vishwavidyalaya
T_7	SI-205-1	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{22}	RJS-44	Jawaharlal Nehru Krishi Vishwavidyalaya
T_8	IS-118	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{23}	SI-3265	Jawaharlal Nehru Krishi Vishwavidyalaya
T_9	IS-107	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{24}	IS-207	Jawaharlal Nehru Krishi Vishwavidyalaya
T_{10}	SI-982	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{25}	SI-3270	Jawaharlal Nehru Krishi Vishwavidyalaya
T_{11}	PCU-34	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{26}	IAVT-14-5	Kerala Agricultural University
T_{12}	PCU-35	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{27}	AVT-15-9	Kerala Agricultural University
T_{13}	PCU-36	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{28}	AVT-14-6	Kerala Agricultural University
T_{14}	PCU-37	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{29}	EVS-12-12	Kerala Agricultural University
T_{15}	PCU-38	Jawaharlal Nehru Krishi Vishwavidyalaya	T_{30}	IVT-13-7	Kerala Agricultural University

Plate 1. Part of field view (Experiment I)

other biometrical traits. For the traits *viz*., days for 50 per cent blooming and maturity days, the observations were taken on per plot basis. The procedures followed for recording observations on different traits are elaborated below.

a. Days for 50 Per cent Blooming

The number of days required from the day of sowing to the day at which 50 per cent of the plants in each plot attained flowering, was recorded.

b. Maturity Days

The total number of days recorded from the date of sowing to physiological maturity when leaves and stem tend to change from green to yellow colour.

c. Height of the Plant (cm)

Height of the plant was measured in centimeters from the base of plant to the tip of main axis at maturity.

d. Number of Primary Branches Plant^{-1}

Branches originating from the main stem were counted at full maturity stage of the plant.

e. Number of Capsules per Leaf Axil

Number of capsules per leaf axil was counted.

f. Number of Capsules Plant^{-1}

Total number of capsules on each plant was counted.

g. Capsule Length

Five capsules were randomly selected plant^{-1} and the length of capsule was measured in centimetres.

h. Number of Seeds Capsule $^{-1}$

Five capsules were already taken randomly for finding the length of capsule. It was also utilized for counting the number of seeds capsule^{-1} in order to determine the average number of seeds capsule^{-1}.

i. Seed Colour

Seed colour was determined by comparing colour of the sesame seeds with different shades reported in the Royal Horticultural Society (RHS) Colour Chart Fan-4.

j. 1000 Seed Weight

The weight of 100 randomly selected seeds (g) was taken and multiplied it by 10.

k. Leaf Area

Plants selected for dry matter study were used for determining the leaf area plant^{-1} at the late bloom stage of the crop (before ripening phase where, most of the leaves fall off from the plants). The leaves were separated and the leaf area was measured by using graph paper method. The leaf area of small, medium and large leaf was measured. The mean leaf area of small, medium and large leaf was calculated and the grand mean was calculated by multiplying mean leaf area with number of respective leaves. The leaf area plant^{-1} was calculated in cm^2.

l. Dry Matter Production

After the removal of the root portion of the plant, the samples were shade dried followed by hot air oven at 60^{0}C till a constant weight was obtained. The average weight was expressed as dry matter production plant^{-1} in gram.

m. Seed Yield Plant^{-1}

Weight of seeds in each plant was taken and expressed as grams.

n. Scoring of Pest and Diseases, if any

3.1.4. Quality Characters

a. Oil Content.

Oil content was estimated by cold percolation method suggested by Kartha and Sethi (1957)

b. Protein Content (%)

The protein content of the sesame seeds was estimated by multiplying N per cent by 6.25 (Simpson *et al.*, 1965). Nitrogen content was determined by Micro kjeldahl digestion and distillation (A.O.A.C. (1970)).

3.1.5 Statistical Analysis

3.1.5.1 Analysis of Variance (ANOVA)

The analysis of variance (Panse and Sukhatme, 1967) was carried out for all biometric characters recorded from the field evaluation for comparison among the genotypes and to estimate variance components as given below.

Sources of variation	**Degrees of freedom**	**Sum of squares**	**Mean square**	**Computed F ratio**
Replications	r-1	SSR	MSR	MSR/MSE
Treatment	t-1	SST	MST	MST/MSE
Error	(r -1) (t -1)	SSE	MSE	
Total	rt-1	TSS		

Where,

r = number of replications

t = number of treatments

SSR = sum of squares for replications

MSR = mean squares for replication

SST = sum of squares for treatments

MST = mean squares for treatments

SSE = sum of squares for error

MSE = mean squares for error

TSS = Total sum of squares

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

Where,

t_{α} = table value of student’s distribution at error degrees of freedom

α = level of significance (5 % or 1 %).

3.1.5.2 Estimation of Genetic Parameters

a. Coefficient of Variation

Analysis of variance provides estimates of phenotypic and genotypic variances, which are used for the estimation of respective coefficient of variation. The phenotypic and genotypic coefficient of variation are computed as follows (Burton, 1952)

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

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

Where, PCV and GCV are phenotypic and genotypic coefficient of variation, respectively; V_P and V_G are corresponding variances; $\bar{X}$ is the mean.

Categorization of the range of variation was followed as reported by Sivasubramanian and Menon (1973).

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

b. Heritability

Heritability in broad sense is the ratio of genotypic variance to the total or phenotypic variance. It was calculated as per the formula suggested by Allard (1960)

$$\text{Heritability, } H^2 = \frac{V_G}{V_P} \times 100$$

Where, V_G and V_P are genotypic and phenotypic variance respectively.

As suggested by Johnson *et al.* (1955) the range of heritability estimates in broad sense were categorized as:

Category	Range
Low	<30%
Moderate	30-60%
High	> 60%

c. Genetic Advance

Genetic advance refers to the improvement in the mean genotypic value of selected plants over the parental population. From the heritability estimates the genetic advance was estimated by the following formula outlined by Burton (1952).

$$\text{GA} \quad = \quad k.H^{2}\sqrt{V_{P}}$$

Where,

k= Standardized selection differential (2.06 at 5 % selection intensity) (Falconer, 1967)

H^2=Heritability

V_P=Phenotypic variance

For visualizing the relative utility of genetic advance among the characters, genetic advance as per cent of mean was also estimated using the formula suggested by Govidaswamy *et al.* (1973).

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

Where,

GA=Genetic advance

$\overline{X}$ = Grand mean

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

Category	**Range**
Low	<10%
Moderate	10-20%
High	> 20%

3.1.5.3 Correlation Analysis

Correlation analysis is a statistical measure which is used to find out magnitude and direction of relationship between two or more variables. The association between any two variables termed as simple correlation include genotypic and phenotypic correlation coefficients which were worked out by using the formula given by Falconer (1964).

Genotypic coefficient of correlation (r_G) = $\frac{COV_G\ (X, Y)}{\sqrt{V_P\,(X).V_P\,(Y)}}$

Phenotypic coefficient of correlation (r_P) = $\frac{COVp\ (X, Y)}{\sqrt{V_G\,(X).V_G\,(Y)}}$

Where,

COV_P (X, Y) = Phenotypic covariance between two traits X and Y

COV_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

3.1.5.4 Path Co-efficient Analysis

Path coefficient analysis is a standardized partial regression coefficient which splits the correlation coefficient in to the measures of direct and indirect effects as applied by Dewey and Lu (1959). The set of equations obtained from the path diagram were solved to get the information regarding the direct and indirect contribution of the casual factors on the effect.

The residual effect is computed as $\mathrm{R} = 1 - (\mathrm{r}_{\mathrm{Y1}}.\mathrm{P}_{\mathrm{Y1}} + \mathrm{r}_{\mathrm{Y2}}.\mathrm{P}_{\mathrm{Y2}} + ... + \mathrm{r}_{\mathrm{Yn}}.\mathrm{P}_{\mathrm{Yn}})$

$$\mathrm{R} = 1- \sum(r_{Y\,i}.P_{Yi})$$

Where, ‘r’ is the correlation between various traits and the direct effect of X_1 on Y is P_{Y1} and so on. Indirect effect of X_1 on Y depends on other correlated factors.

The direct and indirect effects were classified based on range given by Lenka and Mishra (1973)

Category	**Range**
Very high	>1
High	0.30-0.99
Moderate	0.20-0.29
Low	0.10-0.19
Negligible	<0.09

3.2 EXPERIMENT II - SELECTION OF PARENTS AND HYBRIDISATION

3.2.1 Materials

The experimental material comprised of eight parents (Table 2); five females with high yield as lines *viz.*, Gu. Til 4, VRI-3, Punjab Til No.2, RT-346 and PCU-42 (Plate 2) and three males with high oil content as testers *viz.*, PCU-37, PCU-41 and NIC-8322 (Plate 3). Hybridization programme was conducted in a Line x Tester mating design. The seeds of fifteen superior hybrids were produced by hand pollination. Selfed seeds were also collected from the parents.

3.2.2 Methods

Emasculation and hybridization were carried out as per Thangavelu and Nallathambi (1982). The flowers of the female parents were hand emasculated a day prior to anthesis during the evening hour. The corolla tube as well as the four epipetalous stamens was removed and the pistil was covered using a soda straw (4 cm long). Crossing was done on the following day between 5.00 and 7.30 AM. Fresh pollen from the selected male parents were collected and dusted on to the stigma of the emasculated flowers. The crossed flowers were again covered with soda straw to avoid contamination. When it comes to selfing, the corolla has to be propely tied before the anthesis to prevent natural cross contamination. Seeds of the individual parental lines and the hybrid seed obtained from the female plants were harvested, sun dried and stored separately.

3.3 EXPERIMENT III - EVALUATION OF PARENTS AND F_1 HYBRID

3.3.1 Materials

The materials in the third experiment comprised of fifteen F_1 hybrids along with their eight parents and the standard check SVPR-1 (Table 3).

Table 2. List of parents involved in crossing (Experiment II)

Sl. no.	Parents
Lines (Females)	
1	Gu. Til 4
2	VRI-3
3	Punjab Til No.2
4	RT-346
5	PCU-42
Testers (Males)	
1	PCU-37
2	PCU-41
3	NIC-8322

Table 3: List of treatments in Experiment III

Sl. no.	Treatments	Sl. no.	Treatments
1	Gu. Til 4	13	VRI-3 x PCU-41
2	VRI-3	14	VRI-3 x NIC-8322
3	Punjab Til No.2	15	Punjab Til No.2 x PCU-37
4	RT-346	16	Punjab Til No.2 x PCU-41
5	PCU-42	17	Punjab Til No.2 x NIC-8322
6	PCU-37	18	RT-346 x PCU-37
7	PCU-41	19	RT-346 x PCU-41
8	NIC-8322	20	RT-346 x NIC-8322
9	Gu. Til 4 x PCU-37	21	PCU-42 x PCU-37
10	Gu. Til 4 x PCU-41	22	PCU-42 x PCU-41
11	Gu. Til 4 x NIC-8322	23	PCU-42 x NIC-8322
12	VRI-3 x PCU-37	24	SVPR-1 (Standard Check)

Gu. Til 4

VRI-3

Punjab Til No.2

RT-346

PCU-42

Plate 2. Lines (Female parents) used in Experiment II

PCU-37 PCU-41 NIC-8322

Plate 3. Testers (Male parents) used in Experiment II

Plate 4. Part of field view (Experiment III)

3.3.2 Layout and Conduct of Experiment III

The experimental crop was raised during February 2021 at farmer's field at Kayamkulam using randomized block design with three replications. The fifteen F_1 hybrids along with their eight parents (23 treatments) were evaluated in three replications. The plot size was 1.5 m^2. In each replication, parents and F_1 hybrids were sown in five rows with a spacing of 30 cm between rows and 15 cm between plants in a row. Recommended agronomic practices were ensured to be followed during the period of crop growth, as per the "Package of Practices recommendations" of Kerala Agricultural University (KAU, 2016).

3.3.3 Biometric Observation

All the biometric observations recorded in experiment-I was also recorded for this experiment. The data collected was utilised to estimate heterosis, general combining ability of the parents, and specific combining ability of the crosses. The mode of gene action associated with the inheritance of different characters was also studied.

3.3.4. Statistical Analysis

3.3.4.2 Combining Ability Analysis

General and specific combining ability effects of the parents and hybrids respectively were assessed by line × tester analysis (Kempthorne, 1956). The analysis of variance and the mean squares expectations are as follows.

3.3.4.2.1 Analysis of Variance for Combining Ability

Analysis of variance for five lines, three testers and fifteen hybrids were carried out for thirteen characters and the expected mean square due to different sources of variation and their genetic expectation were estimated as indicated in the ANOVA table.

Sources	**df**	**Mean Sum of Squares**	**Expectation of mean squares**
Replications	(r-1)		
Lines	(l-1)	MS_1	σ^2_e + r (Cov. FS - 2 Cov. HS) + rt (Cov. HS)
Testers	(t-1)	MS_2	σ^2_e + r (Cov. FS - 2 Cov. HS) + rl (Cov. HS)
Line x Tester Interaction	(l-1) (t-1)	MS_3	σ^2_e + r (Cov. FS - 2 Cov. HS)
Error	(r-1) (lt-1)	MS_4	σ^2_e
Total	(rlt-1)		

Where,

r = number of replications

l = number of lines

t = number of testers

σ^2_e = Environmental variance

Cov. HS = Covariance of Half sib

Cov. FS = Covariance of Full sib

From the genetic expectation of mean squares, the covariences of full sibs (Cov.F.S) and half sibs (Cov.H.S) were estimated as given below:

$$\text{Cov. HS} = \frac{MS_1 + MS_2 - 2MS_3}{r\,(1+t)}$$

$$\text{Cov. FS} = \frac{MS_1 + MS_2 + MS_3 - 3MS_4 + 6r\,Cov.HS - r\,(1+t)Cov.HS}{3r}$$

$$\text{Cov.FS} – 2\ \text{Cov.HS} = \frac{MS_3 - MS_4}{r}$$

From above parameters, general and specific combining ability variances were computed as follows:

GCA variance (σ^2*gca*) = Cov. HS

SCA variance (σ^2*sca*) = Cov. FS – 2 Cov. HS

From the above variances of GCA and SCA, the gene action was calculated as follows (Assuming there is no epistasis, when the parents are inbreds or purelines):

Additive genetic variance, σ^2D= 2Cov. HS or $2\sigma^2$*gca*

Non-additive genetic variance, σ^2H= Cov. FS – 2 Cov. HS or σ^2*sca*

3.3.4.2.2 Estimation of Combining Ability Effects

The variation among the hybrids was further partitioned into genetic components attributed to general combining ability (*gca*) and specific combining ability (*sca*) as per the method suggested by Kempthorne (1956). The *gca* and *sca* effects of parents and hybrids were estimated based on the following model.

$$X_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$$

Where,

X_{ijk} - Value of ijkth observation

μ - Population mean

g_i - *gca* effect of ith line

g_j – *gca* effect of jth tester

s_{ij} - *sca* of ijth cross

e_{ijk} - Error effects associated with ijkth observation

i - Number of lines

j - Number of testers

k - Number of replications

The individual effects of *gca* and *sca* were obtained from the two-way table of lines *vs* testers in which each figure was calculated as follows:

$$\text{Mean } (\mu) = \frac{X\ldots}{rlt}$$

$$gca \text{ effect of lines } (g_i) = \frac{Xi..}{rt} - \frac{X\ldots}{rlt}$$

$$gca \text{ effect of testers } (g_j) = \frac{X.j.}{rl} - \frac{X\ldots}{rlt}$$

$$sca \text{ effect of hybrids } (s_{ij}) = \frac{Xij.}{r} - \frac{Xi..}{rt} - \frac{X.j.}{rl} + \frac{X\ldots}{rlt}$$

Where,

X… - Sum of all the hybrid combinations over replications

Xi.. = Sum of ith line over 't' testers and 'r'replications

X.j. = Sum of jth tester over 'l' lines and 'r' replications

Xij. = Sum of ijth hybrid over 'r'replications

r - Number of replications

l - Number of lines

t - Number of testers

The standard error pertaining to *gca* effects of lines and testers and *sca* effects of crosses were calculated as follows.

SE for *gca* effect of lines = $\sqrt{\frac{EMS}{rt}}$

SE for *gca* effect of testers = $\sqrt{\frac{EMS}{rl}}$

SE for *sca* effect of hybrids = $\sqrt{\frac{EMS}{r}}$

Where,

S.E. - Standard Error

EMS - Error Mean Square

The significance of various effects was tested using ‘t’test.

$t_{cal} = \frac{\text{Effect}}{\text{SE}}$

This calculated ‘t’ value can be compared with table ‘t’ value at error degrees of freedom.

3.3.4.1. Estimation of Heterosis

The overall mean value for each parent and hybrid for each character was taken for the estimation of heterosis. The magnitude of heterosis in hybrids was expressed as per centage increase or decrease of a character over mid parent (RH), better parent (HB) and standard check (SH) and was estimated using the following formula (Turner ,1953).

a) Heterosis over mid parental value [Relative Heterosis]

Relative heterosis was estimated as per cent deviation of the mean F_1 performance over the mean performance of the mid parents.

Relative heterosis per cent (RH) = $\frac{\overline{F1}-\overline{MP}}{\overline{MP}}$ x 100

Where,

$\overline{F1}$ - the mean value of the F_1 hybrid

$\overline{MP}$ - the mean of mid parental value *i.e.*, $(P_1+P_2)/2$

P_1, P_2 – the mean values of the first and second parent respectively

b) Heterosis over better parent [Heterobeltiosis]

Heterobeltiosis was estimated as per cent deviation of the mean F_1 performance over the mean performance of the better parent**.**

Heterobeltiosis (HB) = $\frac{\overline{F1}-\overline{BP}}{\overline{BP}}$ x 100

Where,

$\overline{BP}$- the mean of better parental value

c) Heterosis over the standard variety [Standard Heterosis]

Standard heterosis was estimated as per cent deviation of the mean F_1 performance over the mean performance of the standard variety or hybrid**.**

Standard Heterosis (SH) = $\frac{\overline{F1}-\overline{SP}}{\overline{SP}}$ x 100

Where,

$\overline{SP}$- the mean of standard check

The significance of Relative heterosis, Heterobeltiosis and Standard heterosis were tested by the formulae suggested by Turner (1953).

t' for Relative heterosis = $\frac{\overline{F_1} - \overline{MP}}{\sqrt{\frac{\sigma^2 e}{r} \times \frac{3}{2}}} \times 100$

't' for Heterobeltiosis = $\frac{\overline{F_1} - \overline{BP}}{\sqrt{\frac{\sigma^2 e}{r} \times 2}} \times 100$

't' for Standard heterosis = $\frac{\overline{F_1} - \overline{SP}}{\sqrt{\frac{\sigma^2 e}{r} \times 2}} \times 100$

Where,

$\sigma^2 e$ - Error variance

r - Number of replications

3.4. EXPERIMENT IV - IDENTIFICATION AND SELECTION OF SUPERIOR RECOMBINANTS IN F_2

3.4.1 Materials

The experimental material consisted F_2 segregants of the crosses *viz.,* Gu. Til 4 x PCU-37, Gu. Til 4 x PCU-41, Gu. Til 4 x NIC-8322, VRI-3 x PCU-37, VRI-3 x PCU-41, VRI-3 x NIC-8322, Punjab Til No.2 x PCU-37, Punjab Til No.2 x PCU-41, Punjab Til No.2 x NIC-8322, RT-346 x PCU-37, RT-346 x PCU-41, RT-346 x NIC-8322, PCU-42 x PCU-37, PCU-42 x PCU-41 and PCU-42 x NIC-8322.

3.4.2 Method

Here pedigree method was followed. By recording the pedigree, detailed relationship between the plant under investigation and their corresponding progenies was maintained. This helped to trace back each progeny to the F_2 plant from which it was originated. Each individual cross progenies were given a number; the first digit refers to the particular year during which the cross was created and rest of the digits denotes the designation (Table 4) and serial number of the cross. In the segregating generations, serial numbers were assigned for the selected plants within individual progenies. Thus, each of the progenies of the selected plant had the serial numbers of all the plants in the previous generations related to it by direct descent. Thus, each selected plants in F_2 were given a serial number and the F_3 progenies derived from these plants were given the serial numbers of their parent and F_2 plant (Singh, 2016).

3.4.3 Biometric Observation

All the observations recorded as in experiment-I were taken in this trial also.

3.5.EXPERIMENT V - IDENTIFICATION AND SELECTION OF SUPERIOR RECOMBINANTS IN F_3

3.5.1 Materials

One hundred and ten superior performing segregants from F_2 population from ten cross combinations were forwarded to F_3 generation and sown in rows (Table 5). The F_3 population included were segregants from the crosses *viz.*, Gu. Til 4 x PCU-37, Gu. Til 4 x PCU-41, Gu. Til 4 x NIC-8322, VRI-3 x PCU-41, VRI-3 x NIC-8322, Punjab Til No.2 x PCU-37, Punjab Til No.2 x PCU-41, RT-346 x PCU-37, PCU-42 x PCU-37, PCU-42 x NIC-8322.

3.5.2 Method

The seeds of F_2 plant progenies were selected based on seed yield and single plant selection was followed and the pedigree was recorded. The plants selected from a progeny in F_3 were given the number of that progeny. From F_2 generation 110 superior single plants were selected based on the yield performance. They were raised as single plant progeny rows separately in F_3. Plate 6 shows a general view of the experimental field.

In both the segregating populations of F_2 and F_3, the number of plants performed better values for seed yield plant^{-1} was noted as superior segregants. From F_3, forty superior segregants with better yield performance were evaluated for protein and oil content (Table 6). The superior segregants based on high seed yield plant^{-1}, oil content and protein content were identified and selected.

x

Plate 5. Part of field view (Experiment IV)

Plate 6. Part of field view (Experiment V)

Table 4. Designation of the crosses

Sl. No.	**Cross**	**Designation of the cross**
1	Gu. Til 4 x PCU-37	01
2	Gu. Til 4 x PCU-41	02
3	Gu. Til 4 x NIC-8322	03
4	VRI-3 x PCU-37	04
5	VRI-3 x PCU-41	05
6	VRI-3 x NIC-8322	06
7	Punjab Til No.2 x PCU-37	07
8	Punjab Til No.2 x PCU-41	08
9	Punjab Til No.2 x NIC-8322	09
10	RT-346 x PCU-37	10
11	RT-346 x PCU-41	11
12	RT-346 x NIC-8322	12
13	PCU-42 x PCU-37	13
14	PCU-42 x PCU-41	14
15	PCU-42 x NIC-8322	15

Table 5. List and number of progenies of the crosses selected from F_2 and forwarded towards F_3

Sl. No.	**Designation of the cross**	**Number of Progenies selected from F_2 and forwarded towards F_3**
1	01	04
2	02	12
3	03	17
4	05	24
5	06	10
6	07	14
7	08	06
8	10	15
9	13	06
10	15	02
Total		110

Table 6. List and number of progenies of the crosses selected from F_3 and evaluated for biometric as well as quality traits

Sl. no.	**Designation of the cross**	**Number of Progenies selected from F_3 generation**
1	01	02
2	02	04
3	03	06
4	05	10
5	06	02
6	07	06
7	08	01
8	10	03
9	13	04
10	15	02
Total		40

3.5.3 Observation

All biometric observations were recorded as in experiment I. Oil and protein content of superior F_3 plants were also analysed as in experiment I.

Results

4. RESULTS

The present investigation on “Development of superior varieties in white seeded sesame for seed yield and oil content” was taken with a view to assess the genotypes and to study the heterosis and combining ability in order to develop superior recombinants of white seeded sesame genotypes with high yield and oil content suitable for transgressive and heterosis breeding. The results of the present study are presented under five major experiments.

4.1. Experiment I - Evaluation of thirty genotypes of white seeded sesame
4.2. Experiment II - Selection of parents and hybridization
4.3. Experiment III - Evaluation of parents and F_1 hybrids
4.4. Experiment IV - Identification and selection of superior recombinants in F_2
4.5. Experiment V - Identification and selection of superior recombinants in F_3

4.1. EXPERIMENT I - EVALUATION OF THIRTY GENOTYPES OF WHITE SEEDED SESAME

The performance of thirty genotypes of white seeded sesame were evaluated for various morphological and yield traits. The results obtained on biometric and quality characters are presented under the following headings.

4.1.1 Analysis of variance
4.1.2 Mean performance of the genotypes
4.1.3 Genetic parameters
    4.1.3.1 Phenotypic and genotypic coefficients of variability
    4.1.3.2 Heritability (broad sense) and genetic advance
4.1.4 Correlation studies
4.1.5 Path coefficient analysis

4.1.1 Analysis of Variance

Analysis of variance (Table 7) revealed that there were significant differences among the thirty genotypes of white seeded sesame for all the biometric characters studied.

Table 7. Analysis of variance of fourteen characters in thirty genotypes of white seeded sesame

Sl. No.	**Characters**	**Mean square**		
		Replication	**Treatment**	**Error**
1.	Days for 50 per cent blooming	22.011	65.419**	10.367
2	Maturity days	12.211	20.885**	5.303
3	Height of the plant (cm)	202.809	781.538**	70.779
4	Primary branches plant^{-1}	0.217	3.635**	0.615
5	Number of capsules per leaf axil	0.012	0.489**	0.010
6	Number of capsules plant^{-1}	162.192	673.998**	58.51
7	Capsule length (cm)	0.001	0.193**	0.008
8	Number of seeds capsule^{-1}	30.900	213.411**	15.705
9	1000 seed weight	0.025	0.295**	0.010
10	Leaf area	64,043.858	4,288,628.561**	67962.355
11	Dry matter production	86.863	254.698**	10.492
12	Seed yield plant^{-1}	6.408	29.130**	2.653
13	Oil content (%)	2.011	29.184**	0.816
14	Protein content (%)	1.076	10.903**	0.113

** Significant at 1 per cent level

* Significant at 5 per cent level

4.1.2 Mean Performance

The mean values of each of the thirty genotypes of white seeded sesame for the following observations are presented in Table 8. It was observed that there was considerable variation among all the thirty genotypes for the characters under study.

4.1.2.1 *Days for 50 Per cent Blooming*

The days for 50 per cent blooming ranged from 28.67 to 48.67 days. The genotype T_{28} (AVT-14-6) was the earliest to come to 50 per cent blooming whereas the genotypes, T_{16} (29.00 days), T_{12} (29.67 days), T_{20} (30.33 days), T_2 (31.33 days), T_5 (31.67 days), T_{10} (32.00 days), T_7 (32.33 days), T_{13} (32.33 days), T_{30} (32.33 days) and T_{23} (33.33 days) were statistically on par with the genotype T_{28} (28.67 days). The genotype T_3 (VRI-3) was the last to come to 50 per cent blooming. None of the genotypes were statistically on par with genotype T_3 (48.67 days). Among the thirty genotypes studied, sixteen genotypes were having values less than the general mean of 35.51 days.

4.1.2.2 *Maturity Days*

The maturity days of thirty genotypes varied from77.67 to 87.00 days. The genotype T_{12} (PCU-35) took the minimum maturity days (77.67 days) and the genotypes T_2 (78.00 days), T_{16} (78.33 days), T_{11} (78.67 days), T_5 (79.00 days), T_{20} (79.00 days), T_{30} (79.67 days), T_1 (80.00 days), T_{13} (80.00 days), T_{23} (80.00 days), T_{28} (80.00 days), T_{19} (80.33 days), T_4 (80.67), T_{10} (80.67), T_6 (81.00 days) and T_{24} (81.33 days) were statistically on par with the minimum value of maturity days. However, genotypes T_{15} (87 days), T_9 (86 days), T_{27} (85.33 days), T_3 (84.67 days), T_{29} (84.33 days), and T_{18} (84.33 days) were statistically on par with the genotype T_{21} (NIC-8322) which took maximum maturity days.

4.1.2.3 *Height of the Plant*

Height of the plant of the thirty genotypes ranged between 89.07 cm and 155.73 cm. The highest mean value for height of the plant was recorded for genotype T_5 (RT-346) which was statistically on par with T_{19} (146.53 cm), T_2

(145.20 cm) andT_{24} (144.73 cm). The height of the plant was lowest for the genotypeT_{16} (PCU-39). However, genotypes T_8 (94.40) and T_1 (98.33) were statistically on par with it.

4.1.2.4 *Primary Branches Plant^{-1}*

Primary branches plant^{-1} was highest for the genotype T_3 (VRI-3) (6.07) which was statistically on par with the genotype T_9 (4.93). The genotypeT_1 (Gu. Til 2) (0.80) had the lowest number of primary branches plant^{-1} which was statistically on par with the genotypesT_{16} (1.80), T_{14} (1.87), T_8 (2.00), T_{11} (2.00), T_{22} (2.00) and T_{10} (2.07).

4.1.2.5 *Number of Capsules per Leaf Axil*

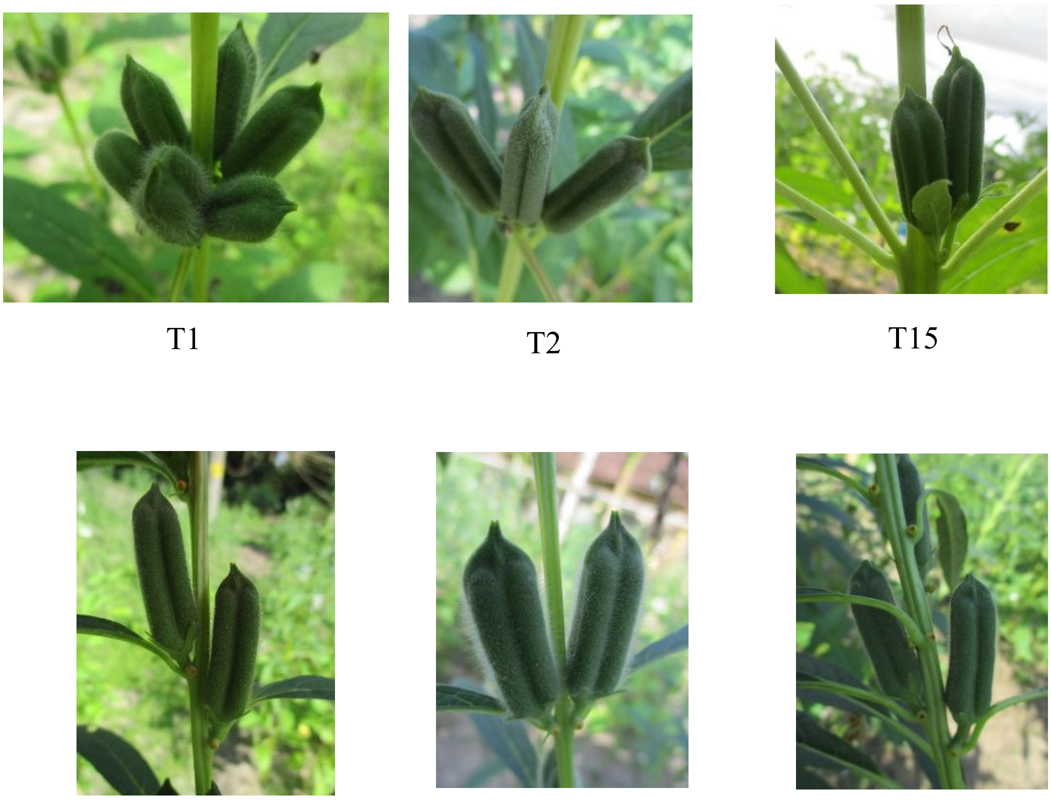
The genotype T_2 (Gu. Til 4) recorded 2.73 number of capsules per leaf axil which was the highest for the trait followed by T_1 (2.40), T_{15} (1.40), T_{11} (1.33) and T_{19} (1.20). All the remaining genotypes possessed only one capsule per leaf axil.

4.1.2.6 *Number of Capsules Plant^{-1}*

Among thirty genotypes, number of capsules plant^{-1} exhibitedsignificant variation with a range of 28.27 to 83.33. The genotypes T_3 (VRI-3) had the maximum number of capsules plant^{-1} and it was statistically on par with T_5 (72.80) and T_2 (70.87). While T_8 (IS-118) was found with the minimum number of capsules plant^{-1}. The genotypes T_{17} (30.47), T_{29} (30.47), T_{23} (30.87), T_{10} (32.13), T_{16} (33.60), T_{14} (34.80), T_9 (35.93), T_{30} (36.40), T_{11} (36.60), T_{26} (38.40), T_{22} (39.00), T_{21} (40.73) and T_{15} (40.80) were statistically on par with the genotype T_8 (28.27).

4.1.2.7 *Capsule Length*

The genotype T_{17} (PCU-40) had the longer capsules (3.17 cm) which was statistically on par with the genotype PCU-42 (3.16 cm). Least capsule length was observed for genotype T_{10} (SI-982) which was statistically on par with the genotypes T_{26} (2.27 cm), T_8 (2.29 cm) and T_{27} (2.30 cm).



T1 T2 T15

T17 T23 T28

Plate 7. Variability in capsule arrangement and number of capsules per leaf axil

Plate 8. Variability in flowers of thirty genotypes

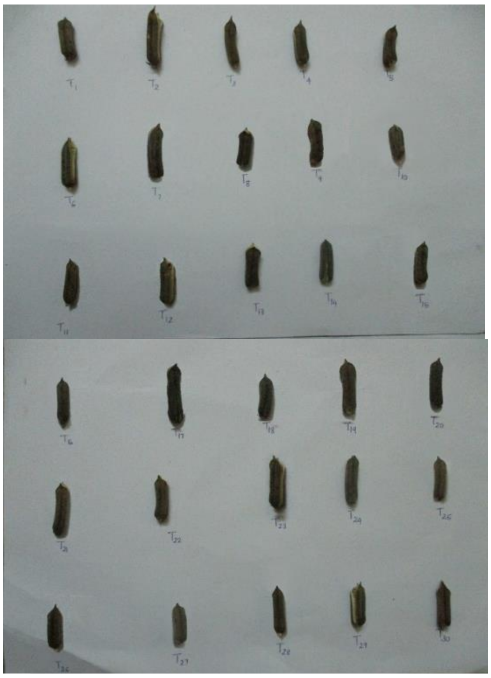


Plate 9. Variability in capsule length of the thirty genotypes

4.1.2.8 *Number of Seeds Capsule^{-1}*

The genotype T_2 (Gu. Til 4) recorded highest number of seeds capsule^{-1}(84.33). The genotypes T_{24} (80.67), T_7 (78.67) and T_{21} (78.00) were statistically on par with it. The genotype T_{25} (SI-3270) was had the least number of seeds capsule^{-1} (52.67) and it was on par withT_{17} (54.00), T_{11} (55.67), T_1 (56.33) and T_{27} (58.67).

4.1.2.9 *Seed Colour*

The morphological character seed colour was studied in the thirty white seeded sesame genotypes and it was found that yellowish-white was the characteristic colour in the seeds of all the white seeded sesame genotypes (Plate 10).

4.1.2.10 *1000 Seed Weight*

The mean value of 1000 seed weight ranged from 2.51g to 3.54g. The genotype T_{22} (RJS-44) had the highest value for 1000 seed weight. However, genotypes T_4 (3.48g), T_{19} (3.45g) and T_{17} (3.45g) were statistically on par with it. It was the least for T_{24} (IS-207) and statistically on par with the genotypes T_{14} (2.52g), T_{10} (2.57g), T_{20} (2.61g) and T_{12} (2.67g).

4.1.2.11 *Leaf Area*

Leaf area varied from 1834.17 cm^2 to 5842.67 cm^2 among the thirty genotypes evaluated. The maximum leaf area was found in the genotype T_7 (SI-205-1) and the genotypes T_4 (5696.67 cm^2) and T_3 (5499.00cm^2) were statistically on par with it. The minimum leaf area was observed in the genotype T_1 (Gu. Til 2) and the genotypes T_{16} (1871.00cm^2), T_{29} (1944.83cm^2), T_{14} (2063.67 cm^2) and T_{10} (2240.67cm^2) were statistically on par with T_1 (1834.178 cm^2).

4.1.2.12 *Dry Matter Production*

Among the thirty genotypes studied, genotype T_3 (VRI-3) registered the highest value for dry matter production (46.21g). It was statistically on par with the genotypes T_5 (43.47g), T_2 (42.86g), T_7 (42.13g) and T_{24} (41.17 g). The lowest amount of dry matter production was by the genotype T_{16} (PCU-39). The genotypes T_{29} (15.96 g), T_{22} (17.31g), T_8 (17.68g), T_{10} (17.86g) and T_{14} (18.84) were statistically on par with T_{16} (14.26g).

4.1.2.13 *Seed yield Plant^{-1}*

The range obtained for the character seed yield plant^{-1}wasfrom 2.97g to 15.27g (Fig.1). The genotype T_2 (Gu. Til 4) had maximum seed yield plant^{-1}and was statistically on par with the genotypes T_3 (14.34 g) and T_{21} (13.15 g). Whereas, T_{10} (SI-982) recorded minimum seed yield plant^{-1}and was statistically on par with the genotypes T_{23} (3.36 g), T_{17} (3.54 g), T_{29} (3.72 g), T_{16} (3.78 g), T_{25} (4.14 g), T_{14} (4.26g), T_8 (4.34g), T_{11} (4.72g), T_{30} (5.12g) and T_9 (5.23 g).

4.1.2.14 *Scoring of Pest and Diseases*

There was only negligible incidence of pest and diseases which were not scorable.

4.1.2.15 *Oil Content* (%)

The mean performance data for oil content ranged from 43.67% to 55.33%. The genotype T_{14} (PCU-37) showed the highest mean value for oil content which was statistically on par with the genotypes T_{21} (55.00%) and T_{18} (54.00%). The genotype T_{28} (AVT-14-6) exhibited the lowest mean value for oil content and was statistically on par with the genotypes T_{12} (44.67%) and T_6 (45.00%).

4.1.2.16 *Protein Content* (%)

For protein content, the genotype T_2 (Gu. Til 4) exhibited the highest mean value (26.66%) while T_6 (SI-44) recorded lowest mean value (19.54%). None of the genotypes were statistically on par with the highest and the lowest mean performance.

Fig.1. Mean performance of thirty genotypes of white seeded sesame for seed yield plant^{-1}(g)

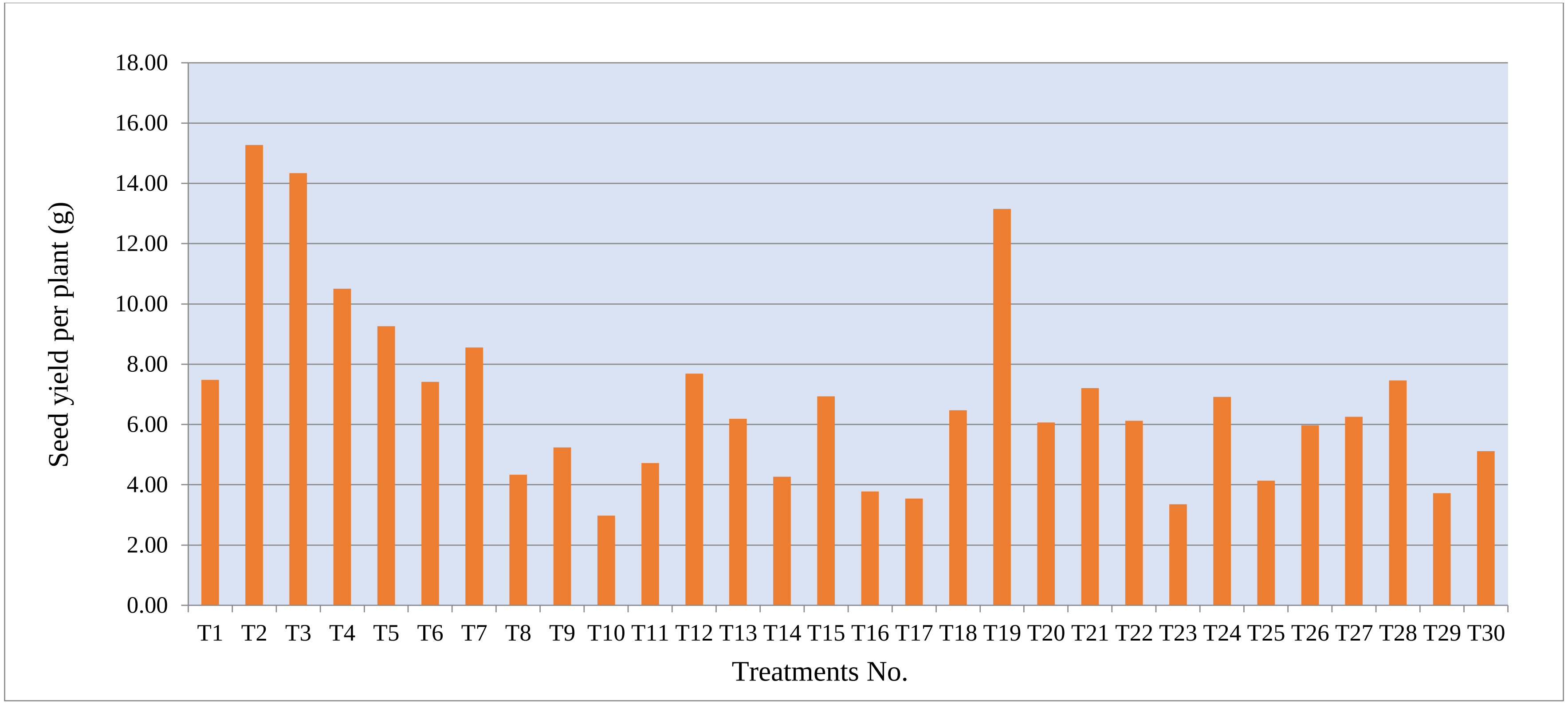
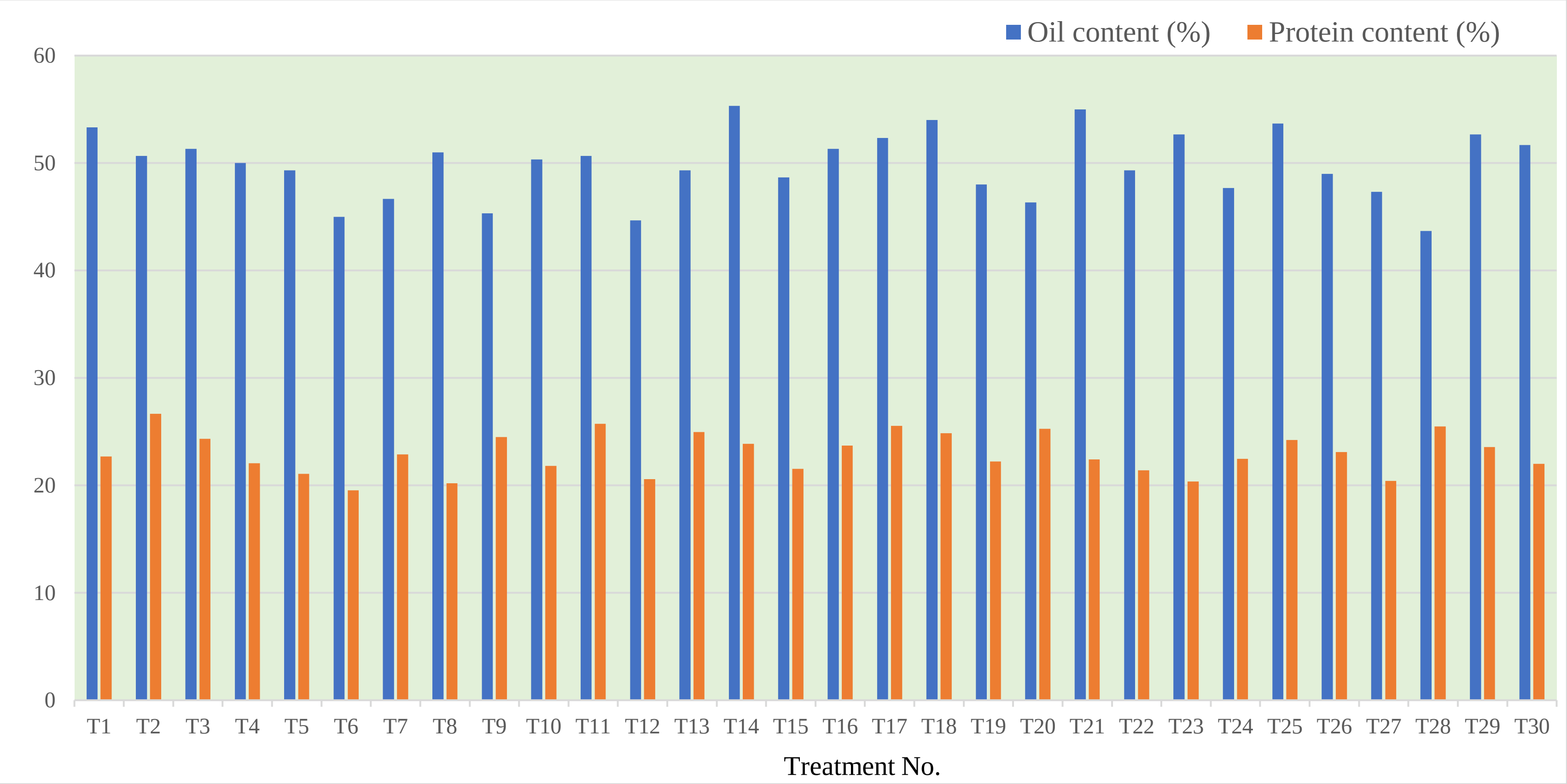
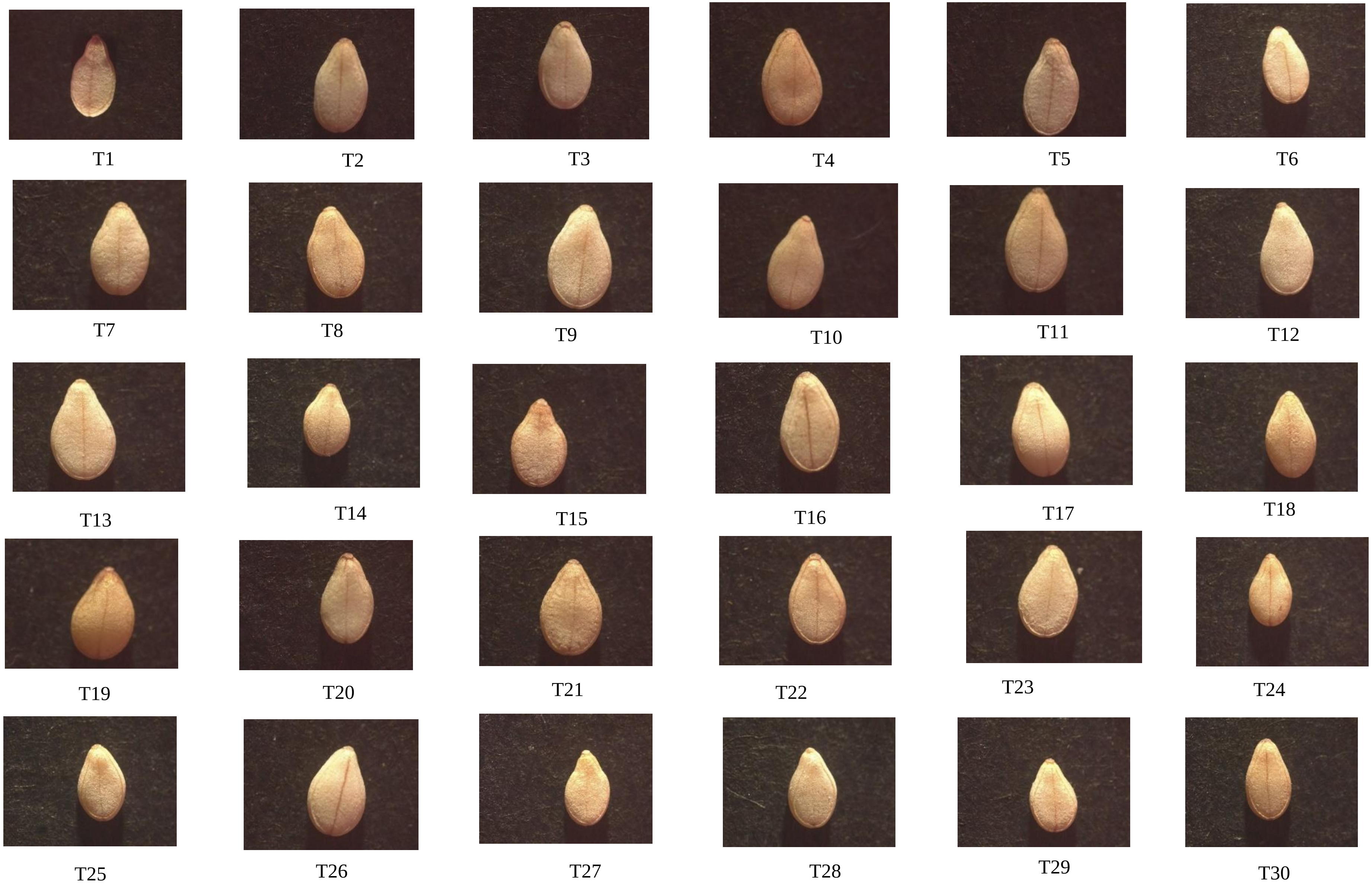


Fig.2. Mean performance of thirty genotypes of white seeded sesame for oil and protein content




T1 T2 T3 T4 T5 T6

T7 T8 T9 T10 T11 T12

T13 T14 T15 T16 T17 T18

T19 T20 T21 T22 T23 T24

T25 T26 T27 T28 T29 T30

Plate 10. Seed colour of the thirty sesame genotypes

Table 8. Mean performance of thirty white seeded sesame genotypes for fourteen characters

	X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**Seed colour**	**X9**	**X10**	**X11**	**X12**	**X13**	**X14**
T_1	36.00	80.00	98.33	0.80	2.40	65.93	2.64	56.33	Yellowish white	2.91	1834.17	32.64	7.48	53.33	22.69
T_2	31.33	78.00	145.40	2.47	2.73	70.87	2.87	84.33	Yellowish white	3.20	3358.67	42.86	15.27	50.67	26.66
T_3	48.67	84.67	137.80	6.07	1.00	83.33	2.78	72.67	Yellowish white	3.01	5499.00	46.21	14.34	51.33	24.33
T_4	34.67	80.67	129.93	3.07	1.00	62.27	2.71	61.67	Yellowish white	3.48	5696.67	31.53	10.50	50.00	22.05
T_5	31.67	79.00	155.73	3.67	1.00	72.80	2.62	59.33	Yellowish white	2.74	5062.50	43.47	9.26	49.33	21.06
T_6	37.67	81.00	118.40	3.13	1.00	49.13	2.56	76.33	Yellowish white	2.68	3410.00	27.26	7.41	45.00	19.54
T_7	32.33	81.67	126.40	3.87	1.00	50.93	2.96	78.67	Yellowish white	2.87	5842.67	42.13	8.56	46.67	22.87
T_8	34.33	83.00	94.40	2.00	1.00	28.27	2.29	68.67	Yellowish white	3.37	2854.67	17.68	4.34	51.00	20.19
T_9	36.33	86.00	129.87	4.93	1.00	35.93	2.79	67.33	Yellowish white	3.24	4369.33	26.44	5.23	45.33	24.50
T_{10}	32.00	80.67	110.07	2.07	1.00	32.13	2.21	62.00	Yellowish white	2.57	2240.67	17.86	2.97	50.33	21.82
T_{11}	37.00	78.67	127.73	2.00	1.33	36.60	2.79	55.67	Yellowish white	3.37	2781.67	37.39	4.72	50.67	25.73
T_{12}	29.67	77.67	134.20	2.27	1.00	67.60	2.55	60.33	Yellowish white	2.67	5216.50	40.08	7.69	44.67	20.59
T_{13}	32.33	80.00	117.27	3.20	1.00	48.53	2.70	64.67	Yellowish white	2.98	4067.17	30.76	6.19	49.33	24.97
T_{14}	36.00	82.33	108.33	1.87	1.00	34.80	2.60	74.67	Yellowish white	2.52	2063.67	18.84	4.26	55.33	23.86

Table 8. Continued

	X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**Seed colour**	**X9**	**X10**	**X11**	**X12**	**X13**	**X14**
T_{15}	40.33	87.00	125.93	2.20	1.40	40.80	2.48	76.67	Yellowish white	3.15	3844.00	30.59	6.94	48.67	21.53
T_{16}	29.00	78.33	89.07	1.80	1.00	33.60	2.37	67.33	Yellowish white	2.89	1871.00	14.26	3.78	51.33	23.69
T_{17}	35.33	83.00	139.20	2.67	1.00	30.47	3.17	54.00	Yellowish white	3.45	4163.67	32.67	3.54	52.33	25.55
T_{18}	34.00	84.33	141.20	2.93	1.00	48.07	2.41	62.33	Yellowish white	3.28	3629.50	37.81	6.47	54.00	24.85
T_{19}	37.00	80.33	146.53	3.13	1.20	69.33	3.16	68.33	Yellowish white	3.45	3287.67	39.42	13.15	48.00	22.23
T_{20}	30.33	79.00	128.73	3.47	1.00	53.60	2.94	71.33	Yellowish white	2.61	3094.17	38.16	6.07	46.33	25.26
T_{21}	41.33	87.00	117.80	3.73	1.00	40.73	2.90	78.00	Yellowish white	3.10	2675.33	29.54	7.21	55.00	22.40
T_{22}	38.33	82.00	104.07	2.00	1.00	39.00	2.73	59.67	Yellowish white	3.54	4061.00	17.31	6.12	49.33	21.41
T_{23}	33.33	80.00	128.33	2.73	1.00	30.87	2.98	65.67	Yellowish white	2.84	3198.50	20.72	3.36	52.67	20.36
T_{24}	43.33	81.33	144.73	4.60	1.00	52.60	2.85	80.67	Yellowish white	2.51	5384.33	41.17	6.91	47.67	22.46
T_{25}	34.33	82.33	132.47	4.00	1.00	46.87	2.73	52.67	Yellowish white	3.17	4732.00	30.33	4.14	53.67	24.21
T_{26}	37.33	83.00	126.07	3.27	1.00	38.40	2.27	64.00	Yellowish white	3.36	3428.00	28.76	5.97	49.00	23.10
T_{27}	44.67	85.33	123.73	2.80	1.00	55.53	2.30	58.67	Yellowish white	2.95	4558.67	24.65	6.25	47.33	20.42

Table 8. Continued

	X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**Seed colour**	**X9**	**X10**	**X11**	**X12**	**X13**	**X14**
T_{28}	28.67	80.00	135.33	4.60	1.00	42.60	2.85	75.33	Yellowish white	3.12	3036.00	36.37	7.46	43.67	25.49
T_{29}	35.67	84.33	109.73	2.87	1.00	30.47	2.45	68.00	Yellowish white	2.72	1944.83	15.96	3.72	52.67	23.57
T_{30}	32.33	79.67	114.20	2.27	1.00	36.40	2.61	62.67	Yellowish white	3.27	2646.00	29.41	5.12	51.67	21.99
Mean	35.51	81.68	124.70	3.02	1.14	47.62	2.68	66.93		3.03	3661.73	30.74	6.81	49.88	22.98
Range	28.67-48.67	77.67-87.00	89.07-155.73	0.80-6.07	1.00-2.73	28.27-83.33	2.21-3.17	52.67-84.33		2.51-3.54	1834.17-5842.67	14.26-46.21	2.97-15.27	43.67-55.33	19.54-26.66
S.E.	2.63	1.88	6.87	0.64	0.08	6.25	0.07	3.24		0.08	212.86	2.65	1.33	0.74	0.28
C.D. (5%)	5.28	3.78	13.81	1.29	0.16	12.55	0.15	6.50		0.16	427.84	5.32	2.67	1.48	0.55

X1	Days for 50 per cent blooming
X2	Maturity days
X3	Height of the plant (cm)
X4	Primary branches plant^{-1}
X5	Number of capsules per leaf axil
X6	Number of capsules plant^{-1}
X7	Capsule length (cm)
X8	Number of seeds capsule^{-1}
X9	1000 seed weight
X10	Leaf area
X11	Dry matter production
X12	Seed yield plant^{-1} (g)
X13	Oil content (%)
X14	Protein content (%)

S.E. : Standard Error

C.D. : Critical Difference

4.1.3 Genetic Parameters

To comprehend the degree to which the observed variation was due to genetic factors, the value of phenotypic and genotypic coefficients of variability, heritability (broad sense) and genetic advance for various characters were obtained and given in the Table 9.

4.1.3.1 *Phenotypic and Genotypic Coefficients of Variation*

The phenotypic coefficient of variation (PCV) was found high for seed yield plant^{-1} (49.72), primary branches plant^{-1} (42.26), number of capsules per leaf axil (36.27), number of capsules plant^{-1} (34.10), leaf area (33.17) and dry matter production (31.18). Moderate PCV was observed for days for 50 per cent blooming (15.09), height of the plant (14.07), number of seeds capsule^{-1} (13.50), and 1000 seed weight (10.68). Capsule length (9.87), protein content (8.38), oil content (6.43) and maturity days (3.97) had low PCV. The estimates of PCV were higher than GCV for all the traits studied which is an indicator of additive effect of the environment on the expression of the trait. The value of the genotypic coefficient of variation (GCV) ranged from 2.79 for maturity days to 43.59 for seed yield plant^{-1}. High GCV was observed for seed yield plant^{-1} (43.59), number of capsules per leaf axil (35.17), primary branches plant^{-1} (33.30), leaf area (32.39), number of capsules plant^{-1} (30.08), and dry matter production (29.35). Characters like height of the plant (12.34), number of seeds capsule^{-1} (12.13), days for 50 per cent blooming (12.06) and 1000 seed weight (10.16) showed moderate genotypic coefficient of variation. Low GCV was observed for capsule length (9.29), protein content (8.25), oil content (6.17) and maturity days (2.79).

4.1.3.2 *Heritability and Genetic Advance*

High heritability was obtained for protein content (96.94%) followed by leaf area (95.39%), number of capsules per leaf axil (94.02%), oil content (92.06%), 1000 seed weight (90.48%), capsule length (88.61%), dry matter production (88.58%), number of seeds capsule^{-1} (80.76%), number of capsules plant^{-1}

Fig.3. Phenotypic and genotypic coefficients of variation for fourteen characters in white seeded sesame

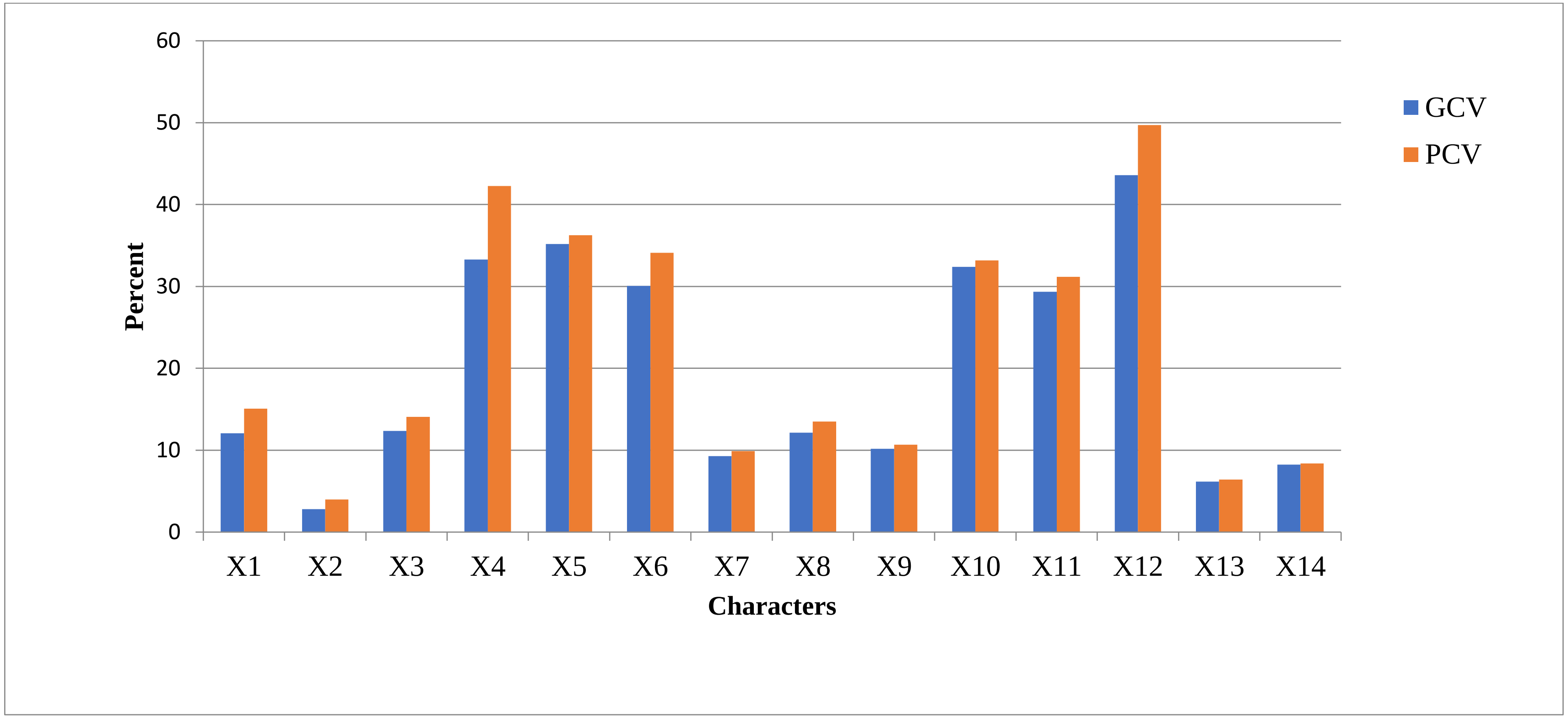


Fig.4. Heritability and genetic advance for fourteen characters in white seeded sesame

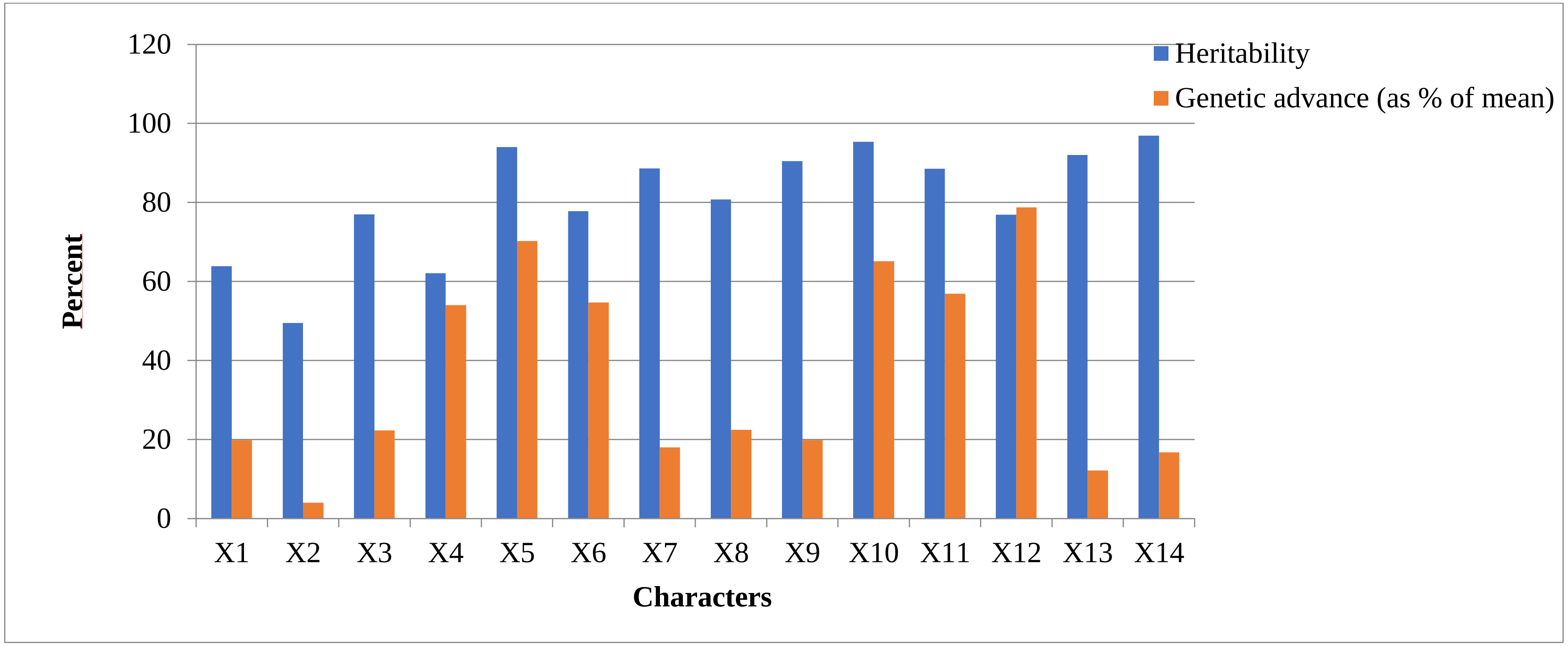


Table 9. Genetic parameters of thirteen characters in thirty genotypes of white seeded sesame

Sl. No.	**Characters**	**PCV**	**GCV**	**Heritability**	**GA (%) of mean**
1	Days for 50 per cent blooming	15.09	12.06	63.90	19.86
2	Maturity days	3.97	2.79	49.48	4.04
3	Height of the plant (cm)	14.07	12.34	77.00	22.31
4	Primary branches plant^{-1}	42.26	33.30	62.10	54.06
5	Number of capsules per leaf axil	36.27	35.17	94.02	70.26
6	Number of capsules plant^{-1}	34.10	30.08	77.81	54.66
7	Capsule length (cm)	9.87	9.29	88.61	18.01
8	Number of seeds capsule^{-1}	13.50	12.13	80.76	22.45
9	1000 seed weight	10.68	10.16	90.48	19.91
10	Leaf area	33.17	32.39	95.39	65.17
11	Dry matter production	31.18	29.35	88.58	56.90
12	Seed yield plant^{-1}	49.72	43.59	76.88	78.74
13	Oil content (%)	6.43	6.17	92.06	12.19
14	Protein content (%)	8.38	8.25	96.94	16.74

(77.81%), height of the plant (77.00%), seed yield plant^{-1} (76.88%), days for 50 per cent blooming (63.9%) and primary branches plant^{-1} (62.10%). Moderate heritability was shown by the trait maturity days (49.48%).

The highest estimate of genetic advance as per cent of mean obtained was 78.74% (seed yield plant^{-1}), followed by 70.26% (number of capsules per leaf axil), 65.17% (leaf area), 56.90% (dry matter production), 54.66% (number of capsules plant^{-1}), 54.06% (primary branches plant^{-1}), 22.45% (number of seeds capsule^{-1}), and 22.31% (height of the plant). In this study, moderate genetic advance was recorded for 1000 seed weight (19.91%), days for 50 per cent blooming (19.86%), capsule length (18.01%), protein content (16.74%) and oil content (12.19 %). Low genetic advance was observed for maturity days (4.04%). High heritability combined with high genetic advance as per cent of mean was recorded for seed yield plant^{-1}, number of capsules per leaf axil, leaf area, dry matter production, number of capsules plant^{-1}, primary branches plant^{-1}, number of seeds capsule^{-1} and height of the plant showed that these traits were controlled by additive genetic influences.

4.1.4 Correlation Studies

The association among yield and yield contributing traits including quality characters were studied by estimating genotypic and phenotypic correlation coefficients. The results of genotypic and phenotypic correlation coefficients which were estimated among the fourteen characters are presented in Table 10 and Table 11.

4.1.4.1 *Correlation between Yield and other Traits*

Highly significant and positive phenotypic and genotypic correlation was recorded between seed yield plant^{-1} and number of capsules plant^{-1} (0.863 and 0.859), dry matter production (0.610 and 0.747), height of the plant (0.438 and 0.578), number of capsules per leaf axil (0.419 and 0.460), leaf area (0.361 and 0.442), primary branches plant^{-1} (0.265 and 0.416), number of seeds capsule^{-1} (0.406 and 0.395) and capsule length (0.286 and 0.369). Days for 50 per cent blooming was found to have significant positive genotypic correlation with seed yield plant^{-1} (0.282). At genotypic level, oil content showed significant and negative genotypic correlation with seed yield plant^{-1} (- 0.230).

4.1.4.2 *Correlation among the yield components*

4.1.4.2.1 *Days for 50 Per cent Blooming*

Days for 50 per cent blooming exhibited significant positive correlation with maturity days (0.487 and 0.813), leaf area (0.232 and 0.284) and primary branches plant^{-1} (0.228 and 0.415) at both phenotypic and genotypic levels. Number of capsules plant^{-1} had significant positive correlation with days for 50 per cent blooming at genotypic level (0.246), while it was not significantly positive at phenotypic level (0.113)

4.1.4.2.2 *Maturity Days*

Maturity days exhibited highly significant positive correlation with days for 50 per cent blooming (0.487 and 0.813). However, primary branches plant^{-1} (0.404), oil content (0.233) and 1000 seed weight (0.228) also had significant and positive correlation with maturity days at genotypic level. It exhibited negative association with number of capsules per leaf axil (-0.213 and -0.291) at phenotypic and genotypic level. While, number of capsules plant^{-1} (-0.300) and dry matter production (-0.252) were also showed significant and negative correlation with maturity days at genotypic level.

4.1.4.2.3 *Height of the Plant*

It was observed that significant positive correlation existed between height of the plant and dry matter production (0.705 and 0.845), leaf area (0.555 and 0.634), number of capsules plant^{-1} (0.460 and 0.581), primary branches plant^{-1} (0.440 and 0.663), capsule length (0.439 and 0.519) and protein content (0.230 and 0.248) at both phenotypic and genotypic level. At both phenotypic and genotypic level, this trait demonstrated significant negative association with oil content (-0.259 and -0.286).

4.1.4.2.4 *Primary Branches Plant^{-1}*

Primary branches plant^{-1} showed significant positive correlation with leaf area (0.511 and 0.625), height of the plant (0.440 and 0.663), dry matter production (0.376 and 0.542), capsule length (0.284 and 0.398), number of seeds capsule^{-1} (0.273 and 0.365), number of capsules plant^{-1} (0.226 and 0.370), protein content (0.211 and 0.243) and days for 50 per cent blooming (0.228 and 0.415) at phenotypic and genotypic level. Significant negative association was observed with number of capsules per leaf axil (-0.321 and -0.394) and oil content (-0.243 and -0.382). Maturity days had significant and positive correlation with primary branches plant^{-1} at genotypic level (0.404).

4.1.4.2.5 *Number of Capsules per Leaf Axil*

Though number of capsules per leaf axil possessed positive correlation with number of capsules plant^{-1} (0.351 and 0.372), protein content (0.261 and 0.284) and dry matter production (0.238 and 0.265), it had negative correlation with primary branches plant^{-1} (-0.321 and -0.394), leaf area (-0.240 and -0.242) and maturity days (-0.213 and -0.291) at phenotypic and genotypic level.

4.1.4.2.6 *Number of Capsules Plant^{-1}*

Significant positive correlation was visible for number of capsules plant^{-1} with dry matter production (0.663 and 0.798) followed by height of the plant (0.460 and 0.581), leaf area (0.450 and 0.542), number of capsules per leaf axil (0.351 and 0.372), and primary branches plant^{-1} (0.226 and 0.370) at both phenotypic and genotypic level and significant negative association with oil content (-0.212 and -0.238) at phenotypic and genotypic level. Capsule length (0.252) and days for 50 per cent blooming showed significant positive correlation with number of capsules plant^{-1} at genotypic level while maturity days showed significant negative association at genotypic level (-0.300).

4.1.4.2.7 *Capsule Length*

Capsule length manifested significant and positive phenotypic and genotypic correlation with dry matter production (0.457 and 0.509), height of the plant (0.439 and 0.519), protein content (0.338 and 0.365), primary branches plant^{-1} (0.284 and 0.398) and leaf area (0.238 and 0.270). Number of capsules plant^{-1} recorded significant positive correlation with capsule length at genotypic level (0.252).

4.1.4.2.8 *Number of Seeds Capsule^{-1}*

At both genotypic and phenotypic level, primary branches plant^{-1} exhibited significant and positive association (0.273 and 0.365) with number of seeds capsule^{-1}. 1000 seed weight showed significant and negative association (-0.271 and -0.315) both in phenotypic and genotypic level. Whereas, oil content had significantly negative correlation with number of seeds capsule^{-1} at genotypic level (-0.237).

4.1.4.2.9 *1000 Seed Weight*

1000 seed weight recorded negative and significant association with number of seeds capsule^{-1} at phenotypic and genotypic level (-0.271 and -0.315). Maturity days expressed significantly positive association with 1000 seed weight at genotypic level.

4.1.4.2.10 *Leaf Area*

The trait leaf area was found to possess significantly positive phenotypic and genotypic correlation with height of the plant (0.555 and 0.634), dry matter production (0.548 and 0.566), primary branches plant^{-1} (0.511 and 0.625), number of capsules plant^{-1} (0.450 and 0.542), capsule length (0.238 and 0.270) and days for 50 per cent blooming (0.232 and 0.284). It showed significantly negative phenotypic and genotypic correlation with oil content (-0.379 and -0.404) and number of capsules per leaf axil (-0.240 and -0.242).

Table 10. Genotypic correlation coefficients

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	1	0.813**	0.096	0.415**	-0.059	0.246*	0.002	0.141	0.1	0.284**	0.084	0.282**	0.121	-0.204
X2		1	-0.049	0.404**	-0.291**	-0.300**	-0.196	0.129	0.228*	0.118	-0.252*	-0.165	0.233*	-0.103
X3			1	0.663**	0.031	0.581**	0.519**	0.129	0.075	0.634**	0.845**	0.578**	-0.286**	0.248*
X4				1	-0.394**	0.370**	0.398**	0.365**	-0.055	0.625**	0.542**	0.416**	-0.382**	0.243*
X5					1	0.372**	0.117	0.166	0.095	-0.242*	0.265*	0.460**	0.163	0.284**
X6						1	0.252*	0.092	-0.091	0.542**	0.798**	0.859**	-0.238*	0.007
X7							1	0.193	0.177	0.270*	0.509**	0.369**	-0.078	0.365**
X8								1	-0.315**	-0.017	0.191	0.395**	-0.237*	0.076
X9									1	0.098	0.039	0.173	0.115	0.195
X10										1	0.566**	0.442**	-0.404**	-0.115
X11											1	0.747**	-0.302**	0.329**
X12												1	-0.230*	0.119
X13													1	0.158
X14														1

X1	Days for 50 per cent blooming	X8	Number of seeds capsule^{-1}
X2	Maturity days	X9	1000 seed weight
X3	Height of the plant (cm)	X10	Leaf area
X4	Primary branches plant^{-1}	X11	Dry matter production
X5	Number of capsules per leaf axil	X12	Seed yield plant^{-1} (g)
X6	Number of capsules plant^{-1}	X13	Oil content (%)
X7	Capsule length (cm)	X14	Protein content (%)

** Significant at 1 per cent level

* Significant at 5 per cent level

Table 11. Phenotypic correlation coefficients

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	1	0.487**	0.087	0.228*	-0.089	0.113	0.004	0.101	0.07	0.232*	0.076	0.147	0.146	-0.165
X2		1	-0.06	0.197	-0.213*	-0.173	-0.109	0.133	0.166	0.073	-0.155	-0.066	0.174	-0.071
X3			1	0.440**	0.016	0.460**	0.439**	0.036	0.078	0.555**	0.705**	0.438**	-0.259*	0.230*
X4				1	-0.321**	0.226*	0.284**	0.273**	-0.031	0.511**	0.376**	0.265*	-0.243*	0.211*
X5					1	0.351**	0.105	0.148	0.096	-0.240*	0.238*	0.419**	0.135	0.261*
X6						1	0.187	0.115	-0.089	0.450**	0.663**	0.863**	-0.212*	0.01
X7							1	0.159	0.182	0.238*	0.457**	0.286**	-0.062	0.338**
X8								1	-0.271**	-0.007	0.165	0.406**	-0.194	0.061
X9									1	0.078	0.02	0.166	0.116	0.182
X10										1	0.548**	0.361**	-0.379**	-0.108
X11											1	0.610**	-0.271**	0.299**
X12												1	-0.194	0.111
X13													1	0.152
X14														1

X1	Days for 50 per cent blooming	X8	Number of seeds capsule^{-1}
X2	Maturity days	X9	1000 seed weight
X3	Height of the plant (cm)	X10	Leaf area
X4	Primary branches plant^{-1}	X11	Dry matter production
X5	Number of capsules per leaf axil	X12	Seed yield plant^{-1} (g)
X6	Number of capsules plant^{-1}	X13	Oil content (%)
X7	Capsule length (cm)	X14	Protein content (%)

** Significant at 1 per cent level

* Significant at 5 per cent level

4.1.4.2.11 *Dry Matter Production*

Dry matter production was found to be in significant positive association with height of the plant (0.705 and 0.845), number of capsules plant^{-1} (0.663 and 0.798), leaf area (0.548 and 0.566), capsule length (0.457 and 0.509), primary branches plant^{-1} (0.376 and 0.542), protein content (0.299 and 0.329) and number of capsules per leaf axil (0.238 and 0.265) at phenotypic and genotypic level. At genotypic and phenotypic level, it showed negative association with oil content (-0.271 and -0.302). While significantly negative association with maturity days (-0.252) was recorded at genotypic level.

4.1.4.2.12 *Oil Content* (%)

Oil content revealed significant and negative correlation with leaf area (-0.379 and -0.404), dry matter production (-0.271 and -0.302), height of the plant (-0.259 and -0.286), primary branches plant^{-1} (-0.243 and -0.382) and number of capsules plant^{-1} (-0.212 and -0.238) at phenotypic and genotypic level. In genotypic level, it showed significantly positive association with maturity days (0.233) and significantly negative association with number of seeds capsule^{-1}.

4.1.4.2.13 *Protein Content* (%)

Protein content expressed significantly positive phenotypic and genotypic correlation with capsule length (0.338 and 0.365) followed by dry matter production (0.299 and 0.329), number of capsules per leaf axil (0.261 and 0.284), height of the plant (0.230 and 0.248) and primary branches plant^{-1} (0.211 and 0.243).

4.1.5 Path Coefficient Analysis

The genotypic correlation coefficients of seed yield plant^{-1} with yield contributing characters were partitioned into different components to find the direct and indirect effect of each character to yield (Table 7). The traits *viz.*, height of the plant, primary branches plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, leaf area and dry matter production which manifested high genotypic correlation with yield were selected for path analysis. Path diagram showing the direct and indirect effects of the component characters on seed yield plant^{-1} is given in Fig 1.

4.1.5.1 *Direct effects*

Number of capsules plant^{-1} (0.7576) recorded the highest positive direct effect on seed yield plant^{-1} followed by number of seeds capsule^{-1} (0.2693), number of capsules per leaf axil (0.2004) and height of the plant (0.1435). The characters *viz.*, capsule length (0.0863), primary branches plant^{-1} (0.0632) and leaf area (0.0357) showed a negligible positive direct effect on seed yield plant^{-1}.

4.1.5.2 *Indirect effects*

Height of the plant had positive indirect effect on seed yield plant^{-1} mainly through high indirect effect of number of capsules plant^{-1} (0.4398). Height of the plant registered negligible indirect effect through all other character.

Primary branches exerted a positive indirect effect on seed yield plant^{-1} through number of capsules plant^{-1} (0.2805). While the indirect effects of number of branches through all other characters were negligible.

Number of capsules per leaf axil showed positive indirect effect through number capsules plant^{-1} (0.2822). It had negligible indirect effect on seed yield plant^{-1} through the remaining characters.

Number of capsules plant^{-1} had low and negative indirect effect through dry matter production (-0.1455). It had negligible indirect effect on seed yield plant^{-1} through other traits.

Capsule length had negligible indirect effect on seed yield plant^{-1} through all the characters except number of capsules plant^{-1} which was low and positive (0.1908).

Number of seeds capsule^{-1} recorded negligible indirect effect on seed yield plant^{-1} through all the characters.

The indirect effect of leaf area *via* number of capsules plant^{-1} was high and positive (0.4052) which nearly accounted for the total genotypic correlation with yield (0.442). It showed negligible indirect effect on seed yield plant^{-1} through the

Table 12. Path analysis (direct diagonal / indirect off diagonal)

	HP	PBP	NCL	NCP	CL	NSC	LA	DMP	**Genotypic correlation co-efficiencies**
HP	**0.1435**	0.0419	0.0062	0.4398	0.0448	0.0346	0.0215	-0.1540	0.578**
PBP	0.0951	**0.0632**	-0.0790	0.2805	0.0344	0.0982	0.0230	-0.0987	0.416**
NCL	0.0045	-0.0249	**0.2004**	0.2822	0.0101	0.0447	-0.0087	-0.0483	0.460**
NCP	0.0833	0.0234	0.0746	**0.7576**	0.0217	0.0247	0.0191	-0.1455	0.859**
CL	0.0745	0.0251	0.0235	0.1908	**0.0863**	0.0520	0.0095	-0.0928	0.369**
NSC	0.0185	0.0230	0.0333	0.0694	0.0167	**0.2693**	-0.0002	-0.0349	0.395**
LA	0.0864	0.0407	-0.0488	0.4052	0.0229	-0.0014	**0.0357**	-0.1050	0.442**
DMP	0.1212	0.0342	0.0531	0.6044	0.0439	0.0515	0.0206	**-0.1823**	0.747**

Residual effect = 0.1301

HP	Height of the plant (cm)
PBP	Primary branches plant^{-1}
NCL	Number of capsules per leaf axil
NCP	Number of capsules plant^{-1}
CL	Capsule length (cm)
NSC	Number of seeds capsule^{-1}
LA	Leaf area
DMP	Dry matter production

remaining characters. Dry matter production exhibited high positive indirect effect *via* number of capsules plant^{-1} (0.6044).

The residual effect obtained was 0.1301 which indicated that selected traits explain the total correlation well and the remaining characters have only minor contribution in the variability of seed yield.

4.2 EXPERIMENT II - SELECTION OF PARENTS AND HYBRIDIZATION

Based on the statistical analysis among the thirty genotypes screened in experiment I, five high seed yielding genotypes were selected as lines *viz.*, Gu. Til 4, VRI-3, Punjab Til No.2, RT-346 and PCU-42 and three genotypes with high oil content were selected as testers *viz.*, PCU-37, PCU-41 and NIC-8322. Hybridization programme was conducted in line x tester mating design.

4.3 EXPERIMENT III - EVALUATION OF PARENTS AND F_1 HYBRIDS

The salient features of the results obtained from the current investigation on evaluation of parents F_1 hybrids along with the check, SVPR1 through line x tester method are presented under following captions:

4.3.1 Analysis of variance for the experimental design
4.3.2 Mean performance of parents and hybrids
4.3.3 Combining ability analysis
4.3.3.1 Analysis of variance for combining ability
4.3.3.2 Combining ability effects
4.3.4 Estimation of heterosis

4.3.1 **Analysis of Variance for the Experimental Design**

Analysis of variance for parents and crosses are presented in Table 13. The genotypic effect was significant for all the characters studied, suggesting the presence of adequate variability in the experimental material. Most of the traits showed significant variations among parents as well as hybrids except days for 50

Table 13. Analysis of variance (mean square) for line x tester design for seed yield and its contributing characters in white seeded sesame

Sources	df	Mean squares for											
		Days for 50 per cent blooming	Maturity days	Height of the plant (cm)	Primary branches plant^{-1}	Number of capsules per leaf axil	Number of capsules plant^{-1}	Capsule length (cm)	Number of seeds capsule^{-1}	1000 seed weight	Leaf area	Dry matter production	Seed yield plant^{-1} (g)
Replication	2	0.275	0.565	18.061	0.475	0.012	73.59	0.018	22.449	0.004	6189.938	8.572	14.486
Treatments	22	53.179**	50.984**	966.924**	6.359**	1.089**	2105.069**	0.119**	216.097**	0.344**	9433003.378**	756.437**	188.470**
Parents	7	91.042**	22.280*	790.207**	3.636**	0.722**	893.537**	0.114**	112.833**	0.286**	7730421.522**	228.645**	50.999**
Parents *vs* Crosses	1	0.873	1.383	2065.802**	13.136**	0.398**	6759.824**	0.005**	0.978	0.085*	15851193.870**	2016.865**	328.553**
Crosses	14	37.984**	68.879**	976.791**	7.236**	1.323**	2378.352**	0.130**	283.095**	0.391**	9825852.129**	930.303**	247.199**
Error	44	12.306	9.247	77.051	0.251	0.007	80.197	0.012	22.313	0.02	53584.783	18.435	5.469

** Significant at 1 per cent level

* Significant at 5 per cent level

per cent blooming (parents *vs* crosses), maturity days (parents *vs* crosses) and number of seeds capsule^{-1} (parents *vs* crosses).

4.3.2. **Mean Performance of Parents and Hybrids**

The mean performance of parents and hybrids for all the twelve traits are presented in Table 14. The character-wise results of mean performance are as under:

4.3.2.1 *Days for 50 Per cent Blooming*

Among the five lines used, the line RT-346 had the lowest days for 50 per cent blooming (29.67 days) and line VRI-3 had the highest days for 50 per cent blooming 47.33). Whereas, among the testers, tester PCU-41 had the lowest days for 50 per cent blooming (32.33 days) and tester NIC-8322 had the highest days for 50 per cent blooming (39.67). Among the hybrids, the cross RT-346 x PCU-41 was the earliest for days for 50 per cent blooming (31 days) and the cross VRI-3 x PCU-41 was the most late for days for 50 per cent blooming (44.67 days). The data on overall mean performance depicted that hybrid (36.44 days) took slightly more days to attain 50 per cent flowering than parents (36.21 days).

4.3.2.2 *Maturity Days*

Maturity days ranged between 80.33 days (RT-346) and 87.33 days (VRI-3) among the lines and from 85.33 days (PCU-41) to 88 days (NIC-8322) among the testers. Among the hybrids, the cross RT-346 x PCU-41 had the lowest maturity days (77.67 days) and VRI-3 x PCU-41 had the highest maturity days (95.00 days). The overall mean performance showed that hybrids (84.24 days) had slightly less days to mature than parents (84.54 days).

4.3.2.3 *Height of the Plant*

Among the lines, Gu. Til 4 was the shortest (141.67 cm) and RT-346 was the tallest (166.87 cm). Whereas among the testers, PCU-37 was the shortest (114.93 cm) and PCU -41 was the tallest (137.00 cm). The mean performance of hybrids varied from 125.80 cm (Gu. Til 4 x PCU-37) to 181.60 cm (RT-346 x PCU-37). The magnitude of mean data for height of the plant indicated that the generated hybrids (153.28) are taller than the parents (141.73 cm).

4.3.2.4 *Primary Branches Plant^{-1}*

The mean performance of lines for primary branches plant^{-1} ranged from 2.67 (Punjab Til No.2) to 5.73(VRI-3), whereas for testers, it ranged from 2.07 (PCU-37) to 3.53 (NIC-8322). Among the hybrids, the cross Gu. Til 4 x PCU-37 had the lowest number of primary branches plant^{-1} (1.60) and the cross VRI-3 x PCU-41 had the highest number of primary branches plant^{-1} (7.27). The magnitude of mean data of parents and hybrids for primary branches plant^{-1} showed that hybrids had higher number of primary branches plant^{-1} (4.26) than parents (3.34).

4.3.2.5 *Number of Capsules per Leaf Axil*

The lines VRI-3, Punjab Til No.2 and RT-346 had only one capsule per leaf axil whereas PCU-42 (1.13) and Gu. Til 4 (2.40) had more than one capsule per leaf axil. All the testers used had only one capsule per leaf axil. Among the hybrids, the cross Gu. Til 4 x PCU-37 had the highest number of capsules per leaf axil (2.73). All the other hybrids except PCU-42 x PCU-41, PCU-42 x PCU-37, Gu. Til 4 x PCU-41, Gu. Til 4 x PCU-37, Gu. Til 4 x NIC-8322 recorded only one capsule per leaf axil. The overall mean of parents and hybrids for number of capsules per leaf axil was 1.19 and 1.35 respectively.

4.3.2.6 *Number of Capsules Plant^{-1}*

Among the lines, Punjab Til No.2 had recorded the lowest number of capsules plant^{-1} (70.53) and VRI-3 had recorded the highest number of capsules plant^{-1} (90.60). Among testers used, PCU-37 had recorded the lowest number of capsules plant^{-1} (41.26) and PCU-41 had recorded the highest number of capsules plant^{-1} (57.60). Among the crosses, VRI-3 x PCU-37 had recorded the lowest number of capsules plant^{-1} (54.46) and Gu. Til 4 x NIC-8322 had recorded the highest number of capsules plant^{-1} (145.60). The mean data for number of capsules plant^{-1} revealed that hybrids had a greater number of capsules plant^{-1} (87.17) compared to parents (66.39) used in the experiment.

4.3.2.7 *Capsule Length*

The capsule length ranged from 2.58 cm (RT-346) to 3.12 cm (PCU-42) among lines and from 2.47 cm (PCU-41) to 2.8 cm (NIC-8322) among testers. Among the hybrids generated, it ranged from 2.38 cm (RT-346 x NIC-8322) to 3.11 cm (PCU-42 x PCU-37). The data from mean value for capsule length showed that parents (2.71 cm) and hybrids (2.73 cm) had almost equal length for the trait.

4.3.2.8 *Number of Seeds Capsule^{-1}*

Among the lines, RT-346 had lowest number of seeds capsule^{-1} (61.67) and Gu. Til 4 had highest number of seeds capsule^{-1} (80.67). Among the testers used, PCU-41 had lowest number of seeds capsule^{-1} (65.00) and NIC-8322 had highest number of seeds capsule^{-1} (72.67). Among hybrids, RT-346 x PCU-41 had lowest number of seeds capsule^{-1} (52.00) and Gu. Til 4 x PCU-41 had highest number of seeds capsule^{-1}(86.00). The data on overall mean performance indicated that hybrids (68.66) had slightly high number of seeds capsule^{-1} than parents (68.42).

4.3.2.9 *Seed Colour*

The seed colour of parents and hybrids were studied and it was found that yellowish white was the characteristic colour in the seeds of all parents and crosses.

4.3.2.10 *1000 Seed Weight*

Among lines used, the mean value for thousand weight was found to be lowest in RT-346 (2.80 g) and highest in PCU-42 (3.57 g). In the case of testers used PCU-37 and PCU-41 expressed lowest (2.65 g) and highest (3.34 g) 1000 seed weight respectively. Among the hybrids generated, PCU-42 x PCU-41 recorded minimum 1000 seed weight (2.67 g) and PCU-42 x PCU-37 recorded maximum 1000 seed weight (3.82 g). The mean performance of parents and hybrids showed that hybrids had slightly high 1000 seed weight (3.24 g) than parents (3.17 g)

4.3.2.11 *Leaf Area*

The minimum leaf area was recorded by PCU-42 (2896.167cm^2) and the maximum leaf area was recorded by Punjab Til No.2 (6004.50 cm^2) among the lines. Among the testers PCU-37 recorded minimum leaf area (2286.5 cm^2) and PCU-41 recorded maximum leaf area (3892 cm^2). The leaf area of hybrids ranged from 867.33 cm^2 (Gu. Til 4 x PCU-37) to 7238.50 cm^2(RT-346 x PCU-37). The mean data of parents and hybrids for leaf area showed that parents had more leaf area (4036.60 cm^2) compared to the hybrids (3030.27 cm^2) generated.

4.3.2.12 *Dry Matter Production*

Among the lines, Punjab Til No.2 had recorded minimum dry matter production (39.66 g) and VRI-3 had recorded the maximum dry matter production (52.37 g). while testers PCU-41 had recorded the minimum and maximum dry matter production (45.12 g). Among the hybrids, VRI-3 x PCU-37 had recorded minimum dry matter production (25.18 g) and RT-346 x PCU-37 had recorded maximum dry matter production (81.24 g). The mean data of parents and hybrids for number of capsules plant^{-1} revealed that hybrids had maximum dry matter production (52.65 g) than parents (41.30 g).

4.3.2.13 *Seed yield Plant^{-1}*

The seed yield plant^{-1} ranged from 11.22 g (RT-346) to 17.46 g (Gu. Til 4) in lines and 5.08g (PCU-37) to 9.21 g (PCU-41) in testers. Among hybrids, the cross PCU-42 x PCU-41 (5.64 g) recorded the lowest seed yield plant^{-1} was whereas the cross Gu. Til 4 x NIC-8322 (32.98 g) recorded the highest seed yield plant^{-1}. The magnitude of mean data of parents and hybrids for seed yield plant^{-1} showed that hybrids had more seed yield plant^{-1} (16.09 g) than parents (11.51 g).

4.3.2.14 *Scoring of pest and diseases*

There was only negligible incidence of pest and diseases which were not scorable.

Table 14. Mean performance of parents and hybrids for twelve characters in white seeded sesame

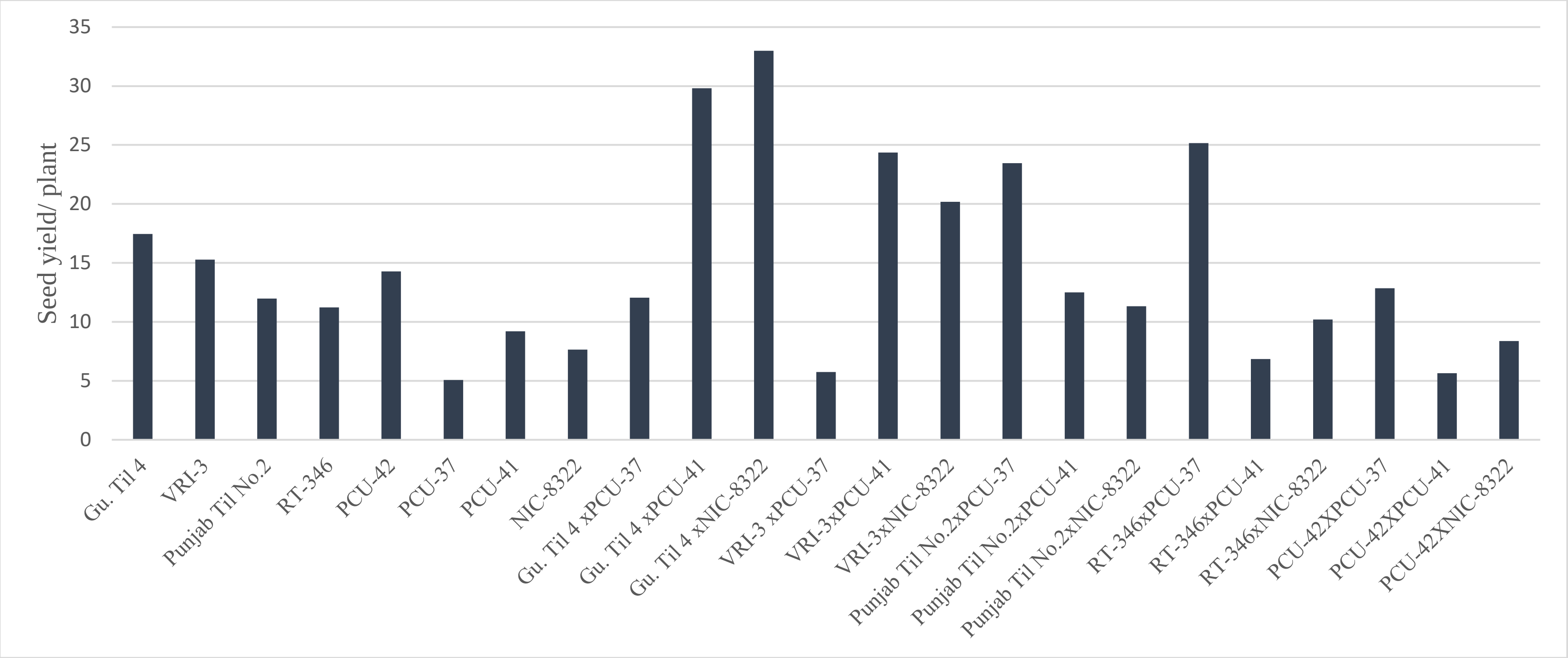
	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	TSW	LA	DMP	SYP
Parents												
Lines												
Gu. Til 4	32.67	81.33	141.67	2.93	2.40	76.27	2.76	80.67	3.32	3036.67	45.05	17.46
VRI-3	47.33	87.33	152.47	5.73	1.00	90.60	2.69	66.33	3.14	5967.83	52.37	15.28
Punjab Til No.2	35.33	83.33	145.60	2.67	1.00	70.53	2.61	63.00	3.39	6004.50	39.66	11.97
RT-346	29.67	80.33	166.87	3.80	1.00	78.13	2.58	61.67	2.80	5692.33	48.07	11.22
PCU-42	34.67	84.67	150.13	2.87	1.13	72.67	3.12	70.33	3.57	2896.17	41.62	14.27
Mean of Lines	35.93	83.40	151.35	3.60	1.31	77.64	2.75	68.40	3.24	4719.50	45.35	14.04
Testers												
PCU-37	38.00	86.00	114.93	2.07	1.00	41.27	2.65	67.67	2.65	2286.50	24.58	5.08
PCU-41	32.33	85.33	137.00	3.13	1.00	57.60	2.47	65.00	3.34	3892.00	45.12	9.21
NIC-8322	39.67	88.00	125.13	3.53	1.00	44.07	2.80	72.67	3.18	2516.83	33.94	7.65
Mean of Testers	36.67	86.44	125.69	2.91	1.00	47.64	2.64	68.44	3.06	2898.44	34.55	7.31
Mean of parents	36.21	84.54	141.73	3.34	1.19	66.39	2.71	68.42	3.17	4036.60	41.30	11.52
Hybrids												
Gu. Til 4 x PCU-37	35.33	81.33	125.80	1.60	2.73	75.40	2.62	62.33	3.41	867.33	34.24	12.06
Gu. Til 4 x PCU-41	41.33	92.00	176.27	5.27	2.47	122.13	3.02	86.00	3.28	4865.17	78.51	29.81
Gu. Til 4 x NIC-8322	37.00	89.33	165.67	6.33	2.67	145.60	2.93	77.33	3.54	3761.67	66.32	32.98
VRI-3 x PCU-37	36.00	80.67	134.80	2.00	1.00	54.47	2.56	59.33	2.87	1767.50	25.18	5.74
VRI-3 x PCU-41	44.67	95.00	156.13	7.27	1.00	128.20	2.65	68.67	3.21	3384.83	54.40	24.37

Table 14. Continued

	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	TSW	LA	DMP	SYP
VRI-3 x NIC-8322	40.33	82.67	144.67	4.67	1.00	86.53	2.74	76.67	3.36	1956.17	47.62	20.18
Punjab Til No.2 x PCU-37	38.00	87.00	160.53	5.47	1.00	95.93	2.86	82.33	3.42	5862.33	64.82	23.46
Punjab Til No.2 x PCU-41	36.33	85.00	167.40	3.87	1.00	61.27	2.90	73.67	3.58	2065.50	55.14	12.50
Punjab Til No.2 x NIC-8322	32.67	79.00	129.73	5.20	1.00	72.80	2.66	64.67	3.04	1394.00	30.72	11.32
RT-346 x PCU-37	34.00	82.00	181.60	4.80	1.00	112.73	2.78	66.33	3.76	7238.50	81.24	25.16
RT-346 x PCU-41	31.00	77.67	155.00	3.67	1.00	67.13	2.63	52.00	3.18	1547.67	42.45	6.84
RT-346 x NIC-8322	35.00	84.67	147.27	4.27	1.00	86.80	2.38	62.33	2.72	2674.00	58.06	10.20
PCU-42 x PCU-37	33.67	82.67	174.07	3.13	1.27	63.60	3.11	76.33	3.82	3936.50	72.63	12.85
PCU-42 x PCU-41	37.33	81.33	151.80	2.80	1.13	56.73	2.68	64.67	2.67	1896.67	36.12	5.64
PCU-42 x NIC-8322	34.00	83.33	128.47	3.53	1.00	78.27	2.40	57.33	2.84	2236.17	42.36	8.37
Mean of hybrids	36.44	84.24	153.28	4.26	1.35	87.17	2.73	68.67	3.25	3030.27	52.65	16.10

DFB	Days for 50 per cent blooming	CL	Capsule length (cm)
MD	Maturity days	NSC	Number of seeds capsule^{-1}
HP	Height of the plant (cm)	TSW	1000 seed weight
PBP	Primary branches plant^{-1}	LA	Leaf area
NCL	Number of capsules per leaf axil	DMP	Dry matter production
NCP	Number of capsules plant^{-1}	SYP	Seed yield plant^{-1} (g)

Fig.6. Mean performance of seed yield plant^{-1} (g) in parents and hybrids



4.3.3 Combining Ability Analysis

4.3.3.1 *Analysis of Variance for Combining Ability*

The analysis of variance for combining ability for all the twelve characters in sesame for seed yield and its components are depicted in Table 15. Partitioning of variance due to the crosses demonstrated that the mean squares due to line were significant only for number of capsules per leaf axil while in the case of testers mean square was not significant for any of the characters. In the case of line x tester interaction, the mean squares were highly significant for all the characters studied.

4.3.3.1.1 *Magnitude of Additive and Dominance Variances*

The estimates of variances due to additive and dominance components were presented in Table 16. The estimates of additive variance were higher than the corresponding dominance variance for number of capsules per leaf axil which denoted the prevalence of additive gene action. For all the remaining characters, estimates of additive components were lower than the corresponding dominance components *i.e.,* days for 50 per cent blooming, maturity days, height of the plant, primary branches plant^{-1}, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight, leaf area, dry matter production and seed yield plant^{-1} indicated the preponderance of non-additive gene action. The ratio between additive and dominance variance was less than one for all the traits except number of capsules per leaf axil.

4.3.3.2 *Combining Ability Effects*

The general combining ability (*gca*) effects of parents and specific combining ability (*sca*) effects of hybrids for all the twelve characters are presented in the Tables 17 to 22.

4.3.3.2.1 *Days for 50 Per cent Blooming*

The general combining ability of lines ranged from -3.11 (RT-346) to 3.89 (VRI-3) and that of testers were from -1.04 (PCU-37) to 1.69 (PCU-41). The estimates of *gca* effects of parents indicated that the line; VRI-3 (3.89) exerted

Table 15. ANOVA for combining ability in LxT

Sources	df	Mean squares for											
		Days for 50 per cent blooming	Maturity days	Height of the plant (cm)	Primary branches plant^{-1}	Number of capsules per leaf axil	Number of capsules plant^{-1}	Capsule length (cm)	Number of seeds capsule^{-1}	1000 seed weight	Leaf area	Dry matter production	Seed yield plant^{-1} (g)
Lines	4	66.556	58.189	315.552	3.89	4.574**	2924.661	0.102	326.056	0.149	2700721.73	514.376	301.542
Testers	2	32.689	47.289	1285.368	8.47	0.028	690.955	0.128	11.667	0.523	9650080.02	168.492	2.958
Lines x Testers	8	25.022**	79.622**	1230.266**	8.600**	0.021**	2527.047**	0.145**	329.472**	0.479**	13432360.360**	1328.718**	281.088**
Error	44	12.306	9.247	77.051	0.251	0.007	80.197	0.012	22.313	0.02	53584.78	18.435	5.469

** Significant at 1 per cent level

* Significant at 5 per cent le

Table 16. Magnitude of Additive and Dominance Variances

Sl. No	**Characters**	**σ^2D (Additive)**	**σ^2H (Dominance)**	**σ^2D/σ^2H**
1	Days for 50 per cent blooming	0.9165	4.2389	0.2162
2	Maturity days	-0.7596	23.4584	-0.0324
3	Height of the plant (cm)	-17.9225	384.4051	-0.0466
4	Primary branches plant^{-1}	-0.0965	2.7832	-0.0347
5	Number of capsules per leaf axil	0.0921	0.0047	19.4898
6	Number of capsules plant^{-1}	-10.5138	815.6167	-0.0129
7	Capsule length (cm)	-0.0010	0.0444	-0.0234
8	Number of seeds capsule^{-1}	-3.2792	102.3864	-0.0320
9	1000 seed weight	-0.0062	0.1531	-0.0407
10	Leaf area	-255005.6	4459592	-0.0572
11	Dry matter production	-28.1708	436.7613	-0.0645
12	Seed yield plant^{-1} (g)	-2.3962	91.8729	-0.0261

significant and positive *gca* effects, indicating it is a good general combiner from the flowering point of view. In the case of testers, none of the testers displayed significant *gca* effect in either direction while among the lines, RT-346 (-3.11) had significant and negative *gca* effect.

The specific combining ability (*sca*) effects of hybrids were observed between -4.02 (RT-346 x PCU-41) and 3.38(Punjab Til No.2 x PCU-37). None of the hybrids showed significant *sca* effect in either of the direction.

4.3.3.2.2 *Maturity Days*

The lines recorded *gca* effects ranging from -2.80 (RT-346) to 3.31 (Gu. Til 4) and the testers ranged from -1.51 (PCU-37) to 1.96 (PCU-41) for maturity days. Among the parents, the line; RT-346 (-2.80) was the good general combiner as it exhibited significant and negative *gca* effect. None of the testers showed significant *gca* effect in negative direction. Whereas, one line Gu. Til 4 (3.31) and one tester PCU-41 (1.96) produced significant and positive *gca* effect.

The *sca* effects of hybrids were observed between -5.73 (RT-346 x PCU-41) and 6.93 (VRI-3 x PCU-41). Total four out of fifteen crosses exhibited significant and negative *sca* effect. The cross RT-346 x PCU-41 (-5.73) exerted the highest, significant negative *sca* effect followed by Gu. Til 4 x PCU-37 (-4.71), Punjab Til No.2 x NIC-8322 (-4.22) and VRI-3 x PCU-37 (-3.93). apart from these, three out of fifteen crosses exhibited significant and positive *sca* effect. The cross VRI-3 x PCU-41 (6.93) recorded the highest, significant and positive *sca* effect followed by Punjab Til No.2 x PCU-37 (4.84) and RT-346 x NIC-8322 (3.67).

4.3.3.2.3 *Height of the Plant*

Height of the plant showed *gca* effect ranging from-8.08 (VRI-3) to 8.01(RT-346) in case of lines and from -10.12 (NIC-8322) to 8.04 (PCU-41) for testers. Estimates of *gca* effect revealed that the parental line RT-346 (8.01) and the tester PCU-41 (8.04) exerted significant and positive *gca* effect and were regarded as good general combiners for height of the plant. On the other hand, the line;

Table 17. Combining ability effects of parents (*gca*) and hybrids (*sca*) for Days for 50 per cent blooming and Maturity days

	Days for 50 Per cent Blooming				**Maturity Days**			
Testers	PCU-37	PCU-41	NIC-8322	*gca* of lines	PCU-37	PCU-41	NIC-8322	*gca* of lines
Lines	*sca* of hybrids				*sca* of hybrids			
Gu. Til 4	-1.51^{ns}	1.76^{ns}	-0.24^{ns}	1.44^{ns}	-4.71*	2.49^{ns}	2.22^{ns}	3.31**
VRI-3	-3.29^{ns}	2.6^{ns}	0.64^{ns}	3.89**	-3.93*	6.93**	-3.00^{ns}	1.87^{ns}
Punjab Til No.2	3.38^{ns}	-1.02^{ns}	-2.36^{ns}	-0.78^{ns}	4.84**	-0.62^{ns}	-4.22*	-0.58^{ns}
RT-346	1.71^{ns}	-4.02^{ns}	2.31^{ns}	-3.11*	2.07^{ns}	-5.73**	3.67*	-2.8**
PCU-42	-0.29^{ns}	0.64^{ns}	-0.36^{ns}	-1.44^{ns}	1.73^{ns}	-3.07^{ns}	1.33^{ns}	-1.8^{ns}
gca of testers	-1.04^{ns}	1.69^{ns}	-0.64^{ns}		-1.51^{ns}	1.96*	-0.44^{ns}	

	Days for 50 Per cent Blooming	**Maturity Days**	**Days for 50 Per cent Blooming**			**Maturity Days**	
				CD (5%)	CD (1%)	CD (5%)	CD (1%)
SE (*gca* of lines)	1.17	1.01	Lines	2.36	3.15	2.04	2.72
SE (*gca* of testers)	0.91	0.79	Testers	1.83	2.45	1.59	2.13
SE (*sca* effects)	2.03	1.76	Hybrids	4.09	5.46	3.55	4.73

VRI-3 (-8.08) and the tester NIC-8322 showed significant and negative *gca* effect for height of the plant.

The *sca* effects of hybrids were found to be between -32.19 (Gu. Til 4 xPCU-37) and 20.54 (PCU-42 x PCU-37). The significant and positive *sca* effect were observed in four out of fifteen crosses examined. The cross PCU-42 x PCU-37 (20.54) ranked first by recording the maximum significant and positive *sca* effect followed by Gu. Til 4 x NIC-8322 (19.88), RT-346 x PCU-37 (18.23), and Gu. Til 4 x PCU-41 (12.32). The cross Gu. Til 4 x PCU-37 (-32.19) recorded highest, significant but negative *sca* effect followed by RT-346 x PCU-41 (-14.33), PCU-42 x NIC-8322 (-12.86), Punjab Til No.2 x NIC-8322 (-12.70) and VRI-3 x PCU-37 (-12.48).

4.3.3.2.4 *Primary Branches Plant^{-1}*

The lines and testers recorded *gca* effect ranging from -1.10 (PCU-42) to 0.59 (Punjab Til No.2) and from -0.86 (PCU-37) to 0.54 (NIC-8322) respectively for primary branches plant^{-1}. In the present investigation the two lines, *viz*; Punjab Til No.2 (0.59) and VRI-3 (0.39) and one tester *viz.*, NIC-8322 (0.54) were found to be good general combiners as they displayed significant and positive *gca* effects. Whereas the parental line PCU-42 (-1.10) and the tester PCU-37 (-0.86) exerted significant but negative *gca* effect.

The *sca* effects of hybrids were observed between -1.94 (Gu. Til 4 x PCU-37) and 2.31 (VRI-3 x PCU-41). Five crosses *viz.*, VRI-3 x PCU-41 (2.31), Punjab Til No.2 x PCU-37 (1.48), RT-346 x PCU-37 (1.41), Gu. Til 4 x NIC-8322 (1.39) and PCU-42 x PCU-37 (0.84) were identified as the best specific combiners as they exerted significant and positive *sca* effects. On the other hand, the crosses Gu. Til 4 x PCU-37 (-1.94), VRI-3 x PCU-37 (-1.79), Punjab Til No.2 x PCU-41 (-1.29), RT-346 x PCU-41 (-0.89) and PCU-42 x PCU-41 (-0.67) showed negatively significant *sca* effects.

Table 18. Combining ability effects of parents (*gca*) and hybrids (*sca*) for Height of the plant (cm) and Primary branches plant^{-1}

	Height of the Plant				**Primary Branches Plant^{-1}**			
Testers	PCU-37	PCU-41	NIC-8322	*gca* of lines	PCU-37	PCU-41	NIC-8322	*gca* of lines
Lines	*sca* of hybrids							
Gu. Til 4	-32.19**	12.32*	19.88**	2.63^{ns}	-1.94**	0.55^{ns}	1.39**	0.14^{ns}
VRI-3	-12.48*	2.89^{ns}	9.59^{ns}	-8.08**	-1.79**	2.31**	-0.52^{ns}	0.39**
Punjab Til No.2	5.90^{ns}	6.80^{ns}	-12.70*	-0.72^{ns}	1.48**	-1.29**	-0.19^{ns}	0.59**
RT-346	18.23**	-14.33**	-3.90^{ns}	8.01**	1.41**	-0.89**	-0.52^{ns}	-0.01^{ns}
PCU-42	20.54**	-7.68^{ns}	-12.86*	-1.84^{ns}	0.84**	-0.67*	-0.16^{ns}	-1.10**
gca of testers	2.08^{ns}	8.04**	-10.12**		-0.86**	0.32^{ns}	0.54**	

	Height of the Plant	**Primary Branches Plant^{-1}**		**Height of the Plant**		**Primary Branches Plant^{-1}**	
				CD (5%)	CD (1%)	CD (5%)	CD (1%)
SE (*gca* of lines)	2.93	0.17	Lines	5.90	7.88	0.34	0.46
SE (*gca* of testers)	2.27	0.13	Testers	4.57	6.11	0.26	0.35
SE (*sca* effects)	5.07	0.29	Hybrids	10.22	13.64	0.58	0.78

4.3.3.2.5 *Number of Capsules per Leaf Axil*

For number of capsules per leaf axil, the line Gu. Til 4 (1.27) and the tester PCU-37 (0.05) were found to be good general combiners as they exhibited significant and positive *gca* effect. Apart from these four parental lines *viz.*, VRI-3 (-0.35), Punjab Til No.2 (-0.35), RT-346 (-0.35) and PCU-42 (-0.22) recorded significant but negative *gca* effect. None of the testers recorded negatively significant *gca* effect.

The *sca* effects of hybrids were observed between -0.12 (Gu. Til 4 x PCU-41, PCU-42 x NIC-8322) to 0.08 (PCU-42 x PCU-37). None of the crosses reported positively significant *sca* effect while the cross Gu. Til 4 x PCU-41 (-0.12) recorded negatively significant *sca* effect.

4.3.3.2.6 *Number of Capsules Plant^{-1}*

The general combining ability of lines showed a range of -20.97 (PCU-42) to 27.20 (Gu. Til 4) and that of testers were from -6.75 (PCU-37) to 6.83 (NIC-8322). For number of capsules plant^{-1}, the parental line Gu. Til 4 (27.20) and the tester NIC-8322 (6.83) were found to be good general combiners as they showed significant positive *gca* effects. While lines *viz.*, PCU-42 (-20.97), Punjab Til No.2 (-10.51) and the tester PCU-37 (-6.75) recorded significant but negative *gca* effect.

The significant and positive *sca* effects were observed in four out of fifteen crosses studied. The cross VRI-3 x PCU-41 (38.55) registered the highest, significant and positive *sca* effect followed by RT-346 x PCU-37 (30.59), Punjab Til No.2 x PCU-37 (26.01) and Gu. Til 4 x NIC-8322 (24.40). Whereas significant but negative *sca* effect were noted in five out of fifteen crosses. The cross Gu. Til 4 x PCU-37 (-32.23) displayed the highest, significant and negative *sca* effect followed by VRI-3 x PCU-37 (-28.52), RT-346 x PCU-41 (-21.68), Punjab Til No.2 x PCU-41 (-15.32) and Punjab Til No.2 x NIC-8322 (-10.69)

Table 19. Combining ability effects of parents (*gca*) and hybrids (*sca*) for Number of capsules leaf per axil and Number of capsules plant^{-1}

	Number of Capsule per Leaf Axils				**Number of Capsules Plant^{-1}**			
Testers	PCU-37	PCU-41	NIC-8322	*gca* of lines	PCU-37	PCU-41	NIC-8322	*gca* of lines
Lines	*sca* of hybrids				*sca* of hybrids			
Gu. Til 4	0.06^{ns}	-0.12*	0.06^{ns}	1.27**	-32.23**	7.84^{ns}	24.40**	27.20**
VRI-3	-0.05^{ns}	0.03^{ns}	0.02^{ns}	-0.35**	-28.52**	38.55**	-10.03^{ns}	2.56^{ns}
Punjab Til No.2	-0.05^{ns}	0.03^{ns}	0.02^{ns}	-0.35**	26.01**	-15.32**	-10.69*	-10.51**
RT-346	-0.05^{ns}	0.03^{ns}	0.02^{ns}	-0.35**	30.59**	-21.68**	-8.92^{ns}	1.72^{ns}
PCU-42	0.08^{ns}	0.03^{ns}	-0.12*	-0.22**	4.15^{ns}	-9.39^{ns}	5.24^{ns}	-20.97**
gca of testers	0.05*	-0.03^{ns}	-0.02^{ns}		-6.75**	-0.08^{ns}	6.83**	

	Number of Capsule per Leaf Axils	**Number of Capsules Plant^{-1}**		**Number of Capsule per Leaf Axils**		**Number of Capsules Plant^{-1}**	
				CD (5%)	CD (1%)	CD (5%)	CD (1%)
SE (*gca* of lines)	0.02	2.99	Lines	0.04	0.05	6.02	8.04
SE (*gca* of testers)	0.02	2.31	Testers	0.04	0.05	4.65	6.21
SE (*sca* effects)	0.05	5.17	Hybrids	0.10	0.13	10.42	13.91

4.3.3.2.7 *Capsule Length*

Capsule length exhibited *gca* effect ranging from -0.13 (RT-346) to 0.13 (Gu. Til 4) in the case of lines and from -0.11(NIC-8322) to 0.06 (PCU-37) for testers. Among the parental lines, Gu. Til 4 (0.13) and Punjab Til No.2 (0.08) were found to be good general combiners while among the testers, PCU-37 (0.06) was found to be a good general combiner as they showed significant and positive *gca* effects. The lines *viz.*, RT-346 (-0.13) and VRI-3 (-0.08) and the tester NIC-8322 (-0.11) exhibited significant and negative *gca* effects.

The *sca* effects of hybrids for capsule length were observed between -0.22 (PCU-42 x NIC-8322) and 0.32 (PCU-42 x PCU-37). Four out of fifteen crosses exhibited significant and positive *sca* effect. The highest, significant and positive *sca* effect was observed in the cross PCU-42 x PCU-37 (0.32) followed by VRI-3 x NIC-8322 (0.20), Gu. Til 4 x NIC-8322 (0.18) and RT-346 x PCU-37 (0.13). Whereas negative *sca* effect was noted in three out of fifteen crosses. The cross Gu. Til 4 x PCU-37 (-0.29) displayed the highest, significant and negative *sca* effect followed by PCU-42 x NIC-8322 (-0.22) and VRI-3 x PCU-37 (-0.15).

4.3.3.2.8 *Number of Seeds Capsule^{-1}*

The general combining ability of lines showed a range of -8.44 (RT-346) to 6.56 (Gu. Til 4) and that of testers were from -1.00 (NIC-8322) to 0.67 (PCU-37). The two parental lines *viz.*, Gu. Til 4 (6.56) and Punjab Til No.2 (4.89) were observed to be good general combiners as they showed significant and positive *gca* effects. Besides, RT-346 (-8.44) recorded significant and negative *gca* effect. None of the testers reported significant *gca* effect in either direction

The significant and positive effects for number of seeds capsule^{-1} were exhibited by five crosses. The highest significant and positive *sca* effects were observed in the cross Gu. Til 4 x PCU-41 (10.44) followed by PCU-42 x PCU-37 (9.56), VRI-3 x NIC-8322 (9.44), Punjab Til No.2 x PCU-37 (8.11) and RT-346 x PCU-37 (5.44). Whereas, significant but negative *sca* effect were also noted in five out of fifteen crosses. The cross Gu. Til 4 x PCU-37 (-13.56) displayed the highest,

Table 20. Combining ability effects of parents (*gca*) and hybrids (*sca*) for Capsule length (cm) and Number of seeds capsule^{-1}

	Capsule Length				**Number of Seeds Capsule^{-1}**			
Testers	PCU-37	PCU-41	NIC-8322	*gca* of lines	PCU-37	PCU-41	NIC-8322	*gca* of lines
Lines	*sca* of hybrids				*sca* of hybrids			
Gu. Til 4	-0.29**	0.12^{ns}	0.18**	0.13**	-13.56**	10.44**	3.11^{ns}	6.56**
VRI-3	-0.15*	-0.05^{ns}	0.20**	-0.08*	-9.56**	0.11^{ns}	9.44**	-0.44^{ns}
Punjab Til No.2	-0.004^{ns}	0.04^{ns}	-0.04^{ns}	0.08*	8.11**	-0.22^{ns}	-7.89**	4.89**
RT-346	0.13*	-0.014^{ns}	-0.11^{ns}	-0.13**	5.44*	-8.56**	3.11^{ns}	-8.44**
PCU-42	0.32**	-0.10^{ns}	-0.22**	0.001^{ns}	9.56**	-1.78^{ns}	-7.78**	-2.56^{ns}
gca of testers	0.06*	0.05^{ns}	-0.11**		0.67^{ns}	0.33^{ns}	-1.00^{ns}	

	Capsule Length	**Number of Seeds Capsule^{-1}**		**Capsule length**		**Number of Seeds Capsule^{-1}**	
				CD (5%)	CD (1%)	CD (5%)	CD (1%)
SE (*gca* of lines)	0.04	1.57	Lines	0.08	0.11	3.16	4.22
SE (*gca* of testers)	0.03	1.22	Testers	0.06	0.08	2.46	3.28
SE (*sca* effects)	0.06	2.73	Hybrids	0.12	0.16	5.50	7.34

significant and negative *sca* effect followed by VRI-3 x PCU-37 (-9.56), RT-346 x PCU-41 (-8.56), Punjab Til No.2 x NIC-8322 (-7.89) and PCU-42 x NIC-8322 (-7.78).

4.3.3.2.9 ***1000 Seed Weight***

The lines and testers recorded *gca* effect ranging from -0.14 (PCU-42) to 0.16 (Gu. Til 4) and from -0.15 (NIC-8322) to 0.21 (PCU-37) respectively for 1000 seed weight. Estimates of *gca* effect showed that the two parental lines *viz.*, Gu. Til 4 (0.16) and Punjab Til No.2 (0.102) and the tester PCU-37 (0.21) exerted significant and positive *gca* effect and were regarded as good general combiners for the trait. On the other hand, the lines PCU-42 (-0.14) and VRI-3 (-0.10) and the tester NIC-8322 (-0.15) showed significant and negative *gca* effect for 1000 seed weight.

The *sca* effects of hybrids were observed between -0.49 (VRI-3 xPCU-37) and 0.5 (PCU-42 x PCU-37). The significant and positive *sca* effects were observed in five out of fifteen crosses evaluated. The crosses *viz.*, PCU-42 x PCU-37 (0.5), VRI-3 x NIC-8322 (0.36), RT-346 x PCU-37 (0.33), Punjab Til No.2 x PCU-41 (0.29) and Gu. Til 4 x NIC-8322 (0.28) were identified as the best specific combiners as they exerted significant and positive *sca* effects. On the other hand, the crosses VRI-3 x PCU-37 (-0.49), PCU-42 x PCU-41 (-0.38), RT-346 x NIC-8322 (-0.35) and Gu. Til 4 x PCU-37 (-0.21) showed negatively significant *sca* effects.

4.3.3.2.10 ***Leaf Area***

Leaf area showed *gca* effect ranging from -660.77 (VRI-3) to 789.79 (RT-346) in case of lines and from -625.87 (NIC-8322) to 904.17 (PCU-37) for testers. In the present study, the lines *viz;* RT-346 (789.79) and the tester PCU-37 (904.17) were found to be good general combiners as they displayed significant and positive *gca* effects. Whereas, two parental lines VRI-3 (-660.77) and PCU-42 (-340.49) and two testers NIC-8322 (-625.87) and PCU-41 (-278.30) exerted significant but negative *gca* effect.

Table 21. Combining ability effects of parents (*gca*) and hybrids (*sca*) for 1000 seed weight and Leaf area

	1000 Seed Weight				**Leaf Area**			
Testers	PCU-37	PCU-41	NIC-8322	*gca* of lines	PCU-37	PCU-41	NIC-8322	*gca* of lines
Lines	*sca* of hybrids				*sca* of hybrids			
Gu. Til 4	-0.21*	-0.07^{ns}	0.28**	0.16**	-3201.56**	1978.74**	1222.81**	134.46^{ns}
VRI-3	-0.49**	0.13^{ns}	0.36**	-0.10*	-1506.17**	1293.63**	212.53^{ns}	-660.77**
Punjab Til No.2	-0.14^{ns}	0.29**	-0.16^{ns}	0.102*	1850.89**	-763.48**	-1087.41**	77.01^{ns}
RT-346	0.33**	0.022^{ns}	-0.35**	-0.03^{ns}	2514.28**	-1994.09**	-520.19**	789.79**
PCU-42	0.50**	-0.38**	-0.13^{ns}	-0.14**	342.56*	-514.81**	172.26^{ns}	-340.49**
gca of testers	0.21**	-0.06^{ns}	-0.15**		904.17**	-278.30**	-625.87**	

	1000 Seed Weight	**Leaf Area**		**1000 Seed Weight**		**Leaf Area**	
				CD (5%)	CD (1%)	CD (5%)	CD (1%)
SE (*gca* of lines)	0.05	77.16	Lines	0.10	0.13	155.48	207.56
SE (*gca* of testers)	0.04	59.77	Testers	0.08	0.11	120.44	160.78
SE (*sca* effects)	0.08	133.65	Hybrids	0.16	0.22	269.30	359.52

The *sca* effects of hybrids were observed between -3201.56 (Gu. Til 4 x PCU-37) and 2514.28 (RT-346 x PCU-37). The significant and positive *sca* effects were observed in six out of fifteen crosses investigated. The highest significant and positive *sca* effects were observed in the cross RT-346 x PCU-37 (2514.28) followed by Gu. Til 4 x PCU-41 (1978.74), Punjab Til No.2 x PCU-37 (1850.89), VRI-3 x PCU-41 (1293.63) and Gu. Til 4 x NIC-8322 (1222.81). Whereas significant but negative *sca* effect were also noted in seven out of fifteen crosses. The cross Gu. Til 4 x PCU-37 (-3201.56) displayed the highest, significant and negative *sca* effect followed by RT-346 x PCU-41 (-1994.09), VRI-3 x PCU-37 (-1506.17), Punjab Til No.2 x NIC-8322 (-1087.41), Punjab Til No.2 x PCU-41 (-763.48), RT-346 x NIC-8322 (-520.19) and PCU-42 x PCU-41 (-514.81).

4.3.3.2.11 *Dry Matter Production*

The general combining ability of lines showed a range of -10.25 (VRI-3) to 7.93 (RT-346) and that of testers was from -3.64 (NIC-8322) to 2.97 (PCU-37). For dry matter production, the two parental lines RT-346 (7.93) and Gu. Til 4 (7.04) and the tester PCU-37 (2.97) were found to be good general combiners as they showed significant positive *gca* effects. While line, VRI-3 (-10.25) the tester NIC-8322 (-3.64) recorded a significant but negative *gca* effect.

The *sca* effects of hybrids for capsule length was observed between -28.42 (Gu. Til 4 x PCU-37) and 19.29 (PCU-42 x PCU-37). Seven out of fifteen crosses exhibited significant and positive *sca* effect. The highest, significant and positive *sca* effect was observed in the cross PCU-42 x PCU-37 (19.29) followed by Gu. Til 4 x PCU-41 (18.15), RT-346 x PCU-37 (17.69), Punjab Til No.2 x PCU-37 (11.63), VRI-3 x PCU-41 (11.33), Gu. Til 4 x NIC-8322 (10.27) and VRI-3 x NIC-8322 (8.86). Whereas, negative *sca* effect was noted in five out of fifteen crosses. The cross Gu. Til 4 x PCU-37 (-28.42) displayed the highest, significant and negative *sca* effect followed by VRI-3 x PCU-37 (-20.19) RT-346 x PCU-41 (-18.80), Punjab Til No.2 x NIC-8322 (-15.87) and PCU-42 x PCU-41 (-14.92).

Table 22. Combining ability effects of parents (*gca*) and hybrids (*sca*) for Dry matter production and Seed yield plant^{-1}

	Dry Matter Production				**Seed Yield Plant^{-1}**			
Testers	PCU-37	PCU-41	NIC-8322	*gca* of lines	PCU-37	PCU-41	NIC-8322	*gca* of lines
Lines	*sca* of hybrids				*sca* of hybrids			
Gu. Til 4	-28.42**	18.15**	10.27**	7.04**	-12.64**	5.13**	7.52**	8.85**
VRI-3	-20.19**	11.33**	8.86**	-10.25**	-10.78**	7.87**	2.90*	0.67^{ns}
Punjab Til No.2	11.63**	4.24^{ns}	-15.87**	-2.43^{ns}	7.95**	-2.99*	-4.95**	-0.34^{ns}
RT-346	17.69**	-18.80**	1.11^{ns}	7.93**	11.34**	-6.96**	-4.38**	-2.03*
PCU-42	19.29**	-14.92**	-4.37^{ns}	-2.29^{ns}	4.14**	-3.05*	-1.09^{ns}	-7.15**
gca of testers	2.97*	0.67^{ns}	-3.64**		-0.25^{ns}	-0.27^{ns}	0.51^{ns}	

	Dry Matter Production	**Seed Yield Plant^{-1}**		**Dry Matter Production**		**Seed Yield Plant^{-1}**	
				CD (5%)	CD (1%)	CD (5%)	CD (1%)
SE (*gca* of lines)	1.43	0.78	Lines	2.88	3.85	1.57	2.10
SE (*gca* of testers)	1.11	0.60	Testers	2.24	2.99	1.21	1.61
SE (*sca* effects)	2.48	1.35	Hybrids	5.00	6.67	2.72	3.63

4.3.3.2.12 *Seed Yield Plant^{-1}*

The range of *gca* effects for seed yield plant^{-1} varied from -7.15 (PCU-42) to 8.85 (Gu. Til 4) in lines and from -0.27 (PCU-41) to 0.51 (NIC-8322) in testers. Among the parents, the line; Gu. Til 4 (8.85) was the good general combiner as it exhibited significant and positive *gca* effect. The lines PCU-42 (-7.15) and RT-346 (-2.03) exhibited significant and negative *gca* effect. None of the testers showed significant *gca* effect in either direction.

The *sca* effects of hybrids were observed between -12.64 (Gu. Til 4 x PCU-37) and 11.34 (RT-346 x PCU-37). Seven out of fifteen crosses exhibited significant and positive *sca* effect. The cross RT-346 x PCU-37 (11.34) exerted the highest, significant positive *sca* effect followed by Punjab Til No.2 x PCU-37 (7.95), VRI-3 x PCU-41 (7.87), Gu. Til 4 x NIC-8322 (7.52), Gu. Til 4 x PCU-41(5.13), PCU-42 x PCU-37 (4.14) and VRI-3 x NIC-8322 (2.90). Apart from these, seven out of fifteen crosses showed significant and negative *sca* effect. The cross Gu. Til 4 x PCU-37 (-12.64) recorded the highest, significant and negative *sca* effect followed by VRI-3 x PCU-37 (-10.78), RT-346 x PCU-41 (-6.96), Punjab Til No.2 x NIC-8322 (4.95), RT-346 x NIC-8322(-4.38), PCU-42 x PCU-41(-3.05) and Punjab Til No.2 x PCU-41 (-2.99).

4.3.4 Estimation of heterosis

The measurement of heterosis was performed as per cent increase or decrease of F_1 hybrid over mid parent (MP), better parent (BP)) and standard check (SC) values for different traits in sesame. The results on heterosis over mid parental value (relative heterosis), over better parent (heterobeltiosis) and over the standard variety (standard heterosis), are given in Table 23 to Table 28. The standard heterosis was estimated based on comparison to check variety; SVPR1 for all traits. The results are furnished character wise under:

4.3.4.1 *Days for 50 Per cent Blooming*

Out of fifteen crosses, the cross Gu. Til 4 x PCU-41 exhibited significant and desirable (positive) relative heterosis (27.18%). The heterosis over midparent ranged from -15.63% (VRI-3 x PCU-37) to 27.18 % (Gu. Til 4 x PCU-41).

The significant heterobeltiosis was recorded in the cross Gu. Til 4 x PCU-41 (26.53%). Heterobeltiosis ranged from -23.94% (VRI-3 x PCU-37) to 26.53% (Gu. Til 4 x PCU-41).

The data from standard heterosis depicted that none of the cross had significant positive standard heterosis in desired direction from all the fifteen crosses evaluated for this particular trait. The standard heterosis ranged from -30.07% (RT-346 x PCU-41) to 0.76 % (VRI-3 x PCU-41). The highest but nonsignificant standard heterosis in desired way was recorded in the cross VRI-3 x PCU-41 (0.76%).

4.3.4.2 *Maturity Days*

The significant heterosis over mid- parent in desired (negative) direction was exhibited by the crosses, Punjab Til No.2 x NIC-8322 (-7.78%), VRI-3 x PCU-37 (-6.92%), and RT-346 x PCU-41 (-6.24%). Relative heterosis ranged from -7.78% (Punjab Til No.2 x NIC-8322) to 10.40% (Gu. Til 4 x PCU-41).

The highest magnitude of significant heterobeltiosis in desired direction was recorded in the cross Punjab Til No.2 x NIC-8322 (-10.23%) followed by RT-346 x PCU-41(-8.98%) and VRI-3 x PCU-37 (-7.63%).

The spectrum of standard heterosis for maturity days ranged from -8.63% (RT-346 x PCU-41) to 11.76% (VRI-3 x PCU-41). The highest significant standard heterosis in expected way was recorded in the cross VRI-3 x PCU-41 (-8.63%) followed by Punjab Til No.2 x NIC-8322 (-7.06%).

Table 23. Per centage of relative heterosis (RH) heterobeltiosis (HB) and standard heterosis (SH) for days for 50 per cent blooming and maturity days

Sl. No.	Hybrids	Days for 50 per cent blooming			Maturity days		
		RH	HB	SH	RH	HB	SH
1	Gu. Til 4 x PCU-37	0.00	-7.02	-20.29**	-2.79	-5.43	-4.31
2	Gu. Til 4 x PCU-41	27.18**	26.53**	-6.76	10.40**	7.81*	8.24*
3	Gu. Til 4 x NIC-8322	2.30	-6.72	-16.54*	5.51*	1.52	5.10
4	VRI-3 x PCU-37	-15.63*	-23.94**	-18.79**	-6.92**	-7.63*	-5.10
5	VRI-3 x PCU-41	12.13	-5.63	0.76	10.04**	8.78**	11.76**
6	VRI-3 x NIC-8322	-7.28	-14.79*	-9.02	-5.70*	-6.06*	-2.75
7	Punjab Til No.2 x PCU-37	3.64	0.00	-14.28*	2.76	1.16	2.35
8	Punjab Til No.2 x PCU-41	7.39	2.83	-18.04**	0.79	-0.39	0.00
9	Punjab Til No.2 x NIC-8322	-12.89	-17.65*	-26.31**	-7.78**	-10.23**	-7.06*
10	RT-346 x PCU-37	0.49	-10.53	-23.30**	-1.40	-4.65	-3.53
11	RT-346 x PCU-41	0.00	-4.12	-30.07**	-6.24*	-8.98**	-8.63**
12	RT-346 x NIC-8322	0.96	-11.76	-21.05**	0.59	-3.79	-0.39
13	PCU-42 x PCU-37	-7.34	-11.40	-24.05**	-3.13	-3.88	-2.75
14	PCU-42 x PCU-41	11.44	7.69	-15.78*	-4.31	-4.69	-4.31
15	PCU-42 x NIC-8322	-8.52	-14.29	-23.30**	-3.47	-5.30	-1.96
	S.E.	2.48	2.86	2.86	2.15	2.48	2.48
	CD at 5%	5.01	5.78	5.78	4.34	5.01	5.01
	CD at 1%	6.67	7.69	7.69	5.78	6.67	6.67
	Range	-15.63 – 27.18	-23.94 – 26.53	-30.07 - 0.76	-7.78 - 10.4	-10.23 - 8.78	-8.63 - 11.76
	No. of crosses in desirable direction	1	1	0	3	3	3

4.3.4.3 *Height of the Plant*

Out of fifteen crosses, six crosses exhibited significant and desirable(positive) relative heterosis. The heterosis over mid parent ranged from -6.66% (PCU-42 x NIC-8322) to 31.34% (PCU-42 x PCU-37). The highest significant relative heterosis was recorded in the cross PCU-42 x PCU-37 (31.34%) followed by RT-346 x PCU-37 (28.89%), Gu. Til 4 x PCU-41 (26.27%), Gu. Til 4 x NIC-8322 (24.19%), Punjab Til No.2 x PCU-37 (23.23 %) and Punjab Til No.2 x PCU-41 (18.25%).

The spectrum of heterobeltiosis varied from -14.43% (PCU-42 x NIC-8322) to 24.42% (Gu. Til 4 x PCU-41). Out of fifteen crosses evaluated, six crosses exhibited significant heterobeltiosis in positive direction. The highest significant heterobeltiosis in desired way was recorded in the cross Gu. Til 4 x PCU-41 (24.42%) followed by Gu. Til 4 x NIC-8322 (16.94%), PCU-42 x PCU-37 (15.94%), Punjab Til No.2 x PCU-41 (14.97%), Punjab Til No.2 x PCU-37 (10.26%), and RT-346 x PCU-37 (8.83%)

Among the fifteen crosses, three had displayed significant standard heterosis in positive direction for height of the plant. The magnitude of standard heterosis was recorded from -20.21% (Gu. Til 4 x PCU-37) to 15.18% (RT-346 x PCU-37) The highest magnitude of standard heterosis in expected direction was exhibited by the cross RT-346 x PCU-37 (15.18%) followed by Gu. Til 4 x PCU-41 (11.79%) and PCU-42 x PCU-37 (10.40%).

4.3.4.4 *Primary Branches Plant^{-1}*

The range of relative heterosis for primary branches plant^{-1} was recorded from -48.72% (VRI-3 x PCU-37) to 130.99% (Punjab Til No.2 x PCU-37). the significant heterosis over mid parent in desired way was recorded in seven out of fifteen crosses evaluated. The highest magnitude of significant and positive relative heterosis was recorded in the cross Punjab Til No.2 x PCU-37 (130.99%) followed by Gu. Til 4 x NIC-8322 (95.88%), Gu. Til 4 x PCU-41 (73.63%), Punjab Til No.2 x NIC-8322

Table 24. Per centage of relative heterosis (RH) heterobeltiosis (HB) and standard heterosis (SH) for height of the plant (cm) and primary branches plant^{-1}

Sl. No.	Hybrids	Height of the plant (cm)			Primary branches plant^{-1}		
		RH	HB	SH	RH	HB	SH
1	Gu. Til 4 x PCU-37	-1.95	-11.20*	-20.21**	-36.00*	-45.39**	-68.00**
2	Gu. Til 4 x PCU-41	26.27**	24.42**	11.79*	73.63**	68.26**	5.33
3	Gu. Til 4 x NIC-8322	24.19**	16.94**	5.07	95.88**	79.41**	26.67**
4	VRI-3 x PCU-37	0.82	-11.59*	-14.50**	-48.72**	-65.10**	-60.00**
5	VRI-3 x PCU-41	7.68	2.40	-0.97	63.91**	26.82**	45.33**
6	VRI-3 x NIC-8322	4.23	-5.12	-8.25	0.72	-18.56*	-6.67
7	Punjab Til No.2 x PCU-37	23.23**	10.26*	1.82	130.99**	104.74**	9.33
8	Punjab Til No.2 x PCU-41	18.25**	14.97**	6.17	33.33**	23.54	-22.67**
9	Punjab Til No.2 x NIC-8322	-4.16	-10.90*	-17.72**	67.74**	47.31**	4.00
10	RT-346 x PCU-37	28.89**	8.83*	15.18**	63.64**	26.32*	-4.00
11	RT-346 x PCU-41	1.84	-7.11	-1.69	5.77	-3.51	-26.67**
12	RT-346 x NIC-8322	0.87	-11.75**	-6.60	16.36	12.28	-14.67
13	PCU-42 x PCU-37	31.34**	15.94**	10.40*	27.03	9.18	-37.33**
14	PCU-42 x PCU-41	5.54	1.11	-3.72	-6.67	-10.54	-44.00**
15	PCU-42 x NIC-8322	-6.66	-14.43**	-18.52**	10.42	0.09	-29.33**
	S.E.	6.21	7.17	7.17	0.35	0.41	0.41
	CD at 5%	12.54	14.48	14.48	0.71	0.83	0.83
	CD at 1%	16.70	19.29	19.29	0.94	1.10	1.10
	Range	-6.66 - 31.34	-14.43 - 24.42	-20.21 - 15.18	-48.72 - 130.99	-65.1 - 104.74	-68 - 45.33
	No. of crosses in desirable direction	6	6	3	7	6	2

(67.74%), VRI-3 x PCU-41 (63.91%), RT-346 x PCU-37 (63.64%) and Punjab Til No.2 x PCU-41 (33.33%).

Among the fifteen crosses, six exhibited significant heterobeltiosis in positive way. The value of it varied from -65.10% (VRI-3 xPCU-37) to 104.74% (Punjab Til No.2 x PCU-37). The highest magnitude of significant heterobeltiosis in desired direction was recorded in the cross Punjab Til No.2 x PCU-37 (104.74%) followed by Gu. Til 4 x NIC-8322 (79.41%), Gu. Til 4 x PCU-41 (68.26%), Punjab Til No.2 x NIC-8322 (47.31%), VRI-3 x PCU-41 (26.82%) and RT-346 x PCU-37 (26.32%)

The spectrum of standard heterosis for primary branches plant^{-1} ranged from -68.00% (Gu. Til 4 x PCU-37) to 45.33% (VRI-3 x PCU-41). Out of fifteen crosses generated, two crosses showed significant standard heterosis in positive direction. The highest significant standard heterosis in desired was recorded in VRI-3 x PCU-41 (45.33%) followed by Gu. Til 4 x NIC-8322 (26.67%).

4.3.4.5 *Number of Capsules per Leaf Axil*

The significant and positive relative heterosis for number of capsules per leaf axil was exhibited by four out of fifteen crosses the value of it ranged from -6.25% (PCU-42 x NIC-8322) to 60.78% (Gu. Til 4 x PCU-37). The highest, significant and positive relative heterosis was recorded in the cross Gu. Til 4 x PCU-37 (60.78%) followed by Gu. Til 4 xNIC-8322 (56.86%), Gu. Til 4 x PCU-41 (45.10%) and PCU-42 x PCU-37(18.75%).

The significant heterosis over better parent in desired way was recorded in three out of fifteen crosses evaluated. It ranged from -11.5% (PCU-42 x NIC-8322) to 13.89% (.Gu. Til 4 x PCU-37). The highest magnitude of significant and positive heterobeltiosis was recorded in the cross Gu. Til 4 x PCU-37 (13.89%) followed by PCU-42 x PCU-37(12.09%) and Gu. Til 4 x NIC-8322 (11.11%).

Out of fifteen crosses evaluated, four crosses exhibited significant and positive heterosis over standard check. Highest significant and positive heterosis over standard check was recorded in the cross Gu. Til 4 x PCU-37 (173.33%)

followed by Gu. Til 4 x NIC-8322 (166.67%), Gu. Til 4 x PCU-41 (146.67%) and PCU-42 x PCU-37 (26.67%).

4.3.4.6 ***Number of Capsules Plant^{-1}***

Among fifteen hybrids evaluated, nine hybrids showed significant relative heterosis in desired direction. It was ranged from -17.39% (VRI-3 x PCU-37) to 141.99% (Gu. Til 4 x NIC-8322). The highest amount of significant and positive relative heterosis for number of capsules plant^{-1} was recorded in Gu. Til 4 x NIC-8322 (141.99%) followed by RT-346 x PCU-37 (88.83%), Gu. Til 4 x PCU-41 (82.47%), VRI-3 x PCU-41 (73.01%), Punjab Til No.2 x PCU-37 (71.62%), RT-346 x NIC-8322 (42.06%), PCU-42 x NIC-8322 (34.09%), VRI-3 x NIC-8322 (28.51%) and Gu. Til 4 x PCU-37 (28.30%).

The heterosis over better parent for this trait varied from -39.88% (VRI-3 x PCU-37) to 90.91% (Gu. Til 4 x NIC-8322). it was observed significant and positive in five out of fifteen crosses evaluated. The highest magnitude of heterobeltiosis was recorded in Gu. Til 4 x NIC-8322 (90.91%) followed by Gu. Til 4 x PCU-41 (60.14%), RT-346 x PCU-37 (44.28%), VRI-3 x PCU-41 (41.50%) and Punjab Til No.2 x PCU-37 (36.01%).

For number of capsules plant^{-1}, only four crosses depicted significant and desired standard heterosis. It ranged from -44.65% (VRI-3 x PCU-37) to 47.97% (Gu. Til 4 x NIC-8322). The highest magnitude of significant and positive standard heterosis was recorded in the cross Gu. Til 4 x NIC-8322 (47.97%) followed by VRI-3 x PCU-41 (30.28%), Gu. Til 4 x PCU-41 (24.12%) and RT-346 x PCU-37 (14.57%).

4.3.4.7 ***Capsule Length***

The spectrum of relative heterosis varied from -18.92% (PCU-42 x NIC-8322) to 15.41% (Gu. Til 4 x PCU-41). Out of fifteen crosses, six crosses had significant and positive relative heterosis. The highest significant and positive heterosis over mid parent was recorded in the cross Gu. Til 4 x PCU-41 (15.41%) followed by Punjab Til No.2 x PCU-41 (14.02%), Punjab Til No.2 x PCU-37

Table 25. Per centage of relative heterosis (RH) heterobeltiosis (HB) and standard heterosis (SH) for number of capsules per leaf axil and number of capsules plant^{-1}

Sl. No.	Hybrids	Number of capsules per leaf axil			Number of capsules plant^{-1}		
		RH	HB	SH	RH	HB	SH
1	Gu. Til 4 x PCU-37	60.78**	13.89**	173.33**	28.30*	-1.14	-23.37**
2	Gu. Til 4 x PCU-41	45.10**	2.78	146.67**	82.47**	60.14**	24.12**
3	Gu. Til 4 x NIC-8322	56.86**	11.11**	166.67**	141.99**	90.91**	47.97**
4	VRI-3 x PCU-37	0.00	0.00	0.00	-17.39	-39.88**	-44.65**
5	VRI-3x PCU-41	0.00	0.00	0.00	73.01**	41.50**	30.28**
6	VRI-3 x NIC-8322	0.00	0.00	0.00	28.51**	-4.49	-12.06
7	Punjab Til No.2 x PCU-37	0.00	0.00	0.00	71.62**	36.01**	-2.51
8	Punjab Til No.2 x PCU-41	0.00	0.00	0.00	-4.37	-13.14	-37.74**
9	Punjab Til No.2 x NIC-8322	0.00	0.00	0.00	27.05*	3.21	-26.02**
10	RT-346 x PCU-37	0.00	0.00	0.00	88.83**	44.28**	14.57
11	RT-346 x PCU-41	0.00	0.00	0.00	-1.08	-14.08	-31.78**
12	RT-346 x NIC-8322	0.00	0.00	0.00	42.06**	11.09	-11.79
13	PCU-42 x PCU-37	18.75**	12.09*	26.67**	11.64	-12.48	-35.37**
14	PCU-42 x PCU-41	6.25	0.29	13.33	-12.9	-21.93*	-42.34**
15	PCU-42 x NIC-8322	-6.25	-11.50	0	34.09**	7.71	-20.46**
	S.E.	0.06	0.07	0.07	6.33	7.31	7.31
	CD at 5%	0.12	0.14	0.14	12.79	14.77	14.77
	CD at 1%	0.16	0.19	0.19	17.03	19.66	19.66
	Range	-6.25 - 60.78	-11.50 - 13.89	0.00 - 173.33	-17.39 - 141.99	-39.88 - 90.91	-44.65 - 47.97
	No. of crosses in desirable direction	4	3	4	10	5	3

(8.75%), PCU-42 x PCU-37 (7.75%), RT-346 x PCU-37 (6.38%) and Gu. Til 4 x NIC-8322 (5.28%).

The observed range for heterosis over better parent was from -23.08% (PCU-42 x NIC-8322) to 11.11% (Punjab Til No.2 x PCU-41). The significant and desired way of heterobeltiosis was recorded in three out of fifteen crosses. The highest and significant positive heterosis over better parent was recorded in the cross Punjab Til No.2 x PCU-41 (11.11%) followed by Gu. Til 4 x PCU-41 (9.42%) and Punjab Til No.2 x PCU-37 (7.92%).

The standard heterosis ranged from -9.85% (RT-346 x NIC-8322) to 17.68% (PCU-42 x PCU-37). The significant and positive standard heterosis was found in five out of fifteen crosses. The highest magnitude of significant and standard heterosis for capsule length was recorded in the cross PCU-42 x PCU-37 (17.68%) followed by Gu. Til 4 x PCU-41 (14.39%), Gu. Til 4 x NIC-8322 (10.86%), Punjab Til No.2 x PCU-41 (9.85%), and Punjab Til No.2 x PCU-37 (8.33%)

4.3.4.8 *Number of Seeds Capsule^{-1}*

The relative heterosis varied from -19.81% (PCU-42 x NIC-8322) to 26.02% (Punjab Til No.2 x PCU-37). Out of fifteen crosses, five crosses reported significant and positive relative heterosis. The highest relative heterosis was recorded in the cross Punjab Til No.2 x PCU-37 (26.02%) followed by Gu. Til 4 x PCU-41 (18.08%), Punjab Til No.2 x PCU-41 (15.10%), PCU-42 x PCU-37 (10.63%) and VRI-3 x NIC-8322 (10.31%).

The magnitude of heterobeltiosis ranged from -22.73% (Gu. Til 4 x PCU-37) to 21.67% (Punjab Til No.2 x PCU-37). The significant and positive heterobeltiosis was found in two out of fifteen crosses. The highest amount of significant and positive heterosis over better parent was recorded in Punjab Til No.2 x PCU-37 (21.67%) followed by Punjab Til No.2 x PCU-41 (13.33%).

The value of standard heterosis was in between -23.90% (RT-346 x PCU-41) and 25.86% (Gu. Til 4 x PCU-41). Out of fifteen crosses, five crosses reported

Table 26. Per centage of relative heterosis (RH) heterobeltiosis (HB) and standard heterosis (SH) for capsule length and number of seeds capsule^{-1}

Sl. No.	Hybrids	Capsule length (cm)			Number of seeds capsule^{-1}		
		RH	HB	SH	RH	HB	SH
1	Gu. Til 4 x PCU-37	-3.08	-5.07	-0.76	-15.96**	-22.73**	-8.78
2	Gu. Til 4 x PCU-41	15.41**	9.42**	14.39**	18.08**	6.61	25.86**
3	Gu. Til 4 x NIC-8322	5.28*	4.52	10.86**	0.87	-4.13	13.18*
4	VRI-3 x PCU-37	-4.12	-4.83	-3.03	-11.44*	-12.32*	-13.17*
5	VRI-3 x PCU-41	2.71	-1.36	0.51	4.57	3.52	0.49
6	VRI-3 x NIC-8322	-0.24	-2.14	3.79	10.31*	5.50	12.20*
7	Punjab Til No.2 x PCU-37	8.75**	7.92*	8.33**	26.02**	21.67**	20.49**
8	Punjab Til No.2 x PCU-41	14.02**	11.11**	9.85**	15.10**	13.33*	7.81
9	Punjab Til No.2 x NIC-8322	-1.72	-5.00	0.76	-4.67	-11.01*	-5.36
10	RT-346 x PCU-37	6.38*	4.91	5.30	2.58	-1.97	-2.92
11	RT-346 x PCU-41	4.22	2.07	-0.25	-17.89**	-20.00**	-23.90**
12	RT-346 x NIC-8322	-11.52**	-15.00**	-9.85**	-7.20	-14.22*	-8.78
13	PCU-42 x PCU-37	7.75**	-0.43	17.68**	10.63*	8.54	11.71*
14	PCU-42 x PCU-41	-4.17	-14.10**	1.52	-4.43	-8.05	-5.36
15	PCU-42 x NIC-8322	-18.92**	-23.08**	-9.09**	-19.81**	-21.10**	-16.09**
	S.E.	0.07	0.08	0.08	3.34	3.86	3.86
	CD at 5%	0.14	0.16	0.16	6.75	7.80	7.80
	CD at 1%	0.19	0.22	0.22	8.98	10.38	10.38
	Range	-18.92 - 15.41	-23.08 - 11.11	-9.85 - 17.68	-19.81 - 26.02	-22.73 - 21.67	-23.90 - 25.86
	No. of crosses in desirable direction	6	2	5	5	2	4

significant and positive standard heterosis. The highest magnitude of significant and positive heterosis was recorded in the cross Gu. Til 4 x PCU-41 (25.86%) followed by Punjab Til No.2 x PCU-37 (20.49%), Gu. Til 4 x NIC-8322 (13.18%), VRI-3 x NIC-8322 (12.20%) and PCU-42 x PCU-37 (11.71%).

4.3.4.9 *1000 Seed Weight*

For 1000 seed weight, out of fifteen hybrids six hybrids exhibited significant and positive relative heterosis. The magnitude of relative heterosis ranged from -22.55% (PCU-42 x PCU-41) to 38.07% (RT-346 x PCU-37). the highest significant and positive heterosis was found in the cross RT-346 x PCU-37 (38.07%) followed by PCU-42 x PCU-37 (22.90%), Gu. Til 4 x PCU-37 (14.24%), Punjab Til No.2 x PCU-37 (13.29%), Gu. Til 4 x NIC-8322 (8.76%) and Punjab Til No.2 x PCU-41 (6.39%).

The heterobeltiosis was significant and positive in two out of fifteen crosses evaluated. It ranged from -25.12% (PCU-42 x PCU-41) to 34.29% (RT-346 x PCU-37). The highest amount of significant and positive heterobeltiosis for 1000 seed weight was recorded in the cross RT-346 x PCU-37 (34.29%) followed by PCU-42 x PCU-37 (7.00%).

Out of fifteen crosses evaluated, four crosses showed significant and positive standard heterosis. The magnitude of standard heterosis varied from -18.25% (PCU-42 x PCU-41) to 16.82% (PCU-42 x PCU-37). The highest magnitude of standard heterosis for this trait was recorded in PCU-42 x PCU-37 (16.82%) followed by RT-346 x PCU-37 (14.98%), Punjab Til No.2 x PCU-41 (9.48%) and Gu. Til 4 x NIC-8322 (8.15%).

4.3.4.10 *Leaf Area*

The observed range of heterosis over mid parent ranged from -67.70% (RT-346 x PCU-41) to 81.44% (RT-346 x PCU-37). The significant and positive relative heterosis was recorded in five out fifteen crosses. The highest and significant positive relative heterosis was recorded in the cross RT-346 x PCU-37

Table 27. Per centage of relative heterosis (RH) heterobeltiosis (HB) and standard heterosis (SH) for 1000 seed weight and leaf area

Sl. No.	Hybrids	1000 seed weight			Leaf area		
		RH	HB	SH	RH	HB	SH
1	Gu. Til 4 x PCU-37	14.24**	2.71	4.28	-67.41**	-71.44**	-82.18**
2	Gu. Til 4 x PCU-41	-1.35	-1.7	0.41	40.44**	25.00**	-0.05
3	Gu. Til 4 x NIC-8322	8.76**	6.53	8.15*	35.47**	23.87**	-22.72**
4	VRI-3 x PCU-37	-0.86	-8.60*	-12.23**	-57.17**	-70.38**	-63.69**
5	VRI-3 x PCU-41	-0.77	-3.79	-1.73	-31.34**	-43.28**	-30.46**
6	VRI-3 x NIC-8322	6.27	5.66	2.75	-53.89**	-67.22**	-59.81**
7	Punjab Til No.2 x PCU-37	13.29**	0.98	4.69	41.41**	-2.37	20.44**
8	Punjab Til No.2 x PCU-41	6.39*	5.6	9.48*	-58.26**	-65.60**	-57.57**
9	Punjab Til No.2 x NIC-8322	-7.45*	-10.23**	-6.93	-67.28**	-76.78**	-71.36**
10	RT-346 x PCU-37	38.07**	34.29**	14.98**	81.44**	27.16**	48.71**
11	RT-346 x PCU-41	3.70	-4.79	-2.75	-67.70**	-72.81**	-68.20**
12	RT-346 x NIC-8322	-9.14**	-14.57**	-16.92**	-34.85**	-53.02**	-45.06**
13	PCU-42 x PCU-37	22.90**	7.00*	16.82**	51.91**	35.92**	-19.13**
14	PCU-42 x PCU-41	-22.55**	-25.12**	-18.25**	-44.12**	-51.27**	-61.03**
15	PCU-42 x NIC-8322	-15.95**	-20.54**	-13.25**	-17.38**	-22.79**	-54.06**
	S.E.	0.10	0.12	0.12	163.68	189.01	189.01
	CD at 5%	0.20	0.24	0.24	330.63	381.80	381.80
	CD at 1%	0.27	0.32	0.32	440.30	508.44	508.44
	Range	-22.55 - 38.07	-25.12 - 34.29	-18.25 - 16.82	-67.70 - 81.44	-76.78 - 35.92	-82.18 - 48.71
	No. of crosses in desirable direction	6	2	4	5	4	2

(81.44%) followed by PCU-42 x PCU-37 (51.91%), Punjab Til No.2 x PCU-37 (41.41%), Gu. Til 4 x PCU-41 (40.44%) and Gu. Til 4 x NIC-8322 (35.47%).

The heterosis over better parent value varied from -76.78% (Punjab Til No.2 x NIC-8322) to 35.92% (PCU-42 x PCU-37). Out of fifteen crosses, four crosses reported significant and positive heterobeltiosis. The maximum significant and positive heterobeltiosis for leaf area was noted in the cross PCU-42PCU-37 (35.92%) followed by RT-346xPCU-37 (27.16%), Gu. Til 4 xPCU-41 (25.00%) and Gu. Til 4 xNIC-8322 (23.87%). The significant and positive standard heterosis over standard check was recorded in two out of fifteen crosses. The recorded range for standard heterosis was -82.18% (Gu. Til 4 x PCU-37) to 48.71% (RT-346 x PCU-37). The highest magnitude of significant and positive standard heterosis was reported in the cross RT-346 x PCU-37 (48.71%) followed by Punjab Til No.2 x PCU-37 (20.44%).

4.3.4.11 *Dry Matter Production*

The spectrum of heterosis over mid parent was from -34.56% (VRI-3 x PCU-37) to123.64% (RT-346 x PCU-37). The significant and positive heterosis over mid parent for this trait was found in six out of fifteen crosses. The highest amount of significant and positive relative heterosis was recorded in the cross RT-346 x PCU-37 (123.64%) followed by PCU-42 x PCU-37 (119.42%), Punjab Til No.2 x PCU-37 (101.81%), Gu. Til 4 x PCU-41 (74.13%), Gu. Til 4 x NIC-8322 (67.92%), RT-346 x NIC-8322 (41.59%) and Punjab Til No.2 x PCU-41 (30.06%).

The significant and positive heterobeltiosis for this character was exhibited in seven out of fifteen crosses. The magnitude of heterosis over better parent ranged from -51.93% (VRI-3 x PCU-37) to 74.50% (PCU-42 x PCU-37). The highest significant and positive heterobeltiosis was observed in the cross PCU-42 x PCU-37 (74.50%) followed by Gu. Til 4 x PCU-41 (74.00%), RT-346 x PCU-37 (69.00%), Punjab Til No.2 x PCU-37 (63.44%), Gu. Til 4 x NIC-8322 (47.21%), Punjab Til No.2 x PCU-41 (22.20%) and RT-346 x NIC-8322 (20.78%).

The heterosis over standard check for this trait varied from -55.71% (VRI-3 x PCU-37) to 42.92% (RT-346 x PCU-37). Out of fifteen crosses five crosses had significant and positive standard heterosis. The highest magnitude of standard heterosis was recorded in the cross RT-346 x PCU-37 (42.92%) followed by Gu. Til 4 x PCU-41(38.12%), PCU-42 x PCU-37 (27.77%), Gu. Til 4 x NIC-8322 (16.68%) and Punjab Til No.2 x PCU-37 (14.04%).

4.3.4.12 *Seed yield Plant^{-1}*

For seed yield plant^{-1}, the spectrum of heterosis over mid parent varied from -51.97% (PCU-42XPCU-41) to 208.71%(RT-346xPCU-37). The significant and positive relative heterosis is found in six out of fifteen crosses. The highest and significant positive heterosis was found in the cross RT-346xPCU-37 (208.71%) followed by Punjab Til No.2xPCU-37 (175.24%), Gu. Til 4 xNIC-8322 (162.69%), Gu. Til 4 xPCU-41 (123.52%), VRI-3xPCU-41 (99.02%) and VRI-3xNIC-8322 (76.04%).

The observed range of heterobeltiosis ranged from -62.43% to 124.24%. The significant and positive heterobeltiosis was observed in six out of fifteen crosses. The highest, significant and positive heterosis over better parent was recorded in the cross RT-346 x PCU-37 (124.24%) followed by Punjab Til No.2 x PCU-37 (95.99%), Gu. Til 4 x NIC-8322 (88.87%), Gu. Til 4 x PCU-41 (70.71%), VRI-3 x PCU-41 (59.49%) and VRI-3 x NIC-8322 (32.07%).

The magnitude of heterosis over standard variety varied from -69.46% to 78.57%. The significant and desired way of standard heterosis was reported in five out of fifteen crosses. The highest magnitude of standard heterosis for seed yield was recorded in the cross Gu. Til 4 x NIC-8322 (78.57%) followed by Gu. Til 4 x PCU-41 (61.41%), RT-346 x PCU-37 (36.25%), VRI-3 x PCU-41 (31.97%) and Punjab Til No.2 x PCU-37 (27.04%).

Table 28. Per centage of relative heterosis (RH) heterobeltiosis (HB) and standard heterosis (SH) for dry matter production and seed yield plant^{-1}

Sl. No.	Hybrids	Dry matter production			Seed yield plant^{-1}		
		RH	HB	SH	RH	HB	SH
1	Gu. Til 4 x PCU-37	-1.66	-24.00**	-39.77**	7.00	-30.95**	-34.71**
2	Gu. Til 4 x PCU-41	74.13**	74.00**	38.12**	123.52**	70.71**	61.41**
3	Gu. Til 4 x NIC-8322	67.92**	47.21**	16.68**	162.69**	88.87**	78.57**
4	VRI-3 x PCU-37	-34.56**	-51.93**	-55.71**	-43.61*	-62.43**	-68.92**
5	VRI-3 x PCU-41	11.60	3.88	-4.29	99.02**	59.49**	31.97**
6	VRI-3 x NIC-8322	10.35	-9.06	-16.22*	76.04**	32.07*	9.28
7	Punjab Til No.2 x PCU-37	101.81**	63.44**	14.04*	175.24**	95.99**	27.04*
8	Punjab Til No.2 x PCU-41	30.06**	22.20**	-3.00	18.04	4.43	-32.31**
9	Punjab Til No.2 x NIC-8322	-16.52	-22.53*	-45.95**	15.45	-5.40	-38.68**
10	RT-346 x PCU-37	123.64**	69.00**	42.92**	208.71**	124.24**	36.25**
11	RT-346 x PCU-41	-8.89	-11.68	-25.31**	-33.02*	-39.01*	-62.94**
12	RT-346 x NIC-8322	41.59**	20.78**	2.15	8.14	-9.06	-44.75**
13	PCU-42 x PCU-37	119.42**	74.50**	27.77**	32.76	-9.97	-30.43**
14	PCU-42 x PCU-41	-16.73*	-19.95*	-36.46**	-51.97**	-60.48**	-69.46**
15	PCU-42 x NIC-8322	12.12	1.78	-25.48**	-23.61	-41.32**	-54.66**
	S.E.	3.04	3.51	3.51	1.65	1.91	1.91
	CD at 5%	6.14	7.09	7.09	3.33	3.86	3.86
	CD at 1%	8.18	9.44	9.44	4.44	5.14	5.14
	Range	-34.56 - 123.64	-51.93 - 74.50	-55.71 - 42.92	-51.97 - 208.71	-62.43 - 124.24	-69.46 - 78.57
	No. of crosses in desirable direction	7	7	5	6	6	5

4.4 EXPERIMENT IV - IDENTIFICATION AND SELECTION OF SUPERIOR RECOMBINANTS IN F_2

The present investigation was undertaken with the objective of identifying the superior F_2 segregants and selection among it for the seed yield improvement of white seeded sesame. Transgressive segregants are produced in F_2 population of white seeded sesame by accumulation of favourable genes from parents involved in the crossing programme. The success of the selection programme relies on the extent to which a breeder can fix these transgressive segregants in early generation. The biometric characters of the 110 high yielding progenies in F_2 generation is presented in the Table 29.

4.4.1 Observations on the Biometric Traits of the Selected F_2 Segregants

4.4.1.1 *Days for 50 Per cent Blooming*

Among the selected F_2 segregants, the F_2 segregant of the cross 05 (VRI-3 x PCU-41); plant number 30 recorded highest value for days for 50 per cent blooming (50 days) followed by segregant of the cross 05; plant number 45 (48 days) and cross 05; plant number 10 (48 days).

4.4.1.2 *Maturity days*

Among the selected F_2 segregant, the F_2 segregant of the cross 10 (RT-346 x NIC-8322); plant number 59 matured earliest (79 days).

4.4.1.3 *Height of the Plant*

Among the selected F_2 segregants, the F_2 segregant of the cross 02 (Gu. Til 4 x PCU-41); plant number 35 had maximum height of the plant (170 cm) followed F_2 segregant of the cross 10 (RT-346 x NIC-8322); plant number 64 (167 cm) and the cross10; plant number 25 (166 cm)

4.4.1.4 *Primary Branches Plant^{-1}*

Among the selected F_2 segregants, two F_2 segregants of the cross 05 (VRI-3 x PCU-41); plant number 27 and plant number 59 had seven primary branches plant^{-1}.

4.4.1.5 *Number of Capsules per Leaf Axil*

Among the selected F_2 segregants, three F_2 segregants of the cross 01 (Gu. Til 4 x PCU-37); plant number 8, plant number 62 and plant number 74 and two F_2 segregants of the cross 02 (Gu. Til 4 x PCU-41); plant number 32 and plant number 82 and one F_2 segregants of the cross 03 (Gu. Til 4 x NIC-8322); plant number 45 recorded three capsules per leaf axil.

4.4.1.6 *Number of Capsules Plant^{-1}*

Among the selected F_2 segregants, the F_2 segregant of the cross 05 (VRI-3 x PCU-41); plant number 10 had the highest number of capsules plant^{-1} (138) followed by the F_2 segregant of the cross 03(Gu. Til 4 x NIC-8322); plant number 58 (126) and the cross2 (Gu. Til 4 x PCU-41); plant number 87 (122).

4.4.1.7 *Capsule Length*

Among the selected F_2 segregants, the F_2 segregant of the cross 13 (PCU-42 x PCU-37) plant number 76 recorded maximum capsule length (3.27 cm) followed by the F_2 segregant of the cross 13; plant number 85 (3.15 cm) and the cross 13; plant number 52 (3.12 cm).

4.4.1.8 *Number of Seeds Capsule^{-1}*

Among the selected F_2 segregants, the F_2 segregants of the cross 02 (Gu. Til 4 x PCU-41); plant number 35 had maximum number of seeds capsule^{-1} (81.33) followed by F_2 segregant of the cross 03 (Gu. Til 4 x NIC-8322); plant number 11 (80.67) and the cross 03; plant number 93 (80.67).

4.4.1.9 *Seed Colour*

All the selected F_2 segregants had yellowish white coloured seeds.

4.4.1.10 *1000 Seed Weight*

Among the selected F_2 segregants, the F_2 segregants of the cross 13 (PCU-42 x PCU-37); plant number 85 exhibited highest 1000 seed weight (3.67 g) followed by F_2 segregant of the cross 13; plant number 52 (3.55 g) and the cross 01 (Gu. Til 4 x PCU-37); plant number 74 (3.54 g).

4.4.1.11 *Leaf Area*

Among the selected F_2 segregants, the F_2 segregant of the cross 05 (VRI-3 x PCU-41); plant number 10 showed maximum leaf area (6254.00 cm^2) followed by F_2 segregant of the cross 02 (Gu. Til 4 x PCU-41); plant number 95 (5975.00 cm^2) and the cross 10 (RT-346 x NIC-8322); plant number 38 (5835.50 cm^2).

4.4.1.12 *Dry Matter Production*

Among the selected F_2 segregants, the F_2 segregant of the cross10 (RT-346 x NIC-8322); plant number 5 recorded maximum dry matter production (67.14 g) followed by F_2 segregant of the cross 10; plant number 25 (64.25 g) and the cross 10; plant number 6 (60.07 g).

4.4.1.13 *Seed yield Plant^{-1}*

Among the selected F_2 segregants, the F_2 segregants of the cross 03 (Gu. Til 4 x NIC-8322); plant number 58 recorded highest seed yield plant^{-1} (27.37 g) followed by F_2 segregant of the cross 02 (Gu. Til 4 x PCU-41); plant number 35(26.84 g) and the cross 03; plant number 44 (26.14 g).

4.4.1.14 *Scoring of Pest and Diseases*

Minute incidence of anthracnose caused by *Alternaria sesami* was observed in all the segregants in F_2.

Table 29. Performance of the selected F_2 segregants

Sl. No.	Designation of the cross	Sl. No, of the selected plants in F_2 for each cross	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP
1	01	8	34	80	124	4	3.0	106	2.61	63.00	Yellowish white	3.42	2061.0	40.85	20.76
2	01	62	37	84	117	3	3.0	92	2.74	68.33	Yellowish white	3.36	1862.5	34.28	18.51
3	01	67	35	82	135	2	2.8	97	2.53	62.33	Yellowish white	3.31	1046.0	27.94	18.04
4	01	74	31	80	121	3	3.0	114	2.70	57.66	Yellowish white	3.54	1385.0	44.71	21.16
5	02	14	40	90	144	6	2.8	102	2.62	74.67	Yellowish white	3.18	3255.0	47.46	22.52
6	02	19	44	96	152	4	2.2	97	2.90	78.00	Yellowish white	3.27	2864.5	56.61	23.08
7	02	32	42	90	159	3	3.0	110	2.71	70.33	Yellowish white	3.11	3752.5	41.80	21.96
8	02	35	35	87	170	3	2.4	116	2.77	81.33	Yellowish white	3.08	4064.5	57.13	26.84
9	02	36	40	92	161	5	2.0	101	2.74	69.33	Yellowish white	3.45	2188.0	54.85	22.71
10	02	41	37	87	147	4	2.8	90	2.65	70.67	Yellowish white	3.42	2463.5	40.28	19.04
11	02	48	39	86	152	5	2.6	86	2.83	77.33	Yellowish white	3.17	4267.0	45.54	18.62
12	02	64	45	94	157	4	2.4	94	2.72	67.33	Yellowish white	3.29	5428.5	42.81	18.14
13	02	82	36	82	148	5	3.0	108	2.88	64.67	Yellowish white	3.44	3671.0	50.45	21.96

Table 29. Continued.

Sl. No.	Designation of the cross	Sl. No, of the selected plants in F_2 for each cross	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP
14	02	87	41	91	151	6	2.8	122	2.64	71.33	Yellowish white	3.21	3018.0	59.78	25.24
15	02	88	41	88	164	4	2.6	90	2.70	76.67	Yellowish white	3.37	4236.5	46.42	20.83
16	02	95	38	87	140	4	2.8	88	2.81	73.33	Yellowish white	3.15	5975.0	44.86	18.31
17	03	2	40	81	162	4	2.4	114	2.72	71.33	Yellowish white	3.36	2764.0	40.51	24.81
18	03	11	35	84	138	6	2.6	97	2.76	80.67	Yellowish white	3.52	3127.5	48.89	25.06
19	03	16	33	80	155	5	2.2	92	2.84	75.67	Yellowish white	3.12	3085.0	36.42	19.52
20	03	20	37	81	146	5	2.4	108	2.66	73.33	Yellowish white	3.46	3746.0	51.60	25.79
21	03	22	41	92	158	4	2.6	86	2.81	77.67	Yellowish white	3.21	3586.5	43.74	18.76
22	03	27	35	85	164	3	2.0	97	2.71	72.33	Yellowish white	3.26	2367.0	41.82	19.51
23	03	36	42	87	151	3	2.4	102	2.76	78.33	Yellowish white	2.97	2572.5	43.52	20.46
24	03	44	37	82	157	3	2.6	117	2.68	73.67	Yellowish white	3.31	4176.0	50.07	26.14
25	03	45	34	80	155	4	3.0	94	2.81	71.67	Yellowish white	3.18	3744.0	39.76	19.52
26	03	58	40	85	144	6	2.6	126	2.73	76.33	Yellowish white	3.14	3061.5	47.41	27.37

Table 29. Continued.

Sl. No.	Designation of the cross	Sl. No, of the selected plants in F_2 for each cross	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP
27	03	62	32	80	149	5	2.8	84	2.64	70.67	Yellowish white	3.54	3572.5	42.54	18.06
28	03	71	38	88	158	4	2.6	78	2.75	68.33	Yellowish white	3.42	3634.5	40.06	16.92
29	03	74	35	86	142	3	2.4	85	2.69	77.67	Yellowish white	3.47	2675.0	38.85	19.87
30	03	82	40	90	151	4	2.4	98	2.71	72.33	Yellowish white	3.36	3954.0	46.92	21.29
31	03	88	37	84	136	5	2.4	90	2.84	78.33	Yellowish white	3.22	3107.5	41.63	19.72
32	03	93	39	88	145	5	2.8	105	2.87	80.67	Yellowish white	3.31	3466.5	56.38	25.94
33	03	94	42	94	157	4	2.6	94	2.76	74.67	Yellowish white	3.52	3062.5	47.67	21.46
34	05	6	40	86	148	5	1.0	96	2.65	60.33	Yellowish white	3.31	4981.0	40.85	16.72
35	05	10	48	94	162	6	1.0	138	2.61	64.00	Yellowish white	3.17	6254.0	57.02	24.37
36	05	21	36	82	140	5	1.0	91	2.53	68.33	Yellowish white	3.26	4762.0	44.36	17.55
37	05	27	43	92	156	7	1.0	107	2.74	62.67	Yellowish white	3.02	3885.5	46.41	17.16
38	05	30	50	96	160	5	1.0	115	2.66	65.33	Yellowish white	3.21	4065.5	50.27	22.35
39	05	36	46	90	144	5	1.0	92	2.58	72.33	Yellowish white	3.38	5496.5	54.84	19.21

Table 29. Continued.

Sl. No.	Designation of the cross	Sl. No, of the selected plants in F_2 for each cross	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP
40	05	37	42	86	158	6	1.0	99	2.69	68.33	Yellowish white	3.14	4682.5	47.38	18.67
41	05	38	47	94	147	5	1.0	95	2.70	65.67	Yellowish white	3.25	3974.5	42.45	17.92
42	05	40	41	90	154	5	1.0	108	2.66	70.67	Yellowish white	3.33	4384.5	51.27	21.81
43	05	42	45	88	142	6	1.0	86	2.59	62.33	Yellowish white	3.10	3576.5	46.62	14.47
44	05	44	42	85	147	6	1.0	90	2.64	64.67	Yellowish white	3.29	3845.0	40.75	16.73
45	05	45	48	91	151	5	1.0	111	2.52	68.67	Yellowish white	3.24	4683.5	54.82	21.05
46	05	49	44	90	148	5	1.0	98	2.71	71.67	Yellowish white	3.09	4036.5	43.37	18.56
47	05	51	38	84	146	4	1.0	86	2.67	66.00	Yellowish white	3.15	3168.5	38.85	15.99
48	05	59	47	96	146	7	1.0	99	2.62	68.33	Yellowish white	3.11	4197.0	41.56	18.46
49	05	70	40	87	151	6	1.0	95	2.58	60.67	Yellowish white	3.26	4482.5	47.34	15.32
50	05	73	37	85	140	5	1.0	84	2.69	64.67	Yellowish white	3.14	3971.5	42.69	14.77
51	05	77	46	88	158	5	1.0	87	2.63	62.33	Yellowish white	3.32	3664.5	39.91	15.81
52	05	81	42	87	151	6	1.0	92	2.57	65.33	Yellowish white	3.27	4137.5	46.74	16.83

Table 29. Continued.

Sl. No.	Designation of the cross	Sl. No, of the selected plants in F_2 for each cross	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP
53	05	84	44	90	164	5	1.0	96	2.74	69.67	Yellowish white	3.05	5182.5	44.82	18.04
54	05	88	44	94	160	6	1.0	115	2.61	70.67	Yellowish white	3.24	4877.5	52.38	23.47
55	05	90	41	87	155	6	1.0	85	2.68	61.33	Yellowish white	3.27	3769.5	46.84	15.76
56	05	95	43	90	152	6	1.0	94	2.62	67.67	Yellowish white	3.16	4183.5	49.42	17.51
57	05	98	39	82	148	5	1.0	87	2.70	65.33	Yellowish white	3.22	4854.5	41.65	15.23
58	06	11	42	85	152	5	1.0	92	2.61	71.33	Yellowish white	3.02	2586.0	35.26	17.01
59	06	19	38	80	147	6	1.0	88	2.68	67.67	Yellowish white	3.21	3181.5	44.91	16.84
60	06	37	43	86	138	5	1.0	94	2.72	65.33	Yellowish white	3.46	2245.5	38.20	18.32
61	06	42	41	91	154	4	1.0	85	2.64	74.33	Yellowish white	3.32	3726.5	43.74	17.45
62	06	59	45	91	148	5	1.0	89	2.61	72.67	Yellowish white	3.41	2892.5	46.27	19.26
63	06	66	42	87	151	4	1.0	84	2.70	74.33	Yellowish white	3.26	3481.5	34.86	17.92
64	06	69	38	82	136	6	1.0	80	2.78	70.33	Yellowish white	3.18	3967.5	37.41	15.87
65	06	71	44	90	142	6	1.0	99	2.59	72.33	Yellowish white	3.11	4018.5	47.94	18.51

Table 29. Continued.

Sl. No.	Designation of the cross	Sl. No, of the selected plants in F_2 for each cross	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP
66	06	80	40	88	147	4	1.0	82	2.73	68.33	Yellowish white	3.20	3672.5	34.36	15.74
67	06	88	41	85	144	6	1.0	87	2.77	75.67	Yellowish white	3.25	3038.0	36.71	18.36
68	07	4	40	88	152	4	1.0	84	2.60	68.67	Yellowish white	2.98	4685.5	41.58	14.76
69	07	9	37	85	149	3	1.0	78	2.71	74.33	Yellowish white	3.24	4182.5	46.21	16.82
70	07	11	42	90	161	4	1.0	87	2.75	65.33	Yellowish white	3.18	3692.5	38.36	15.64
71	07	16	38	87	157	5	1.0	82	2.68	69.67	Yellowish white	3.35	5216.5	40.85	16.35
72	07	23	35	84	145	4	1.0	77	2.74	64.33	Yellowish white	3.22	4012.5	34.61	12.96
73	07	35	32	80	141	4	1.0	79	2.77	76.67	Yellowish white	3.14	4736.0	42.37	15.85
74	07	58	38	86	150	3	1.0	88	2.62	72.67	Yellowish white	3.35	5163.0	46.11	17.96
75	07	64	35	82	147	4	1.0	82	2.65	70.33	Yellowish white	3.20	5372.5	37.79	15.62
76	07	66	37	89	164	4	1.0	86	2.71	67.33	Yellowish white	3.28	4835.5	44.32	16.08
77	07	75	37	85	152	3	1.0	81	2.68	65.67	Yellowish white	3.34	3972.5	48.67	14.76
78	07	84	34	83	146	5	1.0	89	2.74	76.00	Yellowish white	3.17	4687.5	52.85	18.35

Table 29. Continued.

Sl. No.	Designation of the cross	Sl. No, of the selected plants in F_2 for each cross	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP
79	07	90	38	88	144	3	1.0	80	2.80	71.33	Yellowish white	3.15	4142.5	43.72	15.14
80	07	95	35	81	137	3	1.0	76	2.69	74.33	Yellowish white	3.31	3765.5	41.88	16.27
81	07	98	38	86	151	5	1.0	85	2.62	66.67	Yellowish white	3.26	5216.5	49.47	15.82
82	08	12	38	87	142	4	1.0	68	2.67	70.33	Yellowish white	3.34	4682.5	38.62	12.96
83	08	28	36	87	158	3	1.0	74	2.56	67.67	Yellowish white	3.41	3542.0	42.51	14.77
84	08	57	33	82	152	4	1.0	71	2.72	63.67	Yellowish white	3.27	5064.5	40.84	12.52
85	08	72	38	85	145	5	1.0	67	2.64	61.33	Yellowish white	3.45	4166.5	35.47	12.06
86	08	78	37	86	142	4	1.0	68	2.77	71.67	Yellowish white	3.36	3176.5	34.96	14.34
87	08	85	35	82	148	4	1.0	67	2.70	68.33	Yellowish white	3.48	4492.5	39.65	13.66
88	10	5	34	80	153	5	1.0	82	2.58	63.67	Yellowish white	3.42	5583.5	67.14	14.72
89	10	6	37	86	162	4	1.0	86	2.66	61.00	Yellowish white	3.16	4925.0	60.07	13.87
90	10	10	35	86	158	4	1.0	79	2.70	65.67	Yellowish white	2.92	3982.0	47.50	12.92
91	10	18	31	82	147	6	1.0	85	2.61	62.33	Yellowish white	3.32	4152.0	55.46	15.08

Table 29. Continued.

Sl. No.	Designation of the cross	Sl. No, of the selected plants in F_2 for each cross	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP
92	10	25	37	85	166	4	1.0	94	2.67	67.33	Yellowish white	2.87	5265.5	64.25	15.96
93	10	33	33	87	152	4	1.0	87	2.64	62.33	Yellowish white	3.25	4822.0	52.71	14.35
94	10	38	31	80	144	5	1.0	80	2.71	66.33	Yellowish white	3.20	5835.5	49.64	14.54
95	10	40	35	84	149	5	1.0	84	2.61	68.67	Yellowish white	3.08	3765.0	56.13	15.61
96	10	45	37	87	162	5	1.0	92	2.60	61.33	Yellowish white	3.18	4382.0	44.85	16.02
97	10	51	37	82	158	4	1.0	81	2.68	65.33	Yellowish white	3.51	4731.5	41.36	15.94
98	10	59	32	79	150	4	1.0	85	2.61	64.67	Yellowish white	3.35	5512.5	48.69	15.27
99	10	64	36	85	167	4	1.0	88	2.67	64.00	Yellowish white	2.97	4185.0	42.82	13.82
100	10	83	35	81	155	4	1.0	81	2.63	67.33	Yellowish white	3.31	5047.5	46.76	15.49
101	10	91	33	84	151	6	1.0	86	2.72	65.67	Yellowish white	2.78	4966.5	50.22	12.67
102	10	98	37	82	162	4	1.0	80	2.68	60.67	Yellowish white	2.95	4238.5	41.31	12.18
103	13	26	32	85	154	3	1.0	74	2.97	69.67	Yellowish white	3.47	3256.5	48.12	15.72
104	13	34	37	88	148	3	1.0	70	3.08	72.67	Yellowish white	3.28	2985.0	41.57	15.06

Table 29. Continued.

Sl. No.	Designation of the cross	Sl. No, of the selected plants in F_2 for each cross	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP
105	13	52	35	82	144	4	1.0	68	3.12	65.33	Yellowish white	3.55	2262.0	39.44	14.50
106	13	76	31	80	157	4	1.0	80	3.27	70.67	Yellowish white	3.41	3748.5	52.91	17.14
107	13	85	37	86	151	3	1.0	76	3.15	67.33	Yellowish white	3.67	2761.0	44.28	16.35
108	13	89	34	84	146	3	1.0	72	3.11	71.33	Yellowish white	3.52	3137.5	36.72	15.98
109	15	42	39	86	136	4	1.0	80	2.58	64.67	Yellowish white	3.36	2817.5	40.86	15.21
110	15	66	33	82	128	4	1.0	76	2.67	60.33	Yellowish white	3.51	2172.0	32.65	14.88

DFB	Days for 50 per cent blooming	NSC	Number of seeds capsule^{-1}
MD	Maturity days	SC	Seed colour
HP	Height of the plant (cm)	TSW	1000 seed weight
PBP	Primary branches plant^{-1}	LA	Leaf area
NCL	Number of capsules per leaf axil	DMP	Dry matter production
NCP	Number of capsules plant^{-1}	SYP	Seed yield plant^{-1} (g)
CL	Capsule length (cm)		

4.5 EXPERIMENT V - IDENTIFICATION AND SELECTION OF SUPERIOR RECOMBINANTS IN F_3

The 110 promising plant progenies of the crosses were identified and selected from the F_2 population and was forwarded to F_3. Plant number is denoted by the progeny row and its position within the row based on the serial number given in F_2 in order to trace back the pedigree. Selection within these progenies by studying its oil and protein content helped to isolate superior genotypes. The biometric, as well as quality characters of the high yielding progenies in F_3 generation, is presented in Table 30.

4.5.1 Observations on the Biometric and Quality Traits of the Selected F_3 Segregants

4.5.1.1 *Height of the Plant*

Among the selected F_3 segregants, the F_3 progeny with the plant numbers 2105-10, 2105-77,2106-11 took maximum days for 50 per cent blooming (44 days) followed by the plant numbers 2105-90 (42 days) and 2105-95 (41 days).

4.5.1.2 *Maturity Days*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2103-62 matured earliest (74 days) followed by the plant numbers *viz.*, 2101-74, 2106-69 and 2107-84 which took 80 days to mature.

4.5.1.3 *Height of the Plant*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2105-10 had maximum height of the plant (166cm) followed by the plant numbers 2102-35 (158 cm) and 2107-58 (156 cm).

4.5.1.4 *Primary Branches Plant^{-1}*

Among the selected F_3 segregants, the F_3 progenies with the plant numbers 2102-11,2105-10, 2105-90,2105-95 (i) and 2105-95 (ii) produced highest number of primary branches (6).

4.5.1.5 *Number of Capsules per Leaf Axil*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2101-62 recorded highest number of capsules per leaf axil (3).

4.5.1.6 *Number of Capsules Plant^{-1}*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2107-58 had the highest number of capsules plant^{-1} (122) followed by the plant number 2105-10 (102).

4.5.1.7 *Capsule Length*

Among the selected F_3 segregants, F_3 progeny with the plant number 2113-34recorded maximum capsule length (3.04 cm) followed by the plant number 2113-52 (2.98 cm) and 2113-34 (2.92 cm).

4.5.1.8 *Number of Seeds Capsule^{-1}*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2102-35 had maximum number of seeds capsule^{-1} (78.67) followed by the plant numbers 2103-44 (77.67) and 2102-48 (73.67).

4.5.1.9 *Seed Colour*

All the selected F_3 segregants had yellowish white coloured seeds.

4.5.1.10 *1000 Seed Weight*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2108-85 exhibited highest 1000 seed weight (3.52 g) followed by plant numbers2113-52 (3.46 g), and 2115-66 (3.40 g).

4.5.1.11 *Leaf Area*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2103-44 showed maximum leaf area (5246.00 cm^2) followed by plant numbers 2107-98 (5046.50 cm^2), and 2107-58 (4769.50 cm^2).

4.5.1.12 *Dry Matter Production*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2103-44 recorded maximum dry matter production (48.46 g) followed by the plant numbers 2105-40 (47.25 g) and 2102-35 (46.28 g).

4.5.1.13 *Seed yield Plant^{-1}*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2107-58 registered the highest seed yield plant^{-1} (26.04 g) followed by plant numbers 2103-44 (19.76 g) and 2105-10 (19.02 g).

4.5.1.14 *Scoring of Pest and Diseases*

Minute incidence of anthracnose caused by *Alternaria sesami* was observed in all the segregants in F_3.

4.5.1.15 *Oil Content*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2110-64 recorded the highest oil content (54.67%) followed by the plant numbers 2105-81 (54.33%) and 2113-52 (53.00%).

4.5.1.16 *Protein Content*

Among the selected F_3 segregants, the F_3 progeny with the plant number 2103-44 showed highest protein content (25.73%) followed by the plant numbers 2113-34 (25.49%) and 2108-85 (25.26%).

Table 30. Performance of the selected F_3 segregants

Sl. no.	Designation of the cross	Plant number (Pedigree)	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP	OC	PC
1	01	2101-62	34	85	110	0	3.0	84	2.67	70.67	Yellowish white	3.21	1042.5	26.41	16.92	45.67	22.23
2	01	2101-74	30	80	117	2	2.8	80	2.61	64.33	Yellowish white	3.15	1286.0	32.86	14.93	47.33	21.06
3	02	2102-14	38	88	135	4	2.4	86	2.58	72.33	Yellowish white	2.92	2861.5	39.55	15.71	44.33	20.42
4	02	2102-35	32	84	158	3	2.2	88	2.70	78.67	Yellowish white	3.06	3244.5	46.28	17.36	45.33	24.33
5	02	2102-48(i)	35	87	144	4	2.8	84	2.74	71.33	Yellowish white	3.17	3492.5	40.62	16.52	46.33	21.82
6	02	2102-48(ii)	37	84	138	5	2.4	80	2.68	73.67	Yellowish white	3.26	2815.5	38.37	16.07	44.67	21.41
7	03	2102-11	40	88	141	6	2.2	85	2.56	67.00	Yellowish white	3.06	2164.0	44.16	14.81	45.33	23.57
8	03	2102-20	36	85	137	4	2.8	78	2.75	70.33	Yellowish white	3.24	4635.5	40.84	15.64	46.33	24.97
9	03	2103-44	34	88	152	5	2.4	92	2.60	77.67	Yellowish white	3.12	5246.0	48.46	19.76	50.33	25.73
10	03	2103-62(i)	39	87	145	3	2.8	88	2.57	67.67	Yellowish white	3.22	4238.0	46.08	16.09	47.67	20.59
11	03	2103-62(ii)	30	78	136	5	2.6	77	2.61	72.33	Yellowish white	3.38	3806.0	44.21	15.87	42.33	23.10
12	03	2103-71	36	84	141	4	2.8	75	2.69	68.67	Yellowish white	3.20	3164.5	42.74	14.39	46.33	21.53

Table 30. Continued.

Sl. no.	Designation of the cross	Plant number (Pedigree)	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP	OC	PC
13	05	2105-10	44	94	166	6	1.0	102	2.58	67.67	Yellowish white	3.18	3128.0	39.16	19.02	52.67	24.85
14	05	2105-21	38	84	132	4	1.0	82	2.46	62.33	Yellowish white	3.27	3476.5	36.37	14.61	48.33	23.69
15	05	2105-40	40	87	140	5	1.0	80	2.60	65.33	Yellowish white	3.11	3542.5	47.25	14.22	45.00	24.85
16	05	2105-51	36	84	137	4	1.0	77	2.64	62.67	Yellowish white	3.08	2862.5	34.15	13.15	46.67	19.54
17	05	2105-70	40	85	145	4	1.0	86	2.66	68.33	Yellowish white	3.15	3426.0	43.72	16.02	47.33	21.82
18	05	2105-77	44	90	150	4	1.0	82	2.61	58.66	Yellowish white	3.27	3145.5	35.66	13.71	48.67	22.40
19	05	2105-81(i)	38	88	141	4	1.0	92	2.67	66.33	Yellowish white	3.32	2464.5	42.85	18.11	54.33	23.86
20	05	2105-81(ii)	37	82	136	5	1.0	87	2.58	62.67	Yellowish white	3.21	2935.5	36.54	15.27	47.67	22.23
21	05	2105-90	42	89	147	6	1.0	81	2.64	61.00	Yellowish white	3.18	3058.5	32.76	13.52	44.67	24.97
22	05	2105-95	41	92	144	6	1.0	86	2.56	64.33	Yellowish white	3.04	3942.5	40.21	14.38	48.00	21.53
23	06	2106-11	44	87	141	5	1.0	82	2.60	69.67	Yellowish white	2.95	2264.0	32.82	14.69	49.33	24.20
24	06	2106-69	36	80	135	5	1.0	77	2.71	71.67	Yellowish white	3.11	3768.5	30.35	15.12	47.33	21.41

Table 30. Continued.

Sl. no.	Designation of the cross	Plant number (Pedigree)	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP	OC	PC
25	07	2107-04	38	86	148	4	1.0	80	2.62	64.33	Yellowish white	3.06	4062.5	37.27	13.26	44.67	20.36
26	07	2107-23	36	88	142	4	1.0	78	2.70	62.67	Yellowish white	3.18	3458.0	30.61	13.51	48.67	23.68
27	07	2107-58(i)	38	92	156	6	1.0	122	2.68	71.33	Yellowish white	3.36	3364.5	44.42	26.04	52.33	23.57
28	07	2107-58(ii)	36	85	140	4	1.0	90	2.66	68.67	Yellowish white	3.20	4769.5	40.54	16.83	49.00	22.40
29	07	2107-84	32	80	135	5	1.0	76	2.71	72.33	Yellowish white	3.31	3277.0	46.21	13.56	45.67	24.85
30	07	2107-98	38	88	144	4	1.0	80	2.65	64.33	Yellowish white	3.14	5046.5	42.74	14.16	48.33	23.68
31	08	2108-85	34	85	140	4	1.0	90	2.64	67.33	Yellowish white	3.52	3892.5	30.16	18.42	52.67	25.26
32	10	2110-45	38	86	154	5	1.0	86	2.78	62.67	Yellowish white	3.04	3245.5	40.81	13.95	47.67	20.59
33	10	2110-64	35	86	152	3	1.0	90	3.02	68.33	Yellowish white	3.50	4681.5	46.40	19.21	54.67	22.46
34	10	2110-98	35	84	148	4	1.0	77	2.86	64.67	Yellowish white	3.11	3685.5	32.18	12.53	46.33	24.85
35	13	2113-34(i)	34	87	139	3	1.0	74	2.92	70.67	Yellowish white	3.25	2161.5	38.65	14.72	48.33	25.49
36	13	2113-34(ii)	36	85	142	3	1.0	78	3.04	69.67	Yellowish white	3.16	2486.0	40.41	15.04	47.67	23.57

Table 30. Continued.

Sl. no.	Designation of the cross	Plant number (Pedigree)	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	SC	TSW	LA	DMP	SYP	OC	PC
37	13	2113-52(i)	33	87	156	4	1.0	91	2.87	67.33	Yellowish white	3.46	2436.5	42.64	18.76	53.00	22.46
38	13	2113-52(ii)	36	84	144	3	1.0	84	2.98	70.33	Yellowish white	3.20	1982.5	33.42	15.81	47.33	23.68
39	15	2115-42	40	89	130	4	1.0	78	2.51	62.33	Yellowish white	3.27	2135.5	36.25	13.37	45.33	21.99
40	15	2115-66	35	84	122	4	1.0	75	2.62	58.67	Yellowish white	3.40	2048.5	30.62	12.68	46.67	20.06

DFB	Days for 50 per cent blooming
MD	Maturity days
HP	Height of the plant (cm)
PBP	Primary branches plant^{-1}
NCL	Number of capsules per leaf axil
NCP	Number of capsules plant^{-1}
CL	Capsule length (cm)
NSC	Number of seeds capsule^{-1}
SC	Seed colour
TSW	1000 seed weight
LA	Leaf area
DMP	Dry matter production
SYP	Seed yield plant^{-1} (g)
OC	Oil content (%)
PC	Protein content (%)

Discussion

5. DISCUSSION

Developing varieties with high yield involves screening, evaluating and selecting suitable genotypes from a very large collection of germplasm and accumulating the desirable genes in a productive genotype. The breeding programme should be planned efficiently with prior knowledge regarding the pattern of inheritance of yield and its attributing constituents.

In sesame, average productivity continues to be low mainly due to two reasons. The first reason is its cultivation in sub marginal areas and the second reason is the unavailability of superior high yielding varieties having inbuilt resistance to biotic and abiotic stresses. To break the current yield barrier, and to develop superior varieties from genetically heterogenous parents have to be used.

Hence, the present study was aimed at developing superior combinations of white seeded sesame genotypes with higher yield and oil content which is suitable for transgressive and heterosis breeding. The outcome of the current study are discussed here under.

5.1 VARIABILITY STUDIES

5.1.1 Analysis of variance

Significant differences for the thirty genotypes of white seeded sesame was noticed for all the characters studied. *viz.*, days for 50 per cent blooming, maturity days, height of the plant, primary branches plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-1}, capsule length (cm), number of seeds capsule^{-1}, 1000 seed weight, leaf area, dry matter production, seed yield plant^{-1}, oil content (%) and protein content (%). This is in confirmation with the results obtained by Agrawal *et al.*, (2018), Kadvani *et al.* (2020), Kumari *et al*. (2020), Manjeet *et al.* (2020), Mohanty *et al*. (2020), Pavani *et al*. (2020), Aboelkassem *et al.* (2021), Rajitha *et al*. (2021), Kumar *et al.* (2021), Sasipriya *et al.* (2022) and Umamaheswari *et al.* (2019).

The differences were significant and it suggested the adequate heterogeneity among the parents and progenies. The out turn of this research is in tune with the findings of Virani *et al.* (2018) and Sirohi *et al.* (2020) for days for 50 per cent blooming, maturity days, capsule length, number of capsules plant^{-1} and seed yield plant^{-1}. The mean squares due to parents *vs* hybrids were found significant for all the characters except days for 50 per cent blooming, maturity days and number of seeds capsule^{-1} indicating that heterosis could be exploited for most of the characters under study.

Combining ability analysis showed that line x tester interaction was highly significant for all the characters studied. Virani *et al.* (2018), Amarnath *et al.* (2019), Deshmukh *et al.* (2019), Sirohi *et al.* (2020) and Parameshwarappa *et al.* (2021) have also reported significant differences in the mean squares of line x testers for the traits *viz.*, days for 50 per cent blooming, height of the plant, number of branches plant^{-1}, capsule length, number of capsules plant^{-1}, 1000 seed weight and seed yield plant^{-1}.

5.1.2 GCV and PCV

A high genetic variability increases the chances of selection of better genotypes. The phenotypic coefficients of variation were higher than that of genotypic for all the characters which revealed environmental influence in character expression. The studies of Agrawal *et al.*, (2018), Kalaiyarasi *et al.* (2019), Umamaheswari *et al*. (2019), Kadvani *et al.* (2020), Kehie *et al*. (2020), Kumari *et al*. (2020), Manjeet *et al.* (2020), Mohanty *et al*. (2020), Pavani *et al*. (2020), Saravanan *et al*. (2020), Ranjitha *et al.* (2021), Vamshi *et al*. (2021), Kumar *et al.* (2022), Ranjithkumar *et al*. (2022), Roy *et al*. (2022), Sasipriya *et al*. (2022) and Srikanth and Ghodke (2022) supported the present findings.

The estimates of genotypic and phenotypic parameters of variation were high for the characters *viz.*, seed yield plant^{-1}, primary branches plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-1}, leaf area and drymatter production. These findings are in confirmation with that of Kalaiyarasi *et al.* (2019), Kumari *et al*. (2020), Mohanty *et al*. (2020), Saravanan *et al*. (2020), Ranjitha *et al.* (2021), Vamshi *et al*. (2021) for the traits seed yield plant^{-1} and number of capsules plant^{-1}. Kadvani *et al.* (2020) reported high for both coefficient in leaf area plant^{-1} and number of branches plant^{-1}.

The characters *viz*., height of the plant, number of seeds capsule^{-1}, days for 50 per cent blooming and 1000 seed weight showed moderate GCV and PCV. These results are in agreement with Jadhav and Mohrir (2012), Kumari *et al*. (2020) and Sasipriya *et al*. (2022) for days for 50 per cent blooming, and height of the plant. Mohanty *et al*. (2020) and Bamrotiya *et al.* (2016) reported moderate heritability of the character 1000 seed weight and number of seeds capsule^{-1} respectively.

Low estimates of both coefficients were perceived for capsule length, protein content, oil content and maturity days. Similar findings were outlined by Jadhav and Mohrir (2012) and Pavani *et al*. (2020) for maturity days, capsule length and oil content. Agrawal *et al.*, (2018) already revealed the low estimates of GCV and PCV values for the trait protein content.

1.3 Heritability and Genetic advance

High heritability of a character indicates that phenotype of the trait strongly reflects the genotype and shows the low influence of environment in its expression due to the major role of genotypic constitution in the expression of the character. Thereby, heritability supplies the information regarding the degree of inheritance of characters from the parents to the progeny.

In the current study high heritability was obtained for all the attributes except maturity days which possessed moderate heritability. These findings are in line with Mohanty *et al*. (2020) and Ranjithkumar *et al.* (2022) for number of capsules plant^{-1}, seed yield plant^{-1} and oil content; Bamrotiya *et al.* (2016) for number of capsules per leaf axil; Agrawal *et al*. (2018) Kalaiyarasi *et al*. (2019) and Umamaheswari *et al*. (2019) for number of seeds capsule^{-1}; Kadvani *et al.* (2020)

for 1000 seed weight, leaf area plant^{-1} and capsule length; Kumari *et al.,* (2020) for days for 50 per cent blooming, protein content, number of primary branches plant^{-1} and height of the plant. Corroborative findings regarding maturity days were given by Jadhav and Mohrir (2012), Bamrotiya *et al.* (2016) and Mohanty *et al*. (2020).

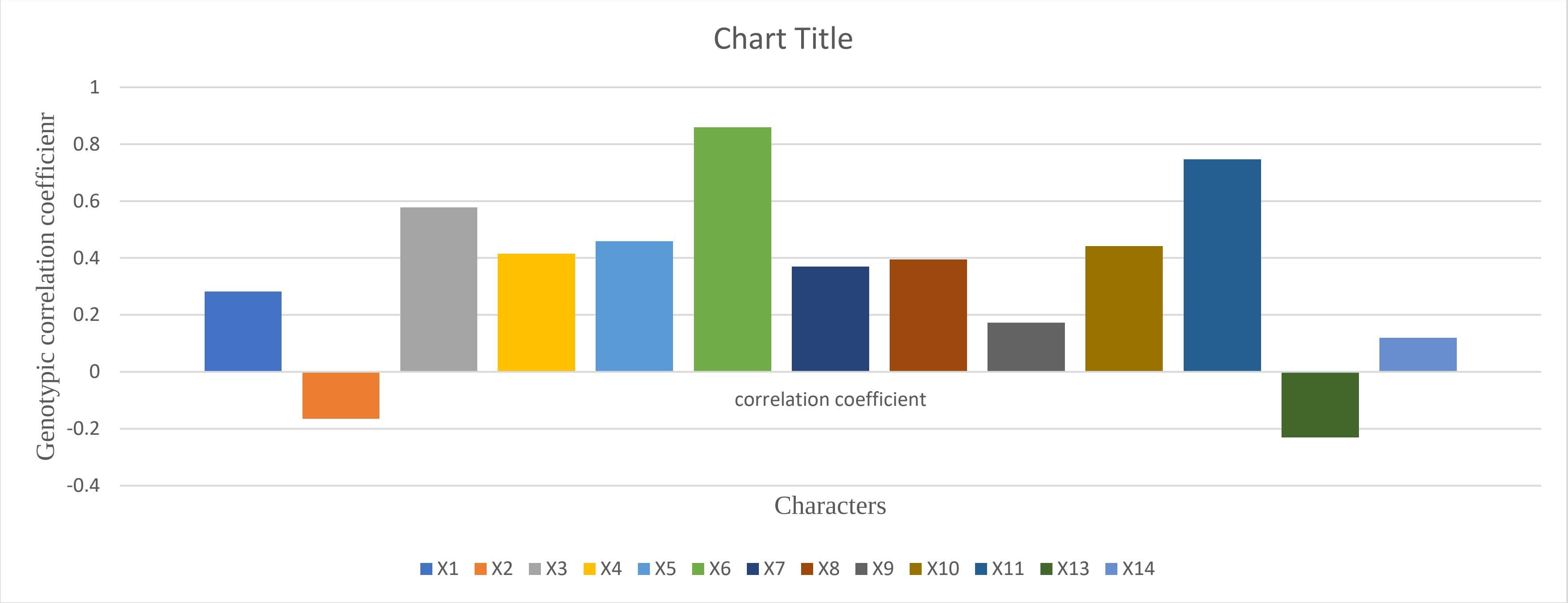
Heritability estimates alone do not provide reliable information regarding the gene action governing the expression of the particular trait as well as it does not give information on the magnitude of genetic progress resulting from the selection of the best individuals. Effective selection procedures depend up on merits of various attributes calculated using the genetic advance. Comparing heritability along with genetic advance indicated that the characters *viz.,* seed yield plant^{-1}, number of capsules per leaf axil, leaf area, dry matter production, number of capsules plant^{-1}, primary branches plant^{-1}, number of seeds capsule^{-1} and height of the plant had high heritability estimates along with high genetic advance as per cent of mean. Similar findings were recorded by Kalaiyarasi *et al.* (2019), Umamaheswari *et al*. (2019), Roy *et al*. (2022) for seed yield plant^{-1}, number of capsules plant^{-1}, number of primary branches, number of seeds capsule^{-1} and height of the plant; Bamrotiya *et al.* (2016) for number of capsules per leaf axil and Kadvani *et al.* (2020) for leaf area plant^{-1}.

Days for 50 per cent blooming, capsule length, 1000 seed weight, oil content and protein content showed high heritability along with moderate genetic advance as per cent of mean. These findings are in agreement with the observations of Kadvani *et al.* (2020) and Ranjithkumar *et al.* (2022) for oil content; Mohanty *et al*. (2020) for 50% flowering; and Sasipriya *et al*. (2022) for capsule length. However, Bindhu *et al.* (2014), Kehie *et al*. (2020), Mohanty *et al*. (2020) and Vamshi *et al*. (2021) observed both heritability and genetic advance as per cent of mean as high for oil content.

5.2 CORRELATION STUDIES

A thorough understanding of the association among the characters is essential for a plant breeder in order to improve the efficiency of selection.

Fig.7. Genotypic correlation of yield contributing traits with seed yield plant^{-1}



Correlation coefficient analysis measures the nature and extent of mutual relationship between plant traits and thereby helps in improving two or more characters simultaneously. A positive correlation shows a change of two variables in the same direction and *vice versa*. If a strong positive correlation exists that implies improvement of one character automatically improves the other character. Correlation among traits may be due to pleiotropy, linkage or physiological association between the characters. Thus, knowledge of the interrelationship among the characters is essential for achieving the desired combination of various components of yield.

In the present study, relationship of seed yield plant^{-1} with thirteen yield attributing components along with their relationship among themselves was examined using correlation coefficient analysis. Seed yield plant^{-1} had highly significant and positive correlation with number of capsules plant^{-1}, dry matter production, height of the plant, number of capsules per leaf axil, leaf area, primary branches plant^{-1}, number of seeds capsule^{-1}, capsule length and days for 50 per cent blooming.

The magnitude of correlation with seed yield was highest in the case of Number of capsules plant^{-1}. Similar findings were reported by Abhijatha *et al.* (2017), Abate (2018), Lalpantluangi and Shah (2018), Navaneetha *et al*., (2019), Umamaheswari *et al.* (2019), Disowja *et al.* (2020), Saravanan *et al*. (2020) and Aboelkassem *et al*. (2021). This distinctly suggest that more capsule number plant^{-1} can enhance seed yield plant^{-1} and therefore, more importance should be given to this character while making the selection for seed yield plant.

Contrary to the present findings, Kalaiyarasi *et al.* (2019), Manjeet *et al.* (2019) and Disowja *et al.* (2020) recorded significant negative correlation of days to fifty per cent flowering with seed yield plant^{-1}. Oil content showed significant and negative genotypic correlation with seed yield plant^{-1} which is in concordance with the reports of Swathy (2018).

For efficient indirect selection for seed yield on the basis of yield attributes, estimates of interrelationships among yield components are essential. Days for 50 per cent blooming had a significant positive inter-correlation with maturity days, leaf area and primary branches plant^{-1}. Kumari *et al*., (2019), Manjeet *et al.* (2019) and Patidar *et al.* (2020) have observed significant and positive association of maturity days with days for 50 per cent blooming.

Significant positive correlation was seen for number of capsules plant^{-1} with dry matter production, height of the plant, leaf area, number of capsules per leaf axil, primary branches plant^{-1}, capsule length and days for 50 per cent blooming. Similar results were reported by Goudappagoudra *et al.* (2011) for days for 50 per cent blooming, height of the plant and number of branches plant^{-1} and Rao *et al.* (2013) for capsule length.

Oil content exhibited a significant and negative inter-correlation with leaf area, dry matter production, height of the plant, primary branches plant^{-1}, number of capsules plant^{-1}, maturity days.

Significant positive inter-correlation was found between height of the plant and dry matter production, leaf area, number of capsules plant^{-1}, primary branches plant^{-1}, capsule length and protein content at both phenotypic and genotypic level. Similar findings were reported by Rao *et al.* (2013), Meenakumari and Ganesamurthy, (2015) and Kalaiyarasi *et al.* (2019) for height of the plant and number of capsules plant^{-1}. Contradictory to the present finding, Manjeet *et al*. (2019) reported significant and negative correlation of height of the plant with number of branches plant^{-1} and number of capsules plant^{-1}.

5.3 PATH COEFFICIENT ANALYSIS

The expression of a complex character such as seed yield plant^{-1} depends upon the interplay of a number of component traits. Sometimes the selection based on the whole correlation existing between yield and its component characters can mislead the research as it might be an over-estimate or an under-estimate due to either the direct or indirect effect of different variables. Therefore, the genotypic correlation was partitioned into direct and indirect effects based on the relationship between dependent variables such as yield and independent variables such as yield components. When many characters are affecting a given character, a better picture of the contribution of each component in building up the yield is obtained through path coefficient analysis. It will help in making the basis of selection more clear by easily identifying the selected traits that provide the most significant contribution to yield.

In the present investigation, path coefficient analysis was utilised to separate the genotypic correlation coefficient of seed yield plant^{-1} with height of the plant, primary branches plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, leaf area and dry matter production. The path coefficient analysis showed that number of capsules plant^{-1} registered maximum positive direct effect on seed yield plant^{-1} followed by number of seeds capsule^{-1}, number of capsules per leaf axil and height of the plant. These findings are supported by Gangadhara *et al.* (2012), Abhijatha *et al.* (2017) and Saravanan *et al*. (2020).

A low to moderate level of direct positive effect on seed yield plant^{-1} was observed for height of the plant and number of capsules per leaf axil whereas the correlation coefficients for this character with seed yield plant^{-1} was found to be high. Height of the plant registered high genotypic correlation with seed yield plant^{-1} *via* the high positive direct effect of number of capsules plant^{-1}. The high correlation coefficient of number of capsules per leaf axil was also assisted by number of capsules plant^{-1}. The traits *viz.,* primary branches plant^{-1}, capsule length and leaf area registered negligible direct effect on seed yield plant^{-1}. The association of dry matter production with seed yield plant^{-1} was significantly high and positive, but its direct effect on seed yield was found to be negative. This direct negative effect was nullified by moderate and high positive indirect effects *via* height of the plant and number of capsules plant^{-1}. In this situation the indirect causal factors have to be taken into consideration simultaneously for selection. In addition, height of the plant, leaf area, and dry matter production exhibited highly significant and positive correlation coefficient with seed yield plant^{-1} because of its high positive indirect effect *via* number of capsules plant^{-1}. The study confirmed that seed yield was mainly a product of high direct effects of number of capsules plant^{-1}. This was in accordance with earlier findings of Ibrahim and Khidir (2012), Abhijatha *et al.* (2017), Umamaheswari *et al.* (2019), Kumari *et al.* (2020), Kumar *et al*. (2022) and Sasipriya *et al*. (2022). Residual effect obtained in this study was low in magnitude indicating that almost all the important yield contributing traits were included in the path analysis.

From the results presented above, it can be inferred that the character, number of capsules plant^{-1} has to be given maximum weightage for the improvement of seed yield plant^{-1} as it showed a significant positive correlation coefficient and a high positive direct effect as compared to other traits.

5.4 STUDIES IN PARENTS AND F$_1$ GENERATION

5.4.1 Evaluation of Parents

Selection of parents is considered as one of the most crucial step in any breeding programme usually aimed for the improvement of seed yield plant^{-1}. Singh *et al*. (1993) suggested the importance of the parents with high mean performance in producing better offspring. The knowledge on *per se* along with *gca* of parents would be of great value in heterosis breeding of sesame. In the present study, eight parents including five lines and three testers were evaluated based on *per se* performance and *gca* effects to identify the superior ones.

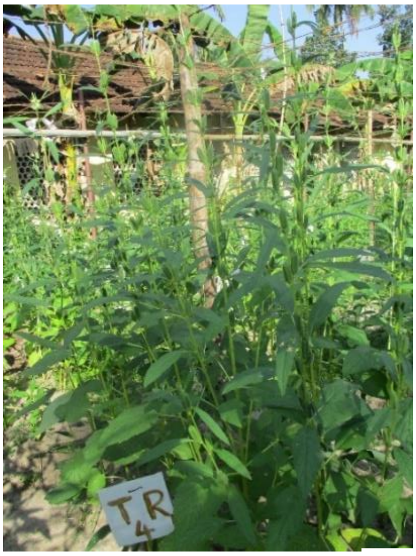
5.4.1.1 Per se Performance of Parents

High mean value has been the primary criterion used by the breeders for the selection of parents. Among the lines, Gu. Til 4 recorded the highest mean value for number of capsules per leaf axil, number of seeds capsule^{-1} and seed yield plant^{-1}. While the line, VRI-3 recorded highest mean value for days for 50 per cent blooming, primary branches plant, number of capsules plant^{-1} and dry matter

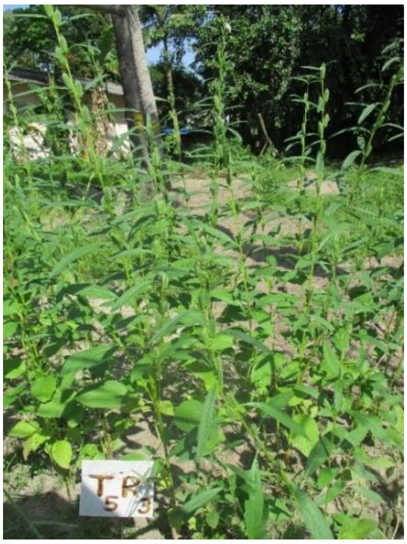
Gu. Til 4

VRI-3

PCU-42



Punjab Til No.2



RT-346

Plate 11. High seed yielding parents (Lines)

PCU-37

PCU-41

NIC-8322

Plate 12. High oil yielding parents (Testers)

production. For the traits, height of the plant and number of seeds capsule^{-1}, RT-346 was identified as the best parent among lines. The line, Punjab Til No.2 recorded maximum leaf area and the line and PCU-42 recorded highest 1000 seed weight and capsule length.

Among the testers, highest mean for seed yield plant^{-1} was recorded NIC-8322. Besides seed yield plant^{-1}, the tester NIC-8322 recorded highest mean values for oil content (experiment 1), primary branches plant^{-1}, capsule length and number of seeds capsule^{-1}. The tester PCU-41was having the highest mean performance for height of the plant, number of capsules plant^{-1}, 1000 seed weight, leaf area and dry matter production. Even though, seed yield plant^{-1} and other yield attributing traits were poor, the tester, PCU-37 recorded high oil content. Hence the above parents were adjudged as superior parents and could be potentially utilized in the development of hybrids.

5.4.1.2 General Combining Ability Effects

Dhillon (1975) opined that combining ability played an important role in selecting parents in order to get hybrids and their progenies with the expected performance. Singh and Singh (1985) reported that parents having high *gca* effects could produce transgressive segregation. The magnitude and nature of combining ability effect aids in recognising superior parents such they can be utilized in further breeding programmes. In the present study estimates of *gca* effect showed that it was hard to choose one good general combiner simultaneously for all the traits together, since the combining ability of parents were not consistent for all the traits.

Choosing the parents for hybridization based on combining ability is of utmost importance in a sound breeding programme. Such a study that is envisioned to ascertain the combining ability not only provides information concerning the choice of parents but also demonstrates the magnitude and nature of the gene action involved. This study was chosen to find out good combiners which can be utilised to make a population with favorable genes for seed yield and yield component characters in sesame. However, on an overall basis, the results of *gca* effect of the parents were categorized as good, average and poor combiners on the basis of their gene effect for different characters. The parent showing desirable and significant *gca* effect was considered as a good general combiner, while those with nonsignificant *gca* effect as an average general combiner and parent with significant but undesirable *gca* effect was considered as poor general combiner (Table 31).

Among the lines, Gu. Til 4 was identified to be a good general combiner for seven traits *viz*., seed yield plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight and dry matter production. The line VRI-3 was good general combiner for days for 50 per cent blooming and primary branches plant^{-1}, while the line Punjab Til No.2 showed desired *gca* effects for primary branches plant^{-1}, capsule length, number of seeds capsule^{-1} and 1000 seed weight. The line RT-346 had desired *gca* effect for four characters *viz*., maturity days, height of the plant, leaf area and dry matter production, while the line PCU-42 did not show desirable *gca* effect on any of the characters.

Among the testers, PCU-37 had given desired *gca* effect for five traits *viz*., number of capsules per leaf axil, capsule length, 1000 seed weight, leaf area and dry matter production. The tester PCU-41 was identified to be good general combiner for only one character *i.e.,* height of the plant. While the tester NIC-8322 gave desirable *gca* effect simultaneously for two characters *viz.,* primary branches plant^{-1} and number of capsules plant^{-1}.

Among the parents, the line Gu. Til 4 is the only one that demonstrated excellent general combining ability effect for seed yield plant^{-1}. None of the parents were identified as a good general combiner simultaneously for all the traits. Results on general combining ability for the traits studied were reported previously by Tripathy *et al*. (2016), Deshmukh *et al.* (2019) and Dela *et al*. (2019) for seed yield plant^{-1}, number of capsules plant^{-1}, number of primary branches plant^{-1}, number of seed capsule^{-1}, capsule length and height of the plant.

Table 31. Classification of parents with respect to *gca* effects for various characteristics in sesame

Sl no.	**Sources**	DFB	MD	HP	PBP	NCL	NCP	CL	NSC	TSW	LA	DMP	SYP
Lines													
1	Gu. Til 4	A	P	A	A	G	G	G	G	G	A	G	G
2	VRI-3	G	A	P	G	P	A	P	A	P	P	P	A
3	Punjab Til No.2	A	A	A	G	P	P	G	G	G	A	A	A
4	RT-346	P	G	G	A	P	A	P	P	A	G	G	P
5	PCU-42	A	A	A	P	P	P	A	A	P	P	A	P
Testers													
1	PCU-37	A	A	A	P	G	P	G	A	G	G	G	A
2	PCU-41	A	P	G	A	A	A	A	A	A	P	A	A
3	NIC-8322	A	A	P	G	A	G	P	A	P	P	P	A

G= Good general combiner having significant *gca* effect in desirable direction
A=Average general combiner having either positive or negative but nonsignificant
P=Poor general combiner having significant *gca* effect in undesirable direction

DFB	Days for 50 per cent blooming	CL	Capsule length
MD	Maturity days	NSC	Number of seeds capsule^{-1}
HP	Height of the plant (cm)	TSW	1000 seed weight
PBP	Primary branches plant^{-1}	LA	Leaf area
NCL	Number of capsules per leaf axil	DMP	Dry matter production
NCP	Number of capsules plant^{-1}	SYP	Seed yield plant^{-1} (g)

5.4.1.3 Based on Per se and gca Effect

In the present study, significantly superior general combining ability along with high mean performance is considered for the identification of superior parents. Among the line, Gu. Til 4 recorded superiority with respect to mean and *gca* for four traits *viz*., number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1} and seed yield plant^{-1}. The line VRI-3 recorded good performance based on *per se* and *gca* effect for the traits *viz*., days for 50 per cent blooming and primary branches plant^{-1}. While the line Punjab Til No.2 showed best performance for the trait 1000 seed weight based on *per se* and desirable *gca* effect. The line RT-346 registered high mean and *gca* estimates for the traits *viz*., maturity days, height of the plant, leaf area and dry matter production. Among the testers, NIC-8322 performed well for the trait primary branches plant^{-1} based on *per se* and desirable *gca* effect. These identified superior lines and testers were showing a positive association between *per se* performance and general combining ability of parents. Since Gu. Til 4 is identified as a good general combiner for seed yield plant^{-1} and other three characters, it can be regarded as the potential parent and may be preferred in subsequent breeding programme so that more number of characters can be combined using fewer number of parents in crossing programme. It is suggested that population involving the parent Gu. Til 4 in a multiple crossing programme will be helpful for isolating desirable recombinants. Further, the lines and testers which show good general combining ability for a particular character can be used in component breeding programme for effective improvement in particular components, ultimately aimed at improving seed yield itself.

The connection between *per se* performance of the parents and their *gca* effect indicated the importance of considering *per se* performance while choosing the parents for hybridization programme. If a character is unidirectionally controlled by a set of alleles and additive effects are important, selection based on *per se* performance is most effective. The parents that possess high *per se* performance may not always be good general combiners. This could be attributed to the intra and inter allelic interaction of the genes associated with the character which can be modified by environmental interference. Linkage at repulsion phase may result in low performing parents with good *gca* estimates also. The ranking based on *per se* performance (Best performing parent) and *gca* effect (Best general combiner) indicated the parents with high *per se* may not have desirable *gca* effect. Though they were not having both parameters, they cannot be eliminated since the *per se* of the parent is an actual value of the character concerned while *gca* effect is a predicted value. Therefore, even if the parents are not having desirable *gca* effects, they can be considered for further exploitation if they have high *per se* performance.

5.4.2 Evaluation of Hybrids

The fundamental objective of hybridization is to merge the favorable genes present in various parents in to a single genotype. These hybrids can be utilized either to exploit heterosis or for the production of superior segregants. The information of three best performing hybrids and good specific combiners are given in Table.

5.4.2.1 Per se Performance of Hybrids

The parents with good *per se* performance would result in good hybrids (Gilbert, 1958). Among the hybrids, Gu. Til 4 x PCU-41 exhibited good mean performance for days for 50 per cent blooming, height of the plant, number of capsules per leaf axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, leaf area, dry matter production and seed yield plant^{-1}; Gu. Til 4 x NIC-8322 for primary branches plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1} and seed yield plant^{-1}; VRI-3 x PCU-37 for maturity days; VRI-3 x PCU-41 for days for 50 per cent blooming, primary branches plant^{-1} and number of capsules plant^{-1}; VRI-3 x NIC-8322 for days for 50 per cent blooming; Punjab Til No.2 x PCU-37 for primary branches plant^{-1}, number of seeds capsule^{-1} and leaf area; Punjab Til No.2 x PCU-41 for 1000 seed weight; Punjab Til No.2 x NIC-8322 for maturity days; RT-346 x PCU-37 for height of the plant, 1000 seed weight, leaf area, dry matter production and seed yield plant^{-1}; RT-346 x PCU-41 for maturity days and PCU-42 x PCU-37 for height of the plant, capsule length, 1000 seed weight and dry matter production.

The present study revealed that even though the better performance of hybrids reflected from parents with high *per se* performance, there were hybrids with poor *per se* performance involving parents with high *per se* performance *viz*., Gu. Til 4 x PCU-37, RT-346 x NIC-8322, PCU-42 x PCU-41 and PCU-42 x NIC-8322 for seed yield plant^{-1}. These hybrids possess at least one parent that was identified to be possessing superiority in seed yield plant^{-1}. Hence, from the current study it was evident that the *per se* performance of F_1 hybrid is decided not only by the genetic architecture of parents but also due to the interaction of genes concerned for the character.

5.4.2.2 Specific Combing Ability Effects

Sprague and Tatum (1942) stated specific combining ability as those effects in certain combinations which significantly departed from what would be expected on the basis of the average performance of the parents involved. The *sca* effect is an important measure for the evaluation of hybrids next to mean performance and it is controlled by non-additive gene action.

Among fifteen hybrids studied, seven cross combinations exhibited significant and positive *sca* effect for seed yield plant^{-1}. The classification of parents with respect to *gca* effects suggested that a contribution of good general combiners was not necessarily the best combination nor a poor x poor combination. In fact, in most of the cross combinations the best specific combinations for different characters were either good x good, good x poor, average x average, average x poor and *vice versa* general combiners.

Selection is rapid if *gca* effect of parents and *sca* effect of crosses are in the same direction. The cross RT-346 x PCU-37 exerted the highest, significant positive *sca* effect which involved poor x average general combining parents for seed yield plant^{-1} followed by Punjab Til No.2 x PCU-37 which involved average x average general combining parents, VRI-3 x PCU-41 which involved average x average general combining parents, Gu. Til 4 x NIC-8322 which involved good x average general combining parents, Gu. Til 4 x PCU-41 which involved good x average general combining parents, PCU-42 x PCU-37 which involved poor x average general combining parents and VRI-3 x NIC-8322 which involved average x average general combining parents. This suggested that information on *gca* effect should be supplemented to *sca* effect.

Besides seed yield plant^{-1}, cross RT-346 x PCU-37 registered significant and desirable *sca* effects for the traits *viz.,* maturity days, height of the plant, primary branches plant^{-1}, number of capsule plant^{-1}, capsule length, number of seeds capsule^{-1}, thousand seed weight, leaf area and dry matter production; Punjab Til No.2 x PCU-37 for the traits *viz.,* primary branches plant^{-1}, number of capsule plant^{-1}, number of seeds capsule^{-1}, leaf area and dry matter production; VRI-3 x PCU-41 for the traits *viz.,* number of primary branches plant^{-1}, number of capsule plant^{-1}, leaf area and dry matter production; Gu. Til 4 x NIC-8322 for the traits *viz* height of the plant, primary branches plant^{-1}, number of capsules plant^{-1}, capsule length, thousand seed weight, leaf area and dry matter production; Gu. Til 4 x PCU-41 for the traits *viz.,* height of the plant, number of seeds capsule^{-1}, leaf area and dry matter production; PCU-42 x PCU-37 for the traits *viz.,* height of the plant, primary branches plant^{-1}, capsule length, number of seeds capsule^{-1}, thousand seed weight, leaf area and dry matter production and VRI-3 x NIC-8322 for the traits *viz.,* capsule length, number of seeds capsule^{-1}, thousand seed weight and dry matter production.

Significant *sca* effects were reported by Kumari *et al.,* (2015) for number of primary branches; Tripathy (2016) for number of capsules plant^{-1}, capsule length, height of the plant, number of seeds capsule^{-1}, and seed yield plant^{-1} and Deshmukh *et al.* (2019) for number of seeds capsule^{-1}.

5.4.2.3 Based on Per se and sca Effect

The high *sca* effect need not guarantee high performance by the hybrid and the estimation of *sca* effect seemed to be redundant, since no additional information was obtained from doing that (Chaudhary *et al*. 1974). In the present study, Gu. Til

4 x NIC-8322 which was the highest yielding hybrid didn't register the highest positive *sca* effect for seed yield plant^{-1}. Therefore, appropriate consideration has to be given to mean value of cross combination during the selection of crosses for specific combing ability effect.

5.4.3 Studies on Heterosis

Information on the magnitude of heterosis is a pre- requisite to filter out the most efficient combination of parents that can provide a higher degree of useful heterosis for seed yield and yield attributing characters. An ideal hybrid needs to show higher amount of heterosis for commercial benefit. Developing better hybrids with the use of stable and high yielding parents will raise the yield ceiling of sesame. In order to obtain high yielding cross combinations, it is vital to assess hybrid combinations for seed yield and its constituents. In the current investigation, per cent increase or decrease over mid parent, better parent (heterobeltiosis) and standard check, SVPR1 (Standard heterosis) was used as a measure of heterosis.

The primary step in exploiting the benefits of heterosis is to understand the direction and magnitude of heterosis. The magnitude and nature of heterosis either help to identify superior cross combinations for their commercial exploitation or for getting better transgressive segregants in segregating generations. The aim of estimation of heterosis in the present study was to identify superior hybrids for future use in the development of hybrids as well as in sesame breeding programme. Significant level of positive and negative relative heterosis, heterobeltiosis and standard heterosis in several crosses for most of the characters indicated genetic diversity of parents used in the crosses. Range of heterosis as well as number of crosses with response to heterotic effects for different traits in sesame are presented in Table 32.

For the traits *viz*., days for 50 per cent blooming, height of the plant, primary branches plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight, leaf area, dry matter production and seed yield plant^{-1} heterosis in the positive direction is considered as

Fig.8. Estimates of heterosis for seed yield plant^{-1}

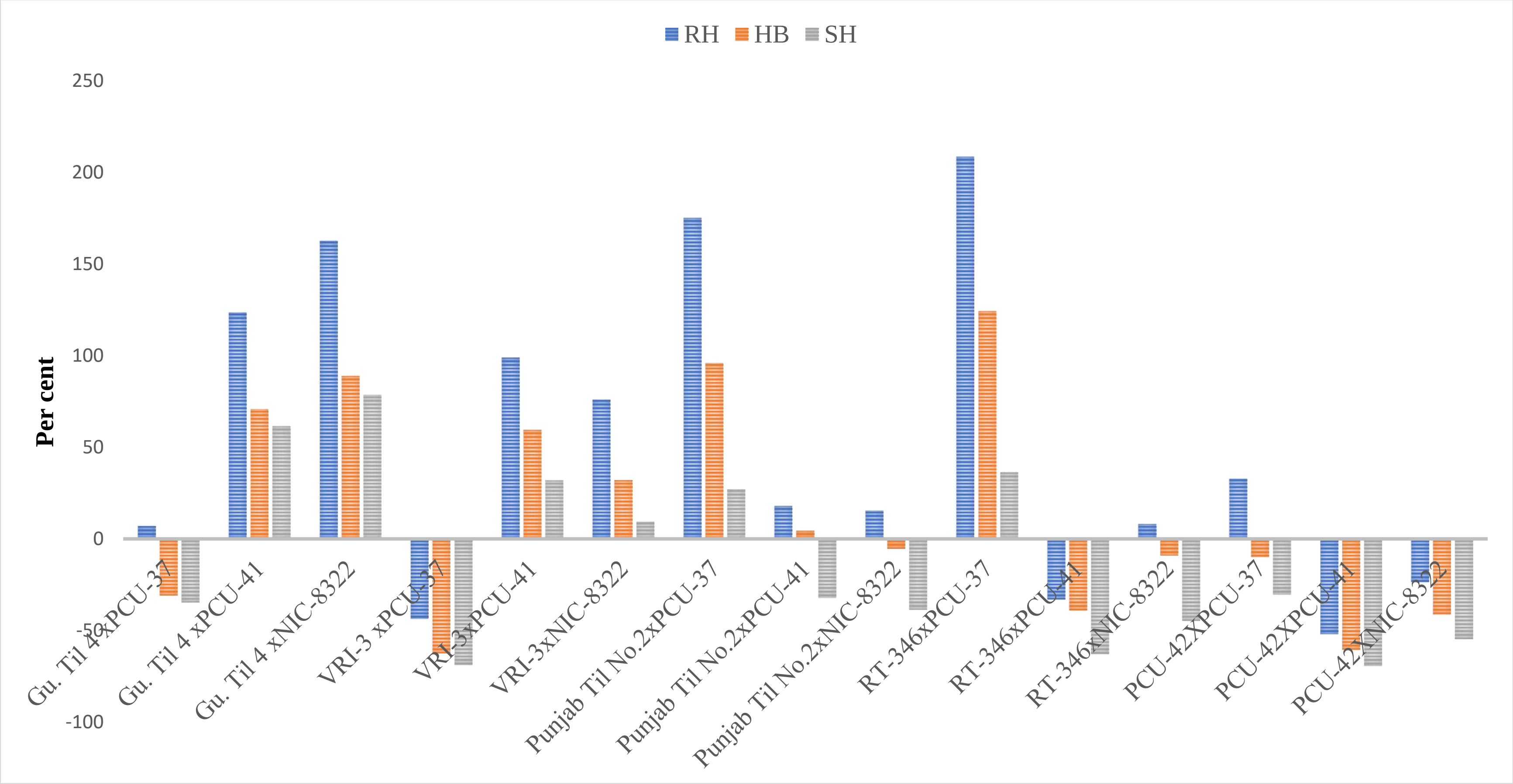


Table 32. Range of heterosis as well as number of crosses with response to heterotic effects for various traits in sesame

Sl. No.	**Characters**	**Range of heterosis**			**No. of crosses with significant heterosis**					
		RH	**HB**	**SH**	**RH**		**HB**		**SH**	
					+ve	-ve	+ve	-ve	+ve	-ve
1.	Days for 50 per cent blooming	-15.63 – 27.18	-23.94 – 26.53	-30.07 - 0.76	**01**	01	**01**	03	00	12
2	Maturity days	-7.78 - 10.4	-10.23 - 8.78	-8.63 - 11.76	03	**04**	02	**04**	02	**02**
3	Height of the plant (cm)	-6.66 - 31.34	-14.43 - 24.42	-20.21 - 15.18	**06**	00	**06**	05	**03**	04
4	Primary branches plant^{-1}	-48.72 - 130.99	-65.1 - 104.74	-68 - 45.33	**07**	02	**06**	03	**02**	07
5	Number of capsules per leaf axil	-6.25 - 60.78	-11.50 - 13.89	0.00 - 173.33	**04**	00	**03**	00	**04**	00
6	Number of capsules plant^{-1}	-17.39 - 141.99	-39.88 - 90.91	-44.65 - 47.97	**10**	00	**05**	02	**03**	08
7	Capsule length (cm)	-18.92 - 15.41	-23.08 - 11.11	-9.85 - 17.68	**06**	02	**03**	03	**05**	02
8	Number of seeds capsule^{-1}	-19.81 - 26.02	-22.73 - 21.67	-23.90 - 25.86	**05**	04	**02**	06	**05**	03
9	1000 seed weight	-22.55 - 38.07	-25.12 - 34.29	-18.25 - 16.82	**06**	04	**02**	05	**05**	04
10	Leaf area	-67.70 - 81.44	-76.78 - 35.92	-82.18 - 48.71	**05**	10	**04**	10	**02**	12
11	Dry matter production	-34.56 - 123.64	-51.93 - 74.50	-55.71 - 42.92	**07**	02	**07**	04	**05**	07
12	Seed yield plant^{-1}	-51.97 - 208.71	-62.43 - 124.24	-69.46 - 78.57	**06**	03	**06**	05	**05**	09

desirable. While for the trait maturity days heterosis in the negative direction is considered as desirable. In practice, selection is weighed in relation to the standard variety (Kadambavanasundaram (1983) and Grakh and Chaudhary (1985)).

In the present study, the five hybrids *viz.*, Gu. Til 4 x NIC-8322, Gu. Til 4 x PCU-41, RT-346 x PCU-37, VRI-3 x PCU-41 and Punjab Til No.2 x PCU-37recorded significant positive standard heterosis over the check SVPR1 for seed yield plant^{-1}. Besides seed yield plant^{-1}, Gu. Til 4 x NIC-8322 showed significant standard heterosis for primary branches plant^{-1}, number of capsules leaf per axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight and dry matter production; Gu. Til 4 x PCU-41 for the traits *viz.*, height of the plant, number of capsules leaf per axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1} and dry matter production; RT-346 x PCU-37 for the traits *viz.*, height of the plant, 1000 seed weight, leaf area and dry matter production; VRI-3 x PCU-41 for the traits *viz.*, primary branches plant^{-1} and number of capsules plant^{-1} and Punjab Til No.2 x PCU-37 for the traits *viz.*, number of seeds capsule^{-1}, leaf area and dry matter production. In the case of days for 50 per cent blooming, none of the crosses reported significant and positive standard heterosis. Virani *et al*. (2017) also reported significant standard heterosis for the traits *viz.*, maturity days, height of the plant, number of branches plant^{-1}, capsule length, number of capsules plant^{-1}, number of capsules per leaf axil, number of seeds capsule^{-1}, 1000 seed weight, and seed yield plant^{-1}.

5.4.3 Studies on Gene Action

The relative amount of *gca* and *sca* effect had a vital role in planning the appropriate and sound breeding programme. Sprague and Tatum (1942) reported that combining ability analysis provides information about the magnitude and nature of different types of gene action that governs various quantitative traits. The nature of gene action helps to decide the breeding procedures for the genetic improvement of such characters. Variance of general combining ability and specific combining ability effects provides a measure of variation due to additive and dominance or non-additive gene action respectively. Additive gene action offers fixable variation, whereas non-additive gene action includes effects of dominance and epistasis, which cannot be fixed. This is helpful for the breeder to know about the relative proportions of additive and non-additive genetic variances related with the inheritance of different characters. It also helps to decide appropriate breeding methods for the utilisation of available genetic variation. The existence of non-additive gene action is the main justification for starting the hybrid breeding programme (Cockerham, 1961).

Ratio of additive (GCA) and dominance (SCA) genetic variances was found to be less than unity for all characters investigated except number of capsules per leaf axil, indicating the preponderance of nonadditive gene action in governing the inheritance of the traits. Similar findings were reported by Joshi *et al*. (2015) and Dela *et al*. (2019) for days for 50 per cent blooming, height of the plant, number of effective branches plant^{-1}, number of capsules plant^{-1}, capsule length, maturity days, number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1}.

In contrary to the findings of the present study Tripathy *et al*. (2016) reported the presence of additive gene action in controlling days to initial flowering, maturity days, height to first capsule, height of the plant, number of primary branches plant^{-1}, number of capsule plant^{-1}, capsule length, number of seeds capsule^{-1} and seed yield plant^{-1}; Jeeva *et al* (2020) for days for 50 per cent blooming, height of the plant, the number of branches plant^{-1}, the number of capsules plant^{-1}, capsule length, the number of seeds capsule^{-1}, 1000 seed weight and seed yield plant^{-1}.; Sirohi *et al.* (2020) for days for 50 per cent blooming, maturity days and 1000 seed weight.

In view of the preponderance of non-additive gene action and high heterosis observed for seed yield and attributing character ensured the profitability and usage of heterosis breeding for the exploiting the hybrid vigour in sesame.

5.4.5. Based on *Per se, sca* Effect and Heterosis

According to standard heterosis and *per se* performance for seed yield plant^{-1}, the hybrid Gu. Til 4 x NIC-8322 ranked first. While, the hybrid RT-346 x PCU-37 ranked first while considering highest, significant and positive relative heterosis, heterobeltiosis and *sca effect* for seed yield plant^{-1}. In such cases, the standard heterosis and *per se* performance indicated the real superiority of hybrids from the commercial point of view (Pethani and Kapoor (1984) and Rogbell *et al.* (1998)). The results revealed best six hybrids on the basis of *per se* performance, heterobeltiosis, standard heterosis and *sca* effect for seed yield plant^{-1} and standard heterosis for component characters in sesame *viz*., Gu. Til 4 x NIC-8322, Gu. Til 4 x PCU-41, RT-346 x PCU-37, VRI-3 x PCU-41, Punjab Til No.2 x PCU-37 andVRI-3 x NIC-8322 (Table 33 and Plate 13).

5.6. *PER SE* PERFORMANCE OF F_2 AND F_3 SEGREGATING POPULATION

The performance of the best segregants was studied in F_2 and F_3 population. Here pedigree method was followed. In pedigree method, there is a conflict of handling a large number of crosses. Pedigree record include the distinguishing features of each progeny. Only promising progenies were included in the record. Poor progenies were simply discarded. It helped to give more focus to the promising progenies.

Among the F_2 segregants studied, cross combinations *viz.*, Gu. Til 4 x PCU-37, Gu. Til 4 x PCU-41, Gu. Til 4 x NIC-8322, VRI-3 x PCU-41, VRI-3 x NIC-8322, Punjab Til No.2 x PCU-37, Punjab Til No.2 x PCU-41, RT-346 x PCU-37, PCU-42 x PCU-37 and PCU-42 x NIC-8322 produced transgressive segregants for seed yield plant^{-1}. In the F_2 generation, the highest count of transgressive segregants for seed yield plant^{-1} was seen in the cross VRI-3 x PCU-41 (24 progenies) which was one among the best hybrids. The remaining progenies of the five hybrids *viz*., VRI-3 x PCU-37, Punjab Til No.2 x NIC-8322, RT-346 x PCU-41, RT-346 x NIC-8322 and PCU-42 x PCU-41 were not proceeded to the subsequent generation because of its poor yield performance.

Gu. Til 4 x NIC-8322 Gu. Til 4 x PCU-41 RT-346 x PCU-37

VRI-3 x PCU-41 Punjab Til No.2 x PCU-37 VRI-3 x NIC-8322

Plate 13. The best performing hybrids for seed yield per plant

VRI-3 x PCU-41
Pedigree - 2105-10

Gu. Til 4 x NIC-8322
Pedigree - 2103-44

Punjab Til No.2 x PCU-37
Pedigree - 2107-58 (i)

VRI-3 x PCU-41
Pedigree - 2105-81 (i)

Punjab Til No.2 x PCU-41
Pedigree - 2108-85

RT-346 x PCU-37
Pedigree - 2110-64

PCU-42 x PCU-37
Pedigree - 2113-52 (i)

Plate 14. Promising segregants recommended for further evaluation and breeding

From the forty superior segregants identified in F_3, seven superior segregants with high seed yield, oil content and protein content were selected from six families of the crosses *viz*., Gu. Til 4 x NIC-8322, VRI-3 x PCU-41, Punjab Til No.2 x PCU-37, Punjab Til No.2 x PCU-41, RT-346 x PCU-37, PCU-42 x PCU-37 (Plate 14). These superior segregants may be forwarded to advanced generations and yield trials for confirming their superiority and release as a variety.

Table 33. Promising parents and F_1 for *per se* performance, combining ability effects and heterosis for various characteristics in sesame

Character	**Rank**	**Best performing parent**	**Best general combiner**	**Per se performance of hybrid**	**Heterosis (%)**			***sca* effect**
					Relative Heterosis	Heterobeltiosis	Standard heterosis	
Days for 50 per cent blooming	**I.**	VRI-3	VRI-3	VRI-3 x PCU-41	Gu. Til 4 x PCU-41	Gu. Til 4 x PCU-41	-	-
	II.	NIC-8322	-	Gu. Til 4 x PCU-41	-	-	-	-
	III.	PCU-37	-	VRI-3 x NIC-8322	-	-	-	-
Maturity days	**I.**	RT-346	RT-346	RT-346 x PCU-41	Punjab Til No.2 x NIC-8322	Punjab Til No.2 x NIC-8322	RT-346 x PCU-41	VRI-3 x PCU-41
	II.	Gu. Til 4	-	Punjab Til No.2 x NIC-8322	VRI-3 x PCU-37	RT-346 x PCU-41	Punjab Til No.2 x NIC-8322	Punjab Til No.2 x PCU-37
	III.	Punjab Til No.2	-	VRI-3 x PCU-37	RT-346 x PCU-41	VRI-3 x PCU-37	-	RT-346 x NIC-8322
Height of the plant (cm)	**I.**	RT-346	PCU-41	RT-346 x PCU-37	PCU-42 x PCU-37	Gu. Til 4 x PCU-41	RT-346 x PCU-37	PCU-42 x PCU-37
	II.	VRI-3	RT-346	Gu. Til 4 x PCU-41	RT-346 x PCU-37	Gu. Til 4 x NIC-8322	Gu. Til 4 x PCU-41	Gu. Til 4 x NIC-8322
	III.	PCU-42	-	PCU-42 x PCU-37	Gu. Til 4 x PCU-41	PCU-42 x PCU-37	PCU-42 x PCU-37	RT-346 x PCU-37

Table 33. Continued

Character	**Rank**	**Best performing parent**	**Best general combiner**	***Per se* performance of hybrid**	**Heterosis (%)**			***sca* effect**
					Relative Heterosis	Heterobeltiosis	Standard heterosis	
Primary branches plant^{-1}	**I.**	VRI-3	Punjab Til No.2	VRI-3 x PCU-41	Punjab Til No.2 x PCU-37	Punjab Til No.2 x PCU-37	VRI-3 x PCU-41	VRI-3 x PCU-41
	II.	RT-346	NIC-8322	Gu. Til 4 x NIC-8322	Gu. Til 4 x NIC-8322	Gu. Til 4 x NIC-8322	Gu. Til 4 x NIC-8322	Punjab Til No.2 x PCU-37
	III.	NIC-8322	VRI-3	Punjab Til No.2 x PCU-37	Gu. Til 4 x PCU-41	Gu. Til 4 x PCU-41	-	RT-346 x PCU-37
Number of capsule per leaf axil	**I.**	Gu. Til 4	Gu. Til 4	Gu. Til 4 x PCU-37	Gu. Til 4 x PCU-37	Gu. Til 4 x PCU-37	Gu. Til 4 x PCU-37	-
	II.	PCU-42	PCU-37	Gu. Til 4 x NIC-8322	Gu. Til 4 x NIC-8322	PCU-42 x PCU-37	Gu. Til 4 x NIC-8322	-
	III.	VRI-3	-	Gu. Til 4 x PCU-41	Gu. Til 4 x PCU-41	Gu. Til 4 x NIC-8322	Gu. Til 4 x PCU-41	-
Number of capsules plant^{-1}	**I.**	VRI-3	Gu. Til 4	Gu. Til 4 x NIC-8322	Gu. Til 4 x NIC-8322	Gu. Til 4 x NIC-8322	Gu. Til 4 x NIC-8322	VRI-3 x PCU-41
	II.	RT-346	NIC-8322	VRI-3 x PCU-41	RT-346 x PCU-37	Gu. Til 4 x PCU-41	VRI-3 x PCU-41	RT-346 x PCU-37
	III.	Gu. Til 4	-	Gu. Til 4 x PCU-41	Gu. Til 4 x PCU-41	RT-346 x PCU-37	Gu. Til 4 x PCU-41	Punjab Til No.2 x PCU-37

Table 33. Continued

Character	**Rank**	**Best performing parent**	**Best general combiner**	***Per se* performance of hybrid**	**Heterosis (%)**			***sca* effect**
					Relative Heterosis	Heterobeltiosis	Standard heterosis	
Capsule length (cm)	**I.**	PCU-42	Gu. Til 4	PCU-42 x PCU-37	Gu. Til 4 x PCU-41	Punjab Til No.2 x PCU-41	PCU-42 x PCU-37	PCU-42 x PCU-37
	II.	NIC-8322	Punjab Til No.2	Gu. Til 4 x PCU-41	Punjab Til No.2 x PCU-41	Gu. Til 4 x PCU-41	Gu. Til 4 x PCU-41	VRI-3 x NIC-8322
	III.	Gu. Til 4	-	Gu. Til 4 x NIC-8322	PCU-42 x PCU-37	Punjab Til No.2 x PCU-37	Gu. Til 4 x NIC-8322	Gu. Til 4 x NIC-8322
Number of seeds capsule^{-1}	**I.**	Gu. Til 4	Gu. Til 4	Gu. Til 4 x PCU-41	Punjab Til No.2 x PCU-37	Punjab Til No.2 x PCU-37	Gu. Til 4 x PCU-41	Gu. Til 4 x PCU-41
	II.	NIC-8322	Punjab Til No.2	Punjab Til No.2 x PCU-37	Gu. Til 4 x PCU-41	Punjab Til No.2 x PCU-41	Punjab Til No.2 x PCU-37	PCU-42 x PCU-37
	III.	PCU-42	-	Gu. Til 4 x NIC-8322	Punjab Til No.2 x PCU-41	-	Gu. Til 4 x NIC-8322	VRI-3 x NIC-8322
1000 seed weight	**I.**	PCU-42	Punjab Til No.2	PCU-42 x PCU-37	RT-346 x PCU-37	RT-346 x PCU-37	PCU-42 x PCU-37	PCU-42 x PCU-37
	II.	Punjab Til No.2	PCU-37	RT-346 x PCU-37	PCU-42 x PCU-37	PCU-42 x PCU-37	RT-346 x PCU-37	VRI-3 x NIC-8322
	III.	PCU-41	Gu. Til 4	Punjab Til No.2 x PCU-41	Gu. Til 4 x PCU-37	-	Punjab Til No.2 x PCU-41	RT-346 x PCU-37

Table 33. Continued

Character	**Rank**	**Best performing parent**	**Best general combiner**	***Per se* performance of hybrid**	**Heterosis (%)**			***sca* effect**
					Relative Heterosis	Heterobeltiosis	Standard heterosis	
Leaf area	**I.**	Punjab Til No.2	PCU-37	RT-346 x PCU-37	RT-346 x PCU-37	PCU-42 x PCU-37	RT-346 x PCU-37	Rt-346 x PCU-37
	II.	VRI-3	RT-346	Punjab Til No.2 x PCU-37	PCU-42 x PCU-37	RT-346 x PCU-37	Punjab Til No.2 x PCU-37	Gu. Til 4 x PCU-41
	III.	RT-346	-	Gu. Til 4 x PCU-41	Punjab Til No.2 x PCU-37	Gu. Til 4 x PCU-41	-	Punjab Til No.2 x PCU-37
Dry matter production	**I.**	VRI-3	RT-346	RT-346 x PCU-37	RT-346 x PCU-37	PCU-42 x PCU-37	RT-346 x PCU-37	PCU-42 x PCU-37
	II.	RT-346	Gu. Til 4	Gu. Til 4 x PCU-41	PCU-42 x PCU-37	Gu. Til 4 x PCU-41	Gu. Til 4 x PCU-41	Gu. Til 4 x PCU-41
	III.	PCU-41	PCU-37	PCU-42 x PCU-37	Punjab Til No.2 x PCU-37	RT-346 x PCU-37	PCU-42 x PCU-37	Rt-346 x PCU-37
Seed yield plant^{-1}	**I.**	Gu. Til 4	Gu. Til 4	Gu. Til 4 x NIC-8322	RT-346 x PCU-37	RT-346 x PCU-37	Gu. Til 4 x NIC-8322	Rt-346 x PCU-37
	II.	VRI-3	-	Gu. Til 4 x PCU-41	Punjab Til No.2 x PCU-37	Punjab Til No.2 x PCU-37	Gu. Til 4 x PCU-41	Punjab Til No.2 x PCU-37
	III.	PCU-42	-	RT-346 x PCU-37	Gu. Til 4 x NIC-8322	Gu. Til 4 x NIC-8322	RT-346 x PCU-37	VRI-3 x PCU-41

Table 34. The best performing hybrids for seed yield per plant along with heterobeltiosis, standard heterosis and *sca* effect and standard heterosis for component characters in sesame

Sl. no.	**Hybrids**	**Seed yield plant^{-1}**	**Hetero-beltiosis**	**Standard heterosis**	***sca* effect**	**Significant desirable standard heterosis for component traits**
1	Gu. Til 4 x NIC-8322	32.98	88.87	78.57	7.52	PBP, NCL, NCP, CL, NSC, TSW, DMP
2	Gu. Til 4 x PCU-41	29.81	70.71	61.41	5.13	HP, NCL, NCP, CL, NSC, DMP
3	RT-346 x PCU-37	25.16	124.24	36.25	11.34	HP, TSW, LA, DMP
4	VRI-3 x PCU-41	24.37	59.49	31.97	7.87	PBP, NCP
5	Punjab Til No.2 x PCU-37	23.46	95.99	27.04	7.95	CL, NSC, LA, DMP
6	VRI-3 x NIC-8322	20.18	32.07	9.28	2.90	NSC

HP	Height of the plant (cm)	NSC	Number of seeds capsule^{-1}
PBP	Primary branches plant^{-1}	LA	Leaf area
NCL	Number of capsules per leaf axil	DMP	Dry matter production
NCP	Number of capsules plant^{-1}	TSW	1000 seed weight (g)
CL	Capsule length (cm)		

Summary

6. SUMMARY

The present investigation on "Development of superior varieties in white seeded sesame for seed yield and oil content' was undertaken to develop superior genotypes in white seeded sesame for high seed yield and oil content. The study was conducted at Onattukara Regional Agricultural Research Station, Kerala Agricultural University during 2019-2022. The study consisted of five experiments.

In the first experiment, thirty white seeded sesame genotypes constituted the experimental material which was evaluated for variability and character association studies. Observations were recorded for biometrical characters *viz.,* days for 50 per cent blooming, maturity days, height of the plant, primary branches plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight, leaf area, dry matter production and seed yield plant^{-1}; and quality characters *viz.,* oil content and protein content (%). From the thirty genotypes evaluated, five high seed yielding genotypes (lines) and three genotypes with high oil content (testers) were selected and crossed in a Line x Tester mating design (Experiment II). In experiment III, fifteen hybrid combinations obtained were raised in the field along with the parents and evaluated for heterosis and combining ability. Identification and selection of superior recombinants in F_2 and F_3 was done in Experiment IV and V respectively. All the biometrical characters were studied in Experiment III and IV while biometrical as well as quality characters were studied in the last experiment. The salient findings of the present investigation are summarized as under

1. Significant differences were found among the genotypes for all the fourteen characters when analysis of variance was performed. This suggests the presence of wide genetic variability in the materials used for evaluation studies. The parents and hybrids also showed significant differences for all the twelve biometric characters. The mean squares due to parents *vs* hybrids were also found significant for the characters height of the plant, primary branches plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-}

^{1}, capsule length, 1000 seed weight, leaf area, dry matter production and seed yield plant^{-1} and it indicates presence of mean heterosis for these characters.

2. The values of genotypic and phenotypic coefficient of variation were high for the traits *viz.*, seed yield plant^{-1}, primary branches plant^{-1}, number of capsules per leaf axil, number of capsules plant^{-1}, leaf area and dry matter production. The characters *viz.*, height of the plant, number of seeds capsule^{-1}, days for 50 per cent blooming and 1000 seed weight showed moderate GCV and PCV. The magnitude of PCV was higher than corresponding GCV for all the characters which indicated the influence of surrounding environment on the character expression.
3. Heritability was high for all the characters except maturity days. The genetic advance was high for all the characters except 1000 seed weight, days for 50 per cent blooming, capsule length, protein content, oil content and maturity days.
4. High heritability along with high values of genetic advance as per cent of mean was recorded for the traits *viz.*, seed yield plant^{-1}, number of capsules per leaf axil, leaf area, dry matter production, number of capsules plant^{-1}, primary branches plant^{-1}, number of seeds capsule^{-1} and height of the plant. Days for 50 per cent blooming, capsule length, 1000 seed weight, oil content and protein content showed high heritability along with moderate genetic advance as per cent of mean.
5. The correlation analysis showed that the seed yield plant^{-1} had significant and positive correlation with number of capsules plant^{-1}, dry matter production, height of the plant, number of capsules per leaf axil, leaf area, primary branches plant^{-1}, number of seeds capsule^{-1}, capsule length and days for 50 per cent blooming. The magnitude of correlation with seed yield was highest in case of number of capsules plant^{-1}. Among the intercorrelations, days for 50 per cent blooming had significant positive

correlation with maturity days, leaf area and primary branches plant^{-1}. Significant positive correlation was observed for number of capsules plant^{-1} with dry matter production, height of the plant, leaf area, number of capsules per leaf axil, primary branches plant^{-1}, capsule length and days for 50 per cent blooming. Oil content exhibited significant and negative correlation with leaf area, dry matter production, height of the plant, primary branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1} and seed yield plant^{-1} while it showed significant and positive genotypic correlation with maturity days.

6. The path coefficient analysis revealed that number of capsules plant^{-1} registered maximum positive direct effect on seed yield plant^{-1} followed by number of seeds capsule^{-1}, number of capsules per leaf axil and height of the plant. Number of capsules plant^{-1} showed high positive indirect effect on seed yield plant^{-1} *via* height of the plant, leaf area and dry matter production.

7. Out of the thirty genotypes evaluated, based on *per se* performance of seed yield plant^{-1} and oil content; five genotypes (lines) *viz.*, Gu-4, VRI-3, Punjab Til No.2, RT-346 and PCU-42 and three genotypes (testers) *viz.*, PCU-37, PCU-38 and NIC-8322 respectively were selected and crossed in Line x Tester mating design.

8. The estimated components of genetic variance indicated that the additive genetic variance was higher than variance due to dominance only for number of capsules per leaf axil which indicated the preponderance of additive gene action. This was further supported by high magnitude of σ^2D/σ^2H ratio (more than 1). For the remaining characters *viz.*, days for 50 per cent blooming, maturity days, height of the plant, primary branches plant^{-1}, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight, leaf area, dry matter production and seed yield plant^{-1}, additive genetic variance was lower than variance due to dominance indicating the

presence of non-additive gene action. This was further confirmed by low magnitude of σ^2D/ σ^2H ratio (less than 1).

9. Among the parents, Gu. Til 4 was identified to be good general combiner for seven traits *viz*., number of capsules per leaf axil, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight, dry matter production and seed yield plant^{-1}.

10. Among the hybrids, Gu. Til 4 x NIC-8322 showed highest *per se* performance for the traits seed yield plant^{-1} followed by Gu. Til 4 x PCU-41 and RT-346 x PCU-37

11. The estimates of *sca* effects of crosses indicated that seven out of fifteen crosses had reported significant and positive *sca* effect for seed yield plant^{-1}. Among them, the highest *sca* effect was manifested by the cross RT-346 x PCU-37 followed by Punjab Til No.2 x PCU-37, VRI-3 x PCU-41, Gu. Til 4 x NIC-8322, Gu. Til 4 x PCU-41, PCU-42 x PCU-37 and VRI-3 x NIC-8322. Besides seed yield plant^{-1}, the cross RT-346 x PCU-37 registered significant and desirable *sca* effects for the traits *viz.,* maturity days, height of the plant, primary branches plant^{-1}, number of capsules plant^{-1}, capsule length, number of seeds capsule^{-1}, 1000 seed weight, leaf area and dry matter production.

12. Significant *sca* effects for seed yield plant^{-1} was observed for the crosses from parental combinations, namely, good x average, average x average, average x poor general combiners

13. Significant estimates of relative heterosis, standard heterosis, and heterobeltiosis were observed in six, six and five cross combinations, respectively for seed yield plant^{-1}. The highest and positive standard heterosis for seed yield plant^{-1} was recorded in the cross Gu. Til 4 x NIC-8322 (78.57%) followed by Gu. Til 4 x PCU-41 (61.41%), RT-346 x PCU-37 (36.25%), VRI-3 x PCU-41 (31.97%) and Punjab Til No.2 x PCU-37

(27.04%). The heterosis for seed yield plant^{-1} was also associated with heterosis for its component traits.

14. The highest magnitude of standard heterosis along with highest *per se* performance for seed yield plant^{-1} was observed in cross Gu. Til 4 x NIC-8322 followed by Gu. Til 4 x PCU-41 and RT-346 x PCU-37.
15. Among the F_2 segregants, the progenies of the crosses Gu. Til 4 x PCU-37, Gu. Til 4 x PCU-41, Gu. Til 4 x NIC-8322, VRI-3 x PCU-41, VRI-3 x NIC-8322, Punjab Til No.2 x PCU-37, Punjab Til No.2 x PCU-41, RT-346 x PCU-37, PCU-42 x PCU-37 and PCU-42 x NIC-8322 produced high yield potential segregants.
16. In the F_2 generation, the highest count of transgressive segregants for seed yield plant^{-1} was found in the cross VRI-3 x PCU-41 (24 progenies).
17. Seven superior segregants with high seed yield, oil content and protein content were selected from six families of the crosses *viz.,* Gu. Til 4 x NIC -8322, VRI-3 x PCU-41, Punjab Til No.2 x PCU-37, Punjab Til No.2 x PCU-41, RT-346 x PCU-37, PCU-42 x PCU-37. These superior segregants may be forwarded to advanced generations and yield trials for confirming their superiority and release as a variety.

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DEVELOPMENT OF SUPERIOR VARIETIES IN WHITE SEEDED SESAME FOR SEED YIELD AND OIL CONTENT

by

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Abstract

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ABSTRACT

The present study entitled "Development of superior varieties in white seeded sesame for seed yield and oil content' was carried out at ORARS, Kayamkulam during 2019-2022. The objectives of the study were collection and evaluation of various genotypes of white seeded sesame for seed yield and oil content, to study the heterosis and combining ability and to develop superior segregants of white seeded sesame genotypes with high seed yield and oil content. The study consisted of five experiments.

In the first experiment, thirty white seeded sesame genotypes obtained from different parts of India were assessed for genetic variability, heritability, genetic advance, correlation and path analysis of seed yield and thirteen other traits. Analysis of variance showed significant differences among the genotypes for all investigated characters. The genotype Gu. Til 4 and PCU-37 recorded highest seed yield plant^{-1} and oil content respectively. The seed yield plant^{-1} exhibited the highest GCV (43.59 %) and PCV (49.72%). Heritability was high for all the characters except maturity days (49.48%). The genetic advance was high for all the characters except 1000 seed weight, days for 50 per cent blooming, capsule length, protein content, oil content and maturity days. High heritability coupled with high genetic advance as per cent of mean was recorded for seed yield plant^{-1}, number of capsules per leaf axil, leaf area, dry matter production, number of capsules plant^{-1}, primary branches plant^{-1}, number of seeds capsule^{-1} and height of the plant indicating additive gene action. Hence selection based on these characters may be rewarding.

The association analysis revealed that seed yield plant^{-1} has significant and positive correlation with number of capsules plant^{-1}, dry matter production, height of the plant, number of capsules per leaf axil, leaf area, primary branches plant^{-1}, number of seeds capsule^{-1} and capsule length. The high significant positive direct effect was recorded by number of capsules plant^{-1}, number of seeds capsule^{-1}, number of capsules per leaf axil and height of the plant with seed yield plant^{-1}.

Among the thirty genotypes evaluated in experiment I, five high seed yielding genotypes (lines) *viz.*, Gu. Til 4, VRI-3, Punjab Til No.2, RT-346 and

PCU-42 and three genotypes with high oil content (testers) *viz.*, PCU-37, PCU-38 and NIC-8322 were chosen and crossed in a Line x Tester mating design (experiment II)

In experiment III, fifteen hybrid combinations obtained were raised in the field along with the parents and evaluated for heterosis and combining ability. The analysis of variance showed significant differences for all the characters among parents and crosses. The cross Gu. Til 4 x NIC-8322 manifested highest seed yield plant^{-1} followed by the crosses Gu. Til 4 x PCU-41 and RT-346 x PCU-37.

Combining ability analysis demonstrated the dominance of non-additive gene action for most of the traits except number of capsules per leaf axil. Among the parents, Gu. Til 4 was the good general combiner as it displayed highly significant and positive *gca* effect for seed yield plant^{-1}. Among the crosses, highest significant *sca* effect for seed yield plant^{-1} was manifested by the cross RT-346 x PCU-37 followed by Punjab Til No.2 x PCU-37 and VRI-3 x PCU-41. The highest magnitude of standard heterosis along with high *per se* performances for seed yield plant^{-1} was observed in the cross Gu. Til 4 x NIC-8322 followed by Gu. Til 4 x PCU-41 and RT-346 x PCU-37.

In experiment IV, F_2 seeds obtained from the F_1 hybrids were raised in the field. The highest number of transgressive segregants in the F_2 generation for seed yield plant^{-1} was observed in the cross VRI-3 x PCU-41. From the F_2 population, 110 transgressive segregants which were superior in yield were selected and forwarded to F_3 generation. Forty superior segregants were identified and selected based on plant growth habit and yield contributing parameters. From the forty segregants, seven superior segregants with high seed yield, oil content and protein content were selected from six families of the crosses *viz.,* Gu. Til 4 x NIC-8322, VRI-3 x PCU-41, Punjab Til No.2 x PCU-37, Punjab Til No.2 x PCU-41, RT-346 x PCU-37, PCU-42 x PCU-37. These superior segregants may be forwarded to advanced generations and yield trials for confirming their superiority and release as a variety.

Appendices

APPENDIX I

Weather data (September 2019 to December 2019)

Month	**Temp**		**RH (%)**		**Wind Velocity (km/h)**	**Sunshine (h/day)**	**Evaporation (mm)**	**Rainfall (mm)**	**Rainy Days**
	Max (C)	Min (C)	FN	AN					
September 2019	31.3	24.4	94	75	1.8	5.4	3.4	324.6	19
October 2019	31.1	23.6	95	75	1.5	5.7	3.5	383.7	18
November 2019	33.0	24.0	95	67	1.3	8.0	3.8	159.8	10
December 2019	32.9	22.6	94	64	1.1	7.5	3.8	82.6	4

APPENDIX II

Weather data (February 2021 to May 2021)

Month	**Temp**		**R.H. (%)**		**Wind Velocity (km/h)**	**Sunshine (h/day)**	**Evaporation (mm)**	**Rainfall (mm)**	**Rainy Days**
	Max (^{O}C)	Min (^{O}C)	FN	AN					
February 2021	33.6	22.7	92	58	1.8	9.6	4.1	00.0	0
March 2021	34.0	23.4	92	59	1.9	9.2	4.0	76.6	5
April 2021	33.0	24.4	94	69	1.4	7.6	3.8	120.2	7
May 2021	31.2	24.5	94	77	1.4	6.6	3.6	863.1	21

APPENDIX III

Weather data (July 2021 to October 2021)

Month	**Temp**		**RH (%)**		**Wind Velocity (km/h)**	**Sunshine (h/day)**	**Evaporation (mm)**	**Rainfall (mm)**	**Rainy Days**
	Max (°C)	Min (°C)	FN	AN					
July 2021	30.4	24.0	95	76	1.8	6.5	3.6	437.5	18
August 2021	29.9	23.8	95	79	1.4	4.9	3.5	430.4	18
September 2021	30.5	24.1	95	77	1.4	6.8	3.6	411.0	21
October 2021	30.3	24.2	95	79	1.3	4.8	3.4	545.1	24

APPENDIX IV

Weather data (October 2021 to January 2022)

Month	**Temp**		**RH (%)**		**Wind Velocity (km/h)**	**Sunshine (h/day)**	**Evaporation (mm)**	**Rainfall (mm)**	**Rainy Days**
	Max (^{O}C)	Min (^{O}C)	FN	AN					
October 2021	30.3	24.2	95	79	1.3	4.8	3.4	545.1	24
November 2021	30.2	24.0	96	78	1.1	4.6	3.4	463.7	17
December 2021	33.1	22.6	94	63	1.1	8.4	3.7	30.0	3
January 2022	33.5	22.4	92	58	1.6	9.4	4.0	02.0	0