PARENTAL SELECTION BY GENETIC ANALYSIS AND PREDICTION OF PERFORMANCE IN SESAME (*Sesamum indicum* L.)

Thesis submitted in part fulfilment of the requirement for the Degree of DOCTOR OF PHILOSOPHY (Agriculture) in PLANT BREEDING AND GENETICS to the Tamil Nadu Agricultural University, Coimbatore

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CERTIFICATE

This to be certify that the thesis entitled ***"Parental selection by genetic analysis and prediction of performance in sesame (Sesamum indicum L.)"*** *submitted in part fulfilment of the requirements for the degree of* **Doctor of Philosophy (Agriculture) in Plant Breeding and Genetics** *to the Tamil Nadu Agricultural University, Coimbatore, is a record of bonafide research work carried out by* **Mrs. Alice John** *under my supervision and guidance and that no part of this thesis has been submitted for the award of any other degree, diploma, fellowship or other similar titles or prizes and that the work has not been published in part or full in any scientific or popular journal or magazine.*

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Alice John

ABSTRACT

ABSTRACT

Alice John, 1998. Parental selection by genetic analysis and prediction of performance in Sesame (***Sesamum indicum*** L.) (Doctor of Philosophy), (Dr. N. Subbaraman).

The study was carried out at Agricultural College and Research Institute, Madurai. It had three parts. In the first part, selected 25 sesame purelines were evaluated for their genetic similarity and diversity in performance for nine economically important traits. The purelines fell into three distinct clusters. They exhibited distinct pattern for seed yield expression. Twenty genotypes of exotic origin fell into one category and the remaining entries showed their variation for yield expression. Dendrogram showed that nine pairs had similar performance for seed yield. Mono/less branched types had similar performance. Additive main effects and multiplicative interaction effects suggested that the genotypes namely EC 351908, EC 357016, EC 357020, EC 351905 and EC 357022 were stable for seasonal influence and less interactive. The summer season has been identified as the best and the least interacting season.

The second part of the study was 6 × 6 diallel cross programme. The analysis showed that additive and dominance effects were important for days to first flowering, height to the first productive node, number of branches per plant and 1000 seed weight. The character such as oil content was influenced by dominance effects. The number of capsules per plant was under the influence of additive gene effects. The heritability estimates were high to moderate for all the nine characters studied.

The parents TMV 3, TMV 6 and SVPR 1 were identified as the best general combiners for plant height and number of branches.

More heterotic hybrids were resulted from good × poor general combiners combinations. High ***sca*** effects were exhibited by TMV 3 × EC 351879, TMV 3 × EC 351906, TMV 6 × EC 351905, EC 351879 × EC 351905 and EC 351905 × EC 351906 for seed yield and other yield contributing attributes.

The component analysis indicated that number of capsules plant^{-1} was the most promising component for realising recombinative heterosis. The same character through complementary determination captured 68 per cent of variations of the complex character such as seed yield.

The recombinative heterosis was high for TMV 3 × SVPR 1, TMV 3 × EC 351905, TMV 3 × EC 351906, TMV 6 × SVPR 1, TMV 6 × EC 351879, TMV 6 × EC 351905, SVPR 1 × EC 351905. SVPR 1 × EC 351906 and EC 351905 × EC 351906.

Probability of net gain of favourable alleles analysis indicated that TMV 3, EC 351879 and EC 351906 were the best donor parents for enhancing seed yield through contributing more favourable alleles. In addition to the above, this analysis suggested that ten cross combinations which involved TMV 3, TMV 6, EC 351879, EC 351905 and EC 351906 as parents were the most suitable combination for developing female inbreds for future crop improvement programme.

The best linear unbiased prediction analysis showed that TMV 3, TMV 6 and SVPR 1 had high prediction value. The combinations TMV 3 × TMV 6, TMV 3 × SVPR 1 and TMV 6 × SVPR 1 were identified as superior cross combinations for wide range of environments.

The F_2 prediction analysis displayed that TMV 3 × EC 351906, TMV 3 × EC 351879 and TMV 6 × SVPR 1 may be exploited for getting superior segregants.

Density tolerance analysis indicated that TMV 3 × EC 351879 and TMV 3 × EC 351906 were highly suitable for thick density cropping.

Forty five double cross hybrids were produced. The analysis of these hybrids revealed that TMV 6 and SVPR 1 were worthy grand parents for improving number of capsules plant^{-1} and seed yield plant^{-1} and SVPR 1 for oil content. The parents EC 351879 and EC 351905 be utilized as grand parents for producing early double cross hybrids.

The 2-line specific effect revealed that TMV 3 × EC 351879 and TMV 3 × EC 351905 combinations may be used as grand parents for the production of double cross hybrids. The 4-line arrangement effect suggested that change of order of parents had drastic effect in the performance of (TMV 3 × TMV 6) (SVPR 1 × EC 351906), (TMV 3 × TMV 6) (EC 351879 × EC 351906), (TMV 3 × SVPR 1) (EC 351879 × EC 351905) and (TMV 6 × SVPR 1) (EC 351879 × EC 351905) double cross hybrids.

The additive, additive × dominance and additive × additive × additive genetic variances had high influence in the inheritance of all nine characters studied.

The double cross prediction analysis revealed that (TMV 3 × EC 351879) (SVPR 1 × EC 351906), (TMV 3 × EC 351905) (TMV 6 × SVPR 1), (TMV 3 × EC 351906) (TMV 6 × SVPR 1), (TMV 3 × EC 351906) (SVPR 1 × EC 351879), (TMV 3 × EC 351906) (EC 351879 × EC 351905), (TMV 6 × EC 351905) (SVPR 1 × EC 351906) and (SVPR 1 × EC 351879) (EC 351905 × EC 351906) were superior hybrids which may produce desirable sesame genotypes.

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INTRODUCTION

CHAPTER I

INTRODUCTION

Breeding and improvement started in sesame (***Sesamum indicum***. L) when people realised the potential of this species for edible oil. Nature would play an important role in the development of sesame strains that were resistant/tolerant to drought, pest and diseases. The traits that people could select and fix are transferable from one local area to another. People and nature would co-operate in developing sesame strains adopted for wide differences in environment.

Accidental mixtures and outbreeding would contribute to the wide variation among sesame varieties. Although many high yielding varieties had replaced varieties of early years, there was concern that a yield plateau had been attained. According to FAO estimate, the productivity of sesame was 331 kg/ha seed in 1990 (Nayar, 1991).

The variability generated through single crosses was not sufficient enough to break the yield plateau in sesame. The recent advancement in plant breeding and genetics offers a wider choice of techniques to be adopted to improve the yield potential of sesame. Many plant breeding programmes operate with austere budgets and breeders must limit the number of environments and other resources used for evaluating and selecting superior genetic materials.

It has therefore become imperative that breeders investigate new techniques and new biometrical approaches that may maximise the accuracy of the estimation of performance of a genotype with few resources. With the above constraints in mind the present study was formulated with the following criteria.

- The genotypes involved in the study must be from various sources and genetically divergent since the extreme sources unfold the genetic variability to the maximum.

- Fewer environments should be used for obtaining informations to predict various aspects of the study.

- To understand the cause behind the heterotic behaviour of the complex character like yield, the recently developed biometrical approaches such as component analysis, recombinative heterosis, estimation of heterosis through probability of net gain of favourable alleles have to be employed.

- Employing prediction methods such as best linear unbiased predictions (BLUP) for the identification of pairs of genotypes with superior yield performance in hybrid combinations.

- As creating variability through single cross is limited, the next logical step would be to adopt double cross.

- Another area of importance is the prediction of performance of double cross from superior single cross as evaluating large number of double crosses is cumbersome.

- In order to break the yield plateau suitable genotypes should be developed to accommodate more number of plants per unit area.

In this context the present study in sesame was programmed with the following objectives

- To study the genetic relationship and their distance among the 25 selected sesame genotypes.

- To assess the genotype-by-environment interactions.

- To study the combining ability and gene action in the randomly selected six parents through diallel mating programme.
- To identify the cause for heterosis in complex characters through components.
- To assess the additive, dominance and epistatic gene actions in the double cross hybrid combinations involving six parents.
- To predict the performance of the crosses by identifying potential parents.

REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

Sesame, ***Sesamum indicum*** L. also known as Gingelly, Til and Simsin, is perhaps the oldest oil seed crop known to man (Weiss, 1983). It belongs to the family Pedaliaceae with a number of wild and cultivated species. The cultivated sesame is an annual and matures in less than 105 days and contains 45-60 per cent oil in its small, oblong seeds which are usually black, brown or white.

Detailed studies on the genetics and inheritance of characters in sesame were conducted in India since 1930. Almost all traits with discernible differences in growth habit, seedling, leaf, stem, flower, capsule and seed characters were thoroughly studied for the dominance relationship. Excellent reviews on the inheritance of simply inherited traits can be found in the treatise of sesame by Brar and Ahuja (1979).

2.1. Variability

Many characters of economic importance are quantitative in nature and are subjected to the environmental influence. The extent of genetic variability and the nature of inheritance displayed by the quantitative characters determine its usefulness in crop improvement.

Variability studies in sesame have well established the existence of distinct genetic differences among the genotypes for almost all characters of economic importance. The genetic expression of these characters was very much influenced by the environment. The extent of genetic variability was substantially large and sufficient enough to practice selection aimed at the improvement of characters (Chandramony and Nayar, 1985;

Govindarasu ***et al.***, 1990; Reddy and Stephen Dorairaj, 1990; Chandrasekhara and Reddy, 1993 b; Bhombe ***et al.***, 1994; Biswas and Akbar, 1995; Mishra ***et al.***, 1995 and Shadakshari ***et al.***, 1995).

Branching habit in sesame is a character of importance to breeders. Plant with branching and non-branching (mono-stemmed) habits are found in sesame. Branching was dominant over non-branching and it was due to a single gene difference (Nohara, 1943).

2.2. Genetic divergence

Success of any hybridisation programme depends upon the wide range of genetic diversity among the parents. Genetic divergence in sesame has been estimated through the adoption of Mahalanobis D^2 analysis of characters. Plant height, days to maturity, number of capsules plant^{-1}, number of primary branches, seed weight, oil content and dry matter production were the most important characters that contributed towards genetic diversity and genetic diversity was not related to geographic diversity (John Joel, 1987; Anitha and Stephen Dorairaj, 1990; Thirugnanakumar, 1991; Mahapatra ***et al.***, 1993; Balan, 1994; Patil and Sheriff, 1994; Ganesh and Thangavelu, 1995; Verma and Mahato, 1995 and Manivannan and Nadarajan, 1996).

Wei Wen Xing ***et al.*** (1994) estimated the genetic divergence among sesame genotypes through principal component and cluster analysis. They observed that the effect of genetic diversity was more beneficial if crossing was carried out between genotypes belonging to different groups and if their genetic distance was greater than 12.5.

quantitative inheritance. Allard (1956) defined a complete diallel cross as n^2 possible matings using n genotypes and explained the utility of Wr, Vr and Wr, Vr graphs in identifying the non-allelic interactions and dominance of the genotypes. Jinks (1956) and Hayman (1958 and 1960 b) extended the scope of diallel analysis to cover later generations like F_2 and back cross also.

Griffing (1956 a) classified the diallel technique into definite groups for the purpose of analysis to estimate the combining ability and provided expectations for different methods. Johnson and Askel (1959) used the standardised deviation graph to support the information on graphic analysis. Askel and Johnson (1962) provided a complete working model for diallel analysis.

The diallel technique was not out of criticism. Gilbert (1958) felt that the utility of diallel technique was exaggerated. Tandon ***et al.*** (1970) opined that the combining ability analysis was found to be better than graphic analysis in predicting the prepotency of cultures especially in the later generations when the expression of dominance effects was reduced. Daniel (1973) appreciated the technique since a complete analysis is obtained from parents and F_1 generations.

Arunachalam (1976) compared the efficiency of the combining ability analysis of diallel with that of graphic and genetic analysis and concluded that the combining ability analysis could be more reliable since it was not restricted to one gene model and it operated with feasible assumptions. Baker (1978) reviewed the critical issue in the use of diallel analysis. He opined that the assumption concerning the independent distribution of genes in the parents to be least acceptable in actual practice and the assumption that there is no epistasis frequently be incorrect. Still, this method has been widely

adopted with a view to get results in a short time which is highly valued in breeding programmes.

Analysis of diallel crosses may be helpful in the study of heterosis which results from various gene actions and interactions as well as in the calculation of degree of heritability (Marinkovic, 1993).

Similar to the situations with other agricultural crops, the analysis of diallel crosses has been found wide application in the genetic analysis of quantitative traits in sesame also (Sharma and Chauhan, 1985; Chandramony and Nayar, 1988; Geetha, 1988; Goyal and Sudhirkumar, 1991; Kadu ***et al.***, 1992; Reddy ***et al.***, 1993; Backiyarani, 1995; Navadhjiya ***et al.***, 1995; Quijada and Layrisse, 1995; Sajjanar ***et al.***, 1995 and Vignesh, 1997).

2.4.1. Combining ability and gene action

Combining ability analysis gives useful information regarding selection of parents in terms of the performance of their hybrids. Further, their analysis elucidated the nature and magnitude of various types of gene action involved in the expression of biometrical traits (Dhillon, 1975). General combining ability is due to additive effects of genes, specific combining ability is due to dominance deviation and epistatic interaction (Sprague and Tatum, 1942). The reported results on combining ability and gene action for various characters by different authors are furnished here.

Nature of gene action for different quantitative traits in sesame.

Nature of gene action	Author(s)
Days to flowering	
Additive	Pathak and Dixit (1988) Dharmalingam and Ramanathan (1993) Backiyarani (1995) Fatteh ***et al.*** (1995) Backiyarani ***et al.*** (1997)
Non-additive	Krishnadoss ***et al.*** (1997) Goyal and Sudhirkumar (1991) Anandakumar(1993) Shinde ***et al.*** (1993) Ramesh ***et al.*** (1995) Ganesh (1996) Shanti(1997) Vignesh (1997).
Additive and non-additive	Das and Sen (1989) Chandramony and Nayar (1994)
Plant height	
Additive	Padmavathy (1987) Deenamani (1989) Shinde ***et al.*** (1991) Dharmalingam and Ramanathan (1993) Shinde ***et al.*** (1993) Backiyarani (1995) Thiyagarajan and Ramanathan (1995) Ganesh (1996) Backiyarani ***et al.*** (1997) Vignesh (1997)
Non-additive	Krishnadoss ***et al.*** (1987) Pathak and Dixit (1988) Manoharan ***et al.*** (1989) Ramakrishnan and Soundarapandian (1990) Balan(1994) Ram (1995) Anandakumar and Sivasamy (1996) Shanti (1997)

Additive and non-additive	Chandramony and Nayar (1988) Das and Sen (1989) Goyal and Sudhirkumar (1991) Geetha and Subramanian (1992) Kadu ***et al.*** (1992) Anandakumar (1993) Fatteh ***et al.*** (1995) Sajjanar ***et al.*** (1995)
Height to first productive node	
Additive	Deenamani (1989)
Non-additive	Padmavathy(1987) Deenamani (1989) Deenamani and Dorairaj (1994) Ganesh (1996) Shanti (1997)
Number of branches plant^{-1}	
Additive	Krishnadoss and Kadambavanasundaram (1987) Chandramony and Nayar (1988) Deenamani (1989) Manoharan ***et al.*** (1989) Subbalakshmi (1989) Narkhedo and Sudhirkumar(1991) Thiyagarajan and Ramanathan(1995) Backiyarani ***et al.*** (1997)
Non-additive	Anandakumar and Rangaswamy (1987) Ramalingam ***et al.*** (1990) Shinde ***et al.*** (1993) Durga ***et al.*** (1994) Backiyarani (1995) Anandakumar and Sivasamy (1996) Ganesh (1996) Vignesh (1997)
Additive and non-additive	Padmavathy (1987) Khorgade ***et al.*** (1988) Das and Sen (1989) Goyal and Sudhirkumar (1991) Narkhedo and Sudhirkumar (1991) Geetha and Subramanian (1992) Kadu ***et al.*** (1992) Backiyarani (1995) Shanti (1997)

Number of capsule plant^{-1}	
Additive	Venkatesh (1987) Subbalakshmi (1989) Kadu ***et al.*** (1992) Shinde ***et al.*** (1993) Backiyarani (1995) Ramesh ***et al.*** (1995)
Non-additive	Krishnadoss ***et al.*** (1987) Ramalingam ***et al.*** (1990) Ramakrishnan and Soundarapandian (1990) Shinde ***et al.*** (1991) Balan (1994) Deenamani and Dorairaj (1994) Quijada and Layrisse (1995) Ganesh (1996)
Additive and non-additive	Khorgade ***et al.*** (1988) Das and Sen (1989) Goyal and Sudhirkumar (1991) Geetha and Subramanian (1992) Anandakumar (1993) Sajjanar ***et al.*** (1995)
Capsule length	
Additive	Padmavathi(1987) Dharmalingam (1990)
Additive and non-additive	Khorgade ***et al.*** (1988) Kadu ***et al.*** (1992) Fatteh ***et al.*** (1995)
1000 seed weight	
Additive	Pathak and Dixit (1988) Deenamani (1989) Kadu ***et al.*** (1992) Dharmalingam and Ramanathan (1993) Haripriya and Reddy (1993) Anandakumar (1994) Mcharo ***et al.*** (1995) Thiyagarajan and Ramanathan (1995

Non-additive	Krishnadoss ***et al.*** (1987) Padmavathy (1987) Ramakrishnan and Soundarapandian (1990) Durga ***et al.*** (1994) Fatteh ***et al.*** (1995) Vignesh (1997)
Additive and non-additive	Mahdy and Bakheit (1987) Khorgade ***et al.***(1988) Das and Sen (1989) Geetha and Subramanian (1992) Sajjanar ***et al.*** (1995) Shanti(1997)
Seed yield plant^{-1}	
Additive	Padmavathi (1987) Deenamani (1989) Das and Sen (1989) Subbalakshmi (1989) Dharmalingam and Ramanathan (1993) Haripriya and Reddy (1993) Ramesh ***et al.*** (1995) Thiyagarajan and Ramanathan (1995) Meenambigai(1996) Vignesh(1997)
Non-additive	Anandakumar and Sree Rangasamy (1987) Manoharan ***et al.*** (1989) Reddy and Haripriya (1990) Shinde ***et al.*** (1993) Durga ***et al.*** (1994) Quijada and Layrisse (1995) Anandakumar and Sivasamy (1996) Ganesh (1996)
Additive and non-additive	Das and Sen (1989) Goyal and Sudhirkumar (1991) Geetha and Subramanian (1992) Kadu ***et al.*** (1992) Anandakumar and Sivasamy (1995) Sajjanar ***et al.*** (1995) Shanti (1997).

Oil content	
Additive	Venkatesh (1987) Anitha (1988) Goyal and Sudhirkumar (1991) Backiyarani (1995) Fatteh ***et al.*** (1995) Meenambigai (1996)
Non-additive	Padmavathy (1987) Ramakrishnan and Soundrapandian (1990) Shanti (1997) Vignesh (1997)
Additive and non-additive	Geetha and Subramanian (1992) Reddy ***et al.*** (1993) Sajjanar ***et al.*** (1995)

2.5. Heterosis

Plant breeding methods have been developed during the last century to take advantage of the manifestation of heterosis in varietal crosses. The method of evaluation and choice of variety included for evaluation of heterosis were changed along with the course of new techniques available. The application of component analysis is an essential and rewarding part of the breeding procedure because it allows exploitation of recombinative heterosis and improves efficiency in the breeding for complex characters by providing the means to predict progeny performance.

2.5.1. Component analysis

Sparnaaij and Bos (1993) proposed a method for identifying components which promise a high degree of recombinative heterosis. A complex character such as yield may be defined as a character for which variation is determined by variation in a number of component traits (Bos and Sparnaaij, 1993). The outcome of complex characters (such as yield) is given by the product of component traits.

Piepho (1995) has introduced a new type of analysis for component characters. The main advantage of this method is its simplicity and straight forwardness in the interpretation of results.

2.5.2. Recombinative heterosis

The phenomenon of recombinative heterosis was first reported by Powers (1944) for tomato and Whitehouse ***et al.*** (1958) for wheat. Williams (1959) explained the new form of heterosis as occurring in hybrids simply as a results of reciprocal inequality of independent gene action in the parents.

Mackey (1976) introduced the term recombinative heterosis for a form of heterosis which he believed to be based on completely independent units of genetic system which by themselves may be only intermediate in reaction compared to the parents.

Bos and Sparnaaij (1993) defined recombinative heterosis as the heterotic performance of a complex character in a family resulting from a cross between parents with complementary component traits.

2.5.3. Estimation of heterosis through Probability of Net Gain (PNG) of favourable alleles

Metz (1994) defined the probability of Net Gain of favourable alleles (PNG_1 and PNG_2) from a donor inbred line as $[\mu_G/(\mu_G+\mu_D)]$, when a new inbred line is developed from $P_1 \times P_D$ and as $[\mu_G/(\mu_G+\mu_F)]$ when a new inbred line is to be developed from $P_2 \times P_D$. The maximum of these statistics (PNG_1 and PNG_2) estimates which parent line should be hybridized to be the donor to maximise the probability of improving the hybrid. If the $PNG_1 > PNG_2$, then greatest gain can be made by hybridizing the donor to P_1, whereas the reverse holds if $PNG_1 < PNG_2$ (Dudley, 1987).

2.6. Prediction of performance

2.6.1. Best linear unbiased prediction (BLUP)

Panter and Allen (1995) found that in self pollinated crops such as soybean, choosing parents typically is accomplished by calculating parental performance from previous yield data and then calculating the mid parental value for potential crosses. When limited or no data exist for parents of interest, precise predictions are difficult or impossible to obtain.

Two methods of selection ***viz.,*** mid parent value (MPV) and best linear unbiased prediction (BLUP) for identifying superior cross combinations when (1) equal and unequal amounts of yield data on all potential parents were available and (2) unequal amounts of yield data are available for some parents and no data were available for others.

The performance of each cross was predicted with MPV and BLUP for each situation. Among the two methods of prediction, prediction from BLUP provide higher rank correlations, lower standard errors and identification of higher percentage of superior crosses than MPV.

BLUP analysis was employed for prediction in Gerbera by Huang ***et al.***(1995) and in maize by Bernardo (1996).

2.7. Relationship between crop yield potential and single plant yield potential

Narayanan and Narayanan(1987) studied the yield variations caused by six cultivars of sesame at three population densities (16, 33 and 66 plants/m^2). He reported that the increase in yield was caused mainly due to the number of plants per unit area rather than the branches.

Yan and Wang (1992) focussed on the relationship that the crop yield (Y_c) per unit area can be expressed as the product of the number of established plants/unit area (D) and the yield /plant (Y_p) in the stand.

Y_p= a–bD where a and b are constants for a given genotype under a given environment.

Dixit ***et al.*** (1997) studied three plant densities ***viz.,*** 30 × 10cm, 30 × 15cm and 30 × 30cm with two varieties of sesame. They reported that the higher seed yield of dense population may be due to more number of plants per unit area.

2.8. Double cross hybrid analysis

Rawlings and Cockerham (1962) defined double cross as first generation progeny of the cross of two unrelated F_1 hybrids and may be symbolised by (A × B) (C × D). They were the first to make a genetic interpretation of the double cross hybrid analysis. This analysis provided a means of obtaining information both genetic and non-genetic from double crosses and classifies the involved interaction system in the double cross hybrid structure.

The order effect of parents and the epistatic components were clearly brought out in this analysis. The 1-line average effects accounts for the total additive effects. Obviously, if the gene action is primarily of the additive type, the estimates of 1-line effects are sufficient to predict the hybrid performance.

The average 2-line effects represent non-additive type of gene action. Similarly, the average 3-line effects are the functions of additive × dominance interactions including all three factors of higher order interactions except, the all dominance type.

The average 4-line effects represent dominance × dominance interactions, all three factor interactions except all additive types. The effects arising due to the arrangement of lines are exclusively the results of dominance effects or interactions involving dominance components.

Apart from the work done in maize, the information on double cross analysis in other crops are very meagre. Giridharan (1986) compared six maize inbreds and their 15 single, 60 three way and 45 double cross hybrids for different types of hybrids, parent order and gene action by subjecting to diallel, triallel and quadriallel analysis. He reported that the parent order affected the estimates of various effects and hybrid means. The different general line effect and 2-line specific effects were helpful in tracing the cross combinations with high 3-line specific effect and high mean yielding hybrids for various cob characters.

Hussain Sahib and Reddy (1989) compared single crosses, three way crosses and double crosses besides parents in sorghum. The yield of all the three groups of crosses were statistically superior to the respective parents.

Subbalakshmi (1989) studied the genetic system governing yield and yield components in sesame through diallel and double cross hybrid analysis and reported that the 1-line general effect was significant for plant height, number of capsules plant^{-1} and oil content.

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

3.1. Materials

Experimental material for this study was 25 genotypes of sesame (***Sesamum indicum*** L.) maintained within a programme of inbreeding through generations from a gene pool established at the Agricultural College and Research Institute, Madurai. The values of genotype for five characters tested are given in Table 1.

3.2. Methods

The study was conducted at Agricultural College and Research Institute, Madurai during 1996-'97. The experimental methods involved three parts, ***viz.***,

i) Evaluation of genotype

ii) Diallel analysis and

iii) Double cross hybrid analysis

3.2.1. Evaluation of parents

The crop was raised in three growing season ***viz.,*** June – July (Kharif), October – November (Rabi), February – march (summer) (Crop Production Guide, 1994) of 1996–'97 employing randomised block design with three replications spaced at 30 × 30 cm. Each genotype was sown in single row of three metre length. Crop was maintained properly by adopting recommended agronomic practices and need based plant protection methods.

Table 1. Source and distinguishing morphological features of the genotypes

Code No.	Genotypes	Source/ Pedigree	Duration (days)	Capsule/ axil	Locule number	Habit	Seed colour
1.	EC 351879	NBPGR* Akola	65-70	1	4	B**	Dull White
2.	EC 351880	,,	,,	1-3	4-8	NB***	,,
3.	EC 351903	,,	60-65	3	4	NB	,,
4.	EC 351904	,,	65-70	1-3	8	B	,,
5.	EC 351905	,,	,,	,,	4-14	NB	,,
6.	EC 351906	,,	,,	,,	4-8	NB	,,
7.	EC 351907	,,	,,	,,	4-8	B	,,
8.	EC 351908	,,	,,	,,	4	NB	,,
9.	EC 357015	,,	,,	,,	,,	NB	Black
10.	EC 357016	,,	,,	,,	,,	NB	Dull White
11.	EC 357017	,,	,,	,,	,,	NB	,,
12.	EC 357018	,,	,,	1	,,	NB	,,
13.	EC 357019	,,	60 – 65	1	,,	B	,,
14.	EC 357020	,,	65 – 70	1-3	,,	B	,,
15.	EC 357021	,,		1-3	4-6	NB	,,
16.	EC 357022	,,		1	,,	NB	,,
17.	EC 357023	,,		1	,,	NB	,,
18.	EC 357024	,,		1 – 3	4 – 8	NB	,,
19.	EC 357025	,,		1 - 2	4	NB	,,
20.	EC 357026	,,		,,	1	4	,,
21.	TMV 3	Thindivanam (Tamil Nadu) South Arcot local x Malabar local	80-85	1	B	B	Brownish black
22.	TMV 4	Thindivanam (Tamil Nadu) Pure line from Sathur local	85-90	1	4	B	Brown
23.	TMV 6	Thindivanam (Tamil Nadu) Pure line selection from Andhra Pradesh variety	85-90	1	4	B	Brown
24.	Co 1	TNAU, Coimbatore Hybrid derivative (TMV 3 x SI 1878) x SI 1878	85-90	1	4	B	Black
25.	SVPR 1	Srivilliputur (Tamil Nadu) Pure line selection from Western ghat	75-80	1	4	B	White

* National Bureau of Plant Genetic Resources

** Branched

*** Non Branched

3.2.2. Diallel crossing programme

Six parents were raised during October 1996 for carrying out hybridisation programme. Three staggered sowings were taken up at weekly intervals. Each parent was sown in five rows with a spacing of 60 cm. A complete diallel set of crosses including selfs were made by hand pollination following emasculation. For hybridisation, the tubular corolla along with epipetalous immature stamens in the flower buds of the female parents that were likely to open in the next day were pulled out by hand. The emasculated buds were covered with butter paper cover to avoid contamination. The next day morning pollination was effected by collecting pollen grains from the male parent and dusted over the stigma of the female parent and covered again with butter paper cover. Parents were selfed following the procedure of smearing technique adopted by Thangavelu and Nallathambi (1982). The smearing technique involved smearing a speck of semi solid clay on the upper portion of the tubular corolla of the unopened matured buds so as to prevent the flower from opening.

The six parents chosen for the study were crossed in all possible ways, p(p-1)/2 without reciprocals so as to provide fifteen direct hybrid combinations (Table 2a). The parents were maintained by selfing.

3.2.3. Trial design

3.2.3.1. Diallel

The field trial had a randomised complete block design with three replications. In each block there was one plot of 30 plants for each self and F_1s making a total of 63 completely randomised plots. The plot consisted of 30 plants each with 30 cm spacing within and

Table 2a. Single cross code numbers of the genotypes used in 6 × 6 diallel

Parental code	Male / Female	TMV3 1	TMV6 2	SVPR 1 3	EC 351879 4	EC 351905 5	EC 351906 6
1.	TMV 3		12	13	14	15	16
2.	TMV 6			23	24	25	26
3.	SVPR 1				34	35	36
4.	EC 351879					45	46
5.	EC 351905						56
6.	EC 351906						

Table 2b. Code number of the crosses made in double cross analysis

Male / Female	23	24	25	26	34	35	36	45	46	56
12					12.34	12.35	12.36	12.45	12.46	12.56
13		13.24	13.25	13.26				13.45	13.46	13.56
14	14.23		14.25	14.26		14.35	14.36			14.56
15	15.23	15.24		15.26	15.34		15.36		15.46	
16	16.23	16.24	16.25		16.34	16.35		16.45		
23								23.45	23.46	23.56
24						24.35	24.36			24.56
25					25.34		25.36		25.46	
26					26.34	26.35		26.45		
34										34.56
35									35.46	
36								36.45		
45										
46										
56										

30 cm between rows. The trial was maintained properly adopting normal cultural and manurial practices (23, 13, 13kg NPK /ha).

3.2.3.2. Relation between crop yield potential and single plant yield potential

A high yielding single F_1 plant of each cross combinations ***viz.***, 1 × 4 (TMV 3 × EC 351879) and 1 × 6 (TMV 3 × EC 351906) was isolated and seeds from these plants were used to raise plants in three densities of planting ***viz.***, 15 × 30 cm, 30 × 30 cm and 45 × 30 cm for assessing the yield potentialities of these cross combinations.

3.2.4. Double cross hybrid

Double cross hybrids are the diallel crosses of the F_1 hybrids with the restriction that no parent can appear twice in the same cross. Considering six parents in the present study there will be 15 single cross hybrids ***i.e.***, F_1 =n (n-1)/2. These single crosses when mated imposing the restriction that only un-related crosses should be involved in the crossing programme, thus 45 double crosses were possible.

The 45 double cross hybrids synthesised from 15 single cross hybrids (Table 2b) were raised in the field during June 1997 employing randomised block design with two replications. Each genotype was sown in single row of three metre length in each replication with 30cm spacing. The agronomic practices recommended for the crop was uniformly followed.

3.3. Characters scored

Observations on the following characters were recorded from ten randomly chosen plants.

3.3.1. Days to first flowering

Number of days was counted from sowing to first flower opening in any single plant in the population.

3.3.2. Plant height

The height of the plant in centimetre was measured from the ground level to the tip of the plant at physiological maturity.

3.3.3. Height to the first productive node

The height from the ground level to the height at which the first capsule arose was measured at the time of physiological maturity and expressed in centimetre.

3.3.4. Number of branches plant^{-1}

Total number of primary and secondary branches were counted at physiological maturity.

3.3.5. Number of capsules plant^{-1}

The total number of capsules per plant was recorded at physiological maturity.

3.3.6. Capsule length

Length of capsule was measured in centimetre from the base to the tip of the capsule.

3.3.7. 1000 seed weight

One thousand healthy seeds were selected at random and weighed in grams.

3.3.8. Seed yield plant^{-1}

The seeds obtained from all the capsules harvested from a single plant were dried, cleaned, weighed and expressed in grams.

3.3.9. Oil content

Oil content of seed was recorded with the help of Nuclear Magnetic Resonance (NMR) method available at Tamil Nadu Agricultural University, Coimbatore and expressed in percentage.

3.4. Statistical Analysis

3.4.1. Analysis of variance

This was computed as follows.

Source	df	Expectations of mean squares
Replication	(r-1)	$\sigma^2_e + g\,\sigma^2_r$
Genotype	(g-1)	$\sigma^2_e + r\,\sigma^2_g$
Error	(r-1)(g-1)	σ^2_e
Total	(rg-1)	

The significance for all the traits were worked out as suggested by Gomez and Gomez (1976)

3.4.2. Pattern analysis

The analysis involved two stages.

i) a classificatory study to determine whether a pattern existed among the genotypes in their response across the test environments.

ii) an ordination study to examine the relationship among individual genotypes.

3.4.2.1. Classification

For each genotype, mean performance in each of the p environment was measured. It was considered that the p environments defined a p-dimensional space and this is analogous to the genotypic stability space of Hanson (1970). Each genotype tested was regarded as a point in this space, the co-ordinates of which were its performance in each of the p environments. The relative proximity of genotypes in this space reflected the degree of similarity of their performance across environments. The mean performance of each genotype in the p environments were thus regarded as p attributes and were used to classify the genotypes into a number of groups. Each group contained genotypes which were relatively close to each other, but more distant from members of other groups in the p-dimensional space.

3.4.2.2. Ordination

In order to display the relative position of genotypes from a p-dimensional space in two or three dimensions, an ordination procedure described by Gower (1966, 1967) as principal co-ordinate analysis was used. By this method the matrix of inter-individual Euclidean distances generated in the previous classification procedure was represented in orthogonal axes. The elements of each vector (axis) were regarded as the co-ordination of the genotypes on that axis.

3.4.3. Additive Main effects and Multiplicative Interaction effects (AMMI)

This model is a combination of ANOVA main effects for genotype and environments and multiplicative interaction effects obtained from a singular value decomposition of the matrix of residuals (Gauch, 1988 and Zobel ***et al***., 1988).

The model is written as,

$$Y_{ijk} = \mu + G_i + E_j + \sum_{n=1}^{N} + \lambda_n a_{ni} b_{nj} + I_{ij} + E_{ijk}$$

where,

Y_{ijk} = yield for the k^{th} replication of the i^{th} p cultivar in the j^{th} trial

μ = the general mean

G_i and E_j = Cultivar and trial effect

λ_n = n^{th} singular value decomposition of the matrix of interaction residuals

a_{ni} and b_{nj} = cultivar and trial scores

N = number of multiplicative terms needed for an adequate description of the interaction

I_{ij} = residual arising from the two way table after correction for the main effects and the extraction of the multiplicative interaction effect

E_{ijk} = intra block error

The 'F' tests to determine the significance of the PCA MS degrees of freedom are calculated by the simple method of Gollob (1968).

$$df = G + E - 1 - 2n$$

where,

G = Genotype

E = Environment

3.4.4. Diallel analysis

3.4.4.1. Genetic analysis

3.4.4.1.1. t^2 test

The validity of the assumptions for genetic and graphic analysis as postulated by Hayman (1954) was tested by

$$t^2 = \frac{(n-2)}{4} \times \frac{(\text{Var Vr} - \text{Var Wr})^2}{\text{Var Vr} \times \text{Var Wr} - \text{Cov}^2(\text{Vr, Wr})}$$

which is an F with 4 and (n-2) degrees of freedom.

Deviation of regression coefficient (b) from zero and unity.

The regression of covariance on variance and its SE were calculated as,

$$b = \frac{\text{Cov (Wr Vr)}}{\text{Var (Vr)}}$$

$$\text{Standard error (b)} = \left[\frac{\text{Var Wr} - b\,\text{Cov(Wr, Vr)}}{\text{Var Vr (n - 2)}}\right]^{1/2}$$

the significance of 'b' from zero and unity was tested as follows.

$$\frac{(b-0)}{SE(b)} \text{ and } \frac{(1-b)}{SE(b)}$$

The values were tested against table value of 't' for n-2 degrees of freedom.

3.4.4.1.2. Estimates of D, F, H_1, H_2, h^2 and E

The method proposed by Hayman (1954) was extended to estimate the genetic parameters using the following formula.

D = Component of variation due to additive effect of the genes

F = The mean of F_r over the arrays, for being the covariance of additive and non additive effects in the r^{th} array

H_1 = Component of variation due to dominance effect of the genes

$H_2 = H_1[1-(u-v)^2]$

where,

u = Proportion of positive genes in the parent

v = Proportion of negative genes in the parent

$u+v=1$

h^2 = Dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses).

E = The expected environmental variation obtained from error variance divided by number of replication.

where,

D = VoLo-E

F = 2 VoLo-4WoLo$_1$-2(n-2)E/n

H_1 = VoLo-4WoLo$_1$+4V$_1$L$_1$-3(m-2)E/n

H_2 = 4 V$_1$L$_1$-4VoL$_1$-2E

h^2 = 4 (ML$_1$-MLo)2-4(n-1)E/n2

The genetic components were tested by 't' test for significance by using the standard error of respective genetic parameters. The standard errors were calculated by using

i) the equation $S^2 = ½$ Var (Wr-Vr) and

ii) the terms of main diagonal of covariance matrix given by Hayman (1954 a) as corresponding multipliers.

3.4.4.1.3. Ratio of genetic components

From the estimated components, the following genetic ratios were calculated.

$(H_1/D)^{\frac{1}{2}}$ = mean degree of dominance over all loci.

$H_2/4H_1$ = the proportion of genes with positive and negative effects in the parents.

$$K_d/K_r = \frac{4(DH_1)^{1/2} + F}{4(DH_1)^{1/2} - F}$$

The proportion of dominant and recessive genes in the parent

Heritability estimates in narrow sense

$$= \frac{\frac{1}{2}D + \frac{1}{2}H_1 + \frac{1}{2}H_2 - \frac{1}{2}F}{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{4}H_2 - \frac{1}{2}F + E}$$

3.4.4.2. Graphical analysis

The graphical analysis as proposed by Jinks and Hayman (1953) and Hayman (1954 a) was adopted.

The Vr (the variance of offspring of the r^{th} parental array) and Wr (the covariance of offspring of r^{th} array with respect to non recurrent parent) were calculated from the diallel table and graphs were drawn for all the characters studied.

The limiting parabola for the Wr, Vr graph was drawn with the formulae.

$$Wr_i = (Vr_i \times VoLo)^{\frac{1}{2}}$$

Standardised deviations of Vr were computed using the formulae $(x_i - \bar{x})/s$ when x_i is the value of the individual parent, $\bar{x}$ is the mean of the parents and s, the standard deviation of the parents. The standardised deviation graphs were drawn utilising these data as proposed by Johnson and Askel (1959).

3.4.4.3. Combining ability estimation

The procedure outlined by Griffing (1956) for method 2 and model 1 was considered appropriate and was adopted for estimation of general and specific combining ability.

The statistical model used for the analysis of combining ability is

$$Y_{ij} = \mu + g_i + g_i + g_j + s_{ij} + \frac{1}{bc}\sum_k \sum_l e_{ijkl}$$

where μ = population mean

g_i = general combining ability effects of i^{th} parent

g_j = general combining ability effects of j^{th} parent

s_{ij} = specific combining ability effects such that $s_{ij}=s_{ji}$.

e_{ijkl} = environment at effect associated with $ijkl^{th}$ the observation

Restrictions imposed are $\sum_i g_i = 0$ and $\sum_j s_{ij} + S_{ii} = 0$ (for each i).

ANOVA for combining ability Method II Model I

Source	df	SS	MS	Expectations of mean square
General combining ability	P-1	Sg	Mg	$\sigma^2 + (p+2)\left(\frac{1}{p-1}\right)\sum_i g_i^2$
Specific combining ability	P(P-1)/2	Ss	Ms	$\sigma^2 + \frac{2}{p(p+1)}\sum_{i \le j}\sum S_{ij}^2$
Error	m		Me'	σ^2

where,

Me'= error mean square from r.b.d/r

$$Sg = \frac{1}{p+2}\left[\sum_i (y_{i.} + Y_{ii})^2 - \frac{4}{p}Y^2..\right]$$

and

$$Ss = \sum_{i \le j}\sum Y_{ij}^2 - \frac{1}{p+2}\sum_i (Y_{i.} + Y_{ii})^2 + \frac{2}{(p+1)(p+2)}Y^2...$$

3.4.4.3.1. Estimation of combining ability effects

3.4.4.3.1.1. General combining ability effects

$$g_i = \frac{1}{p+2}\left[(Y_{i.} + Y_{ii}) - \frac{2}{p}Y..\right]$$

3.4.4.3.1.2. Specific combining ability effects

$$s_{ij} = Y_{ij} - \frac{1}{p+2}(Y_{i.} - Y_{ii} + Y_{.j} + Y_{jj}) + \frac{2}{(p+1)(p+2)}Y..$$

3.4.4.3.2. Standard errors

$$SE(g_i) = \left[(p-1)\sigma_e^2/p(p+2)\right]^{1/2}$$

$$SE(S_{ii}) = \left[(p^2+p+2)\sigma_e^2/(p+1)(p+2)\right]^{1/2}$$

$$SE(g_i\text{-}g_j) = \left[2\sigma_e^2/(p+2)\right]^{1/2}$$

$$SE(s_{ij}) = \left[2(p-1)\sigma_e^2/(p+1)(p+2)\right]^{1/2}$$

$$SE(S_{ii}\text{-}S_{jj}) = \left[2(p-2)\sigma_e^2/(p+2)\right]^{1/2}$$

$$SE(s_{ij}\text{-}s_{ik}) = \left[2(p+1)\sigma_e^2/(p+2)\right]^{1/2}$$

$$SE(s_{ij}\text{-}s_{kj}) = \left[2p\sigma_e^2/(p+2)\right]^{1/2}$$

3.4.5. Component analysis

i) The procedure as proposed by Sparnaaij and Bos (1993) for component analysis was followed. The analysis for four component is

$x_1 \cdot x_2 \cdot x_3 \cdot x_4 = y$ or

$a \quad b/a \quad c/b \quad y/c = y$

3.4.5.1. The calculation of complementary determination (cd)

The above expression is partitioned into three basic equations.

$$a.\frac{y}{a} = x_1 .(x_2.x_3.x_4) = Y$$

$$b.\frac{y}{b} = (x_1.x_2).(x_3.x_4) = Y$$

$$c.\frac{y}{c} = (x_1.x_2.x_3).(x_4) = Y$$

In each successive line a different, more advanced primary character is used as the starting point. The contribution of a more advanced primary character to the variation in 'y' measured by r^2 is larger than that of the previous one. The difference between the r^2 values of two consecutive primary characters is taken to be the complementary determination of variation in 'y' by variation in the intervening component.

$cd\ (x_1,y) = r^2\ (x_1, y) = r^2\ (a, y)$

$cd\ (x_2, y) = r^2\ (x_1.x_2, y) - r^2\ (x_1, y) = r^2\ (b, y) - r^2\ (a, y)$

$cd\ (x_3, y) = r^2\ (x_1.x_2.x_3, y) - r^2\ (x_1.x_2, y) = r^2\ (c, y) - r^2\ (b, y)$

$cd\ (x_4, y) = r^2\ (x_1.x_2.x_3.x_4, y) - r^2\ (x_1.x_2.x_3, y) = 1 - r^2\ (c, y)$

In this way it can be established, which component contribute more to the variation in y.

ii) Another way of analysing components was done as proposed by Piepho (1995). The coefficient of variation of yield (y) defined as the standard deviation of 'y' divided by its mean is approximately equal to the standard deviation of log(y) (Hartung, 1986). This approximate relation may be employed to exploit the straight forward relation between the variance of log(y) and the variances and covariances of the yield components. It may be expressed as

$$\sigma^2 = c_1 + c_2 + \ldots + c_n$$

where, σ^2 is the variance of log(y) and c_i = Cov[log(y), log(xi)], the covariance between yield and the i^{th} yield component on a logarithmic scale. With this result the coefficient of vriation of yield as measured on the untransformed scale, which will be denoted as v, may be approximated by

$$v \approx \sigma = (c_1 + c_2 + \ldots + c_n)^{\frac{1}{2}}$$

This expression suggests that c_i is a measure for the contribution of the i^{th} yield component to the variability of yield, as assessed by the coefficient of variation.

Hence $c_i = \sigma_i^2 + \sum_{j \neq i} \sigma_{ij}$, $(i, j = 1, \ldots, n)$

where, $\sigma_i^2 = Var[(\log(x_i)]$, the variance of the i^{th} component on a logarithmic scale and

$\sigma_{ij} = Cov[\log(x_i), \log(x_j)]$ the covariance between the i^{th} and j^{th} component on a logarithmic scale.

3.4.5.2. Recombinative heterosis

Regression of a component on its preceding primary character indicates the component's dependence on the preceding primary character. The residuals obtained from the regression functions are the component values in as far as independent from their preceding primary character. The predicted progeny value of any component is taken to be the sum of (1) the value calculated from the regression function and (2) the mid parental value of its residuals.

The first component can not be adjusted for the effect of a preceding primary character. The actual mid parent value is therefore taken as the predicted progeny value.

$$\hat{x}_1 = \bar{a} = \hat{a}$$

The predicted value for component x_2 is

$$\hat{x}_2 = fx_2(\hat{a}) + \bar{r}_{x_2}$$

The predicted value for b is

$$\hat{b} = \hat{x}_1 . \hat{x}_2$$

Similarly for the third component

$$\hat{c} = \hat{b} . \hat{x}_3$$

This is continued until all components have been predicted.

3.4.5.3. Hybrid factor (HF) and multiplication factor (MF)

Heterosis of three multiplicative characters were assessed by the formula as suggested by Melchinger ***et al***. (1994).

$$HF_v = MF_{xyz}\, HF_x\, HF_y\, HF_z$$

where,

$$MF_{xyz} = 1/(1 + \Delta_x\, \Delta_y + \Delta_x\, \Delta_z + \Delta_y\, \Delta_z)$$

HF = 1 + hw; hw = relative heterosis of 'w' character

3.4.6. Estimation of heterosis through probability of Net Gain (PNG) favourable alleles

The relative number of favourable allele μ_G was estimated using the formula suggested by Ali and Knapp (1996).

$$\hat{\mu}_G = \left[2(\overline{Y}_{P_1 \times P_D}) - \overline{Y}_{P_1 \times P_2} - \overline{Y}_{P1}\right]/4$$

$$\text{for } (\overline{q}_j = 0, \overline{q}_j = 1)$$

Net merit of a donor inbred line (N_1 or N_2) was estimated following Bernardo (1990).

$$N_1 = (\overline{Y}_{P_2 \times P_D} - \overline{Y}_{P_1 \times P_2})/2 = \hat{\mu}_G - \hat{\mu}_D \text{ and}$$

$$N_2 = (\overline{Y}_{P_1 \times P_D} - \overline{Y}_{P_1 \times P_2})/2 = \hat{\mu}_G - \hat{\mu}_F$$

Probability of Net Gain (PNG) was estimated following Metz (1994).

$$PNG_1 = [\hat{\mu}_G/(\hat{\mu}_G + \hat{\mu}_D)] \text{ and}$$

$$PNG_2 = [\hat{\mu}_G/(\hat{\mu}_G + \hat{\mu}_F)]$$

where,

μ_G = the relative number of favourable allele present in a donor line (P_D) which are not presented in either parent of a single cross hybrid

μ_D or μ_F = the number of favourable allele which could be lost by using a donor to improve parents of a single cross hybrid.

3.4.7. Best Linear Unbiased Predictions (BLUP) (Panter and Allen, 1995)

The mixed model analysis was used to calculate BLUP for each cross with,

i) historical parental data.

ii) environments were considered fixed and genotypes were considered random.

The BLUP for each cross was defined as the mean of the two parental BLUPs. The additive linear mixed model was as follows.

$$Y = \mu + X\beta + Zu + \varepsilon$$

where,

Y = a vector of measured yield

μ = over all mean yield

X = the design matrix of fixed environment

β = the vector of unknown effect due to environments to be estimated

Z = the design matrix of random entries

u = the vector of unknown effects due to parents and progeny

ε = an error vector with a null mean

3.4.8. Prediction for F_2 single plant yield (Halleur and Miranda; 1981)

$$\overline{F}_2 = (\tfrac{1}{4})(\overline{Y}_i + \overline{Y}_j + 2\overline{Y}_{ij})$$

where,

$\overline{Y}_i$ = mean yield of i^{th} parent

$\overline{Y}_j$ = mean yield of j^{th} parent

$\overline{Y}_{ij}$ = mean yield of ij^{th} cross

3.4.9. Relation between crop yield potential and single plant yield potential

The maximum yield potential was assessed as per the formula suggested by Yan and Wallace (1995).

$$Y_{max} = (\tfrac{1}{4})a^2b^{-1}$$

where,

a = interception

b^{-1} = an index of the tolerance of the single plant yield to increase of the plant density

3.4.10. Double cross hybrid analysis

Rawlings and Cockerham (1962) assigned the statistical model for double cross hybrids for estimates of genetic components of epistatic nature and information on order effects of combinations. The model is as follows.

$$Y_{(ij)(kl)_m} = \mu + r_m + G_{(ij)(kl)} + e_{(ij)(kl)_m}$$

where,

$Y_{(ij)(kl)_m}$ = observation on double cross (ij)(kl) grown in replications.

m, m-1, 2 ....., r, i, j, k, l = 1, 2, ... P where no two of i, j, k, and l can be the same

μ = general mean,

r_m = the effect of the m^{th} replication

$G_{(ij)(kl)}$ = the genotypic effect of double cross hybrid (ij) (kl)

$e_{(ij)(kl)}$ = a random error

further,

$$G_{(ij)(kl)} = (g_i + g_j + g_k + g_l)$$
$$+ (s_{ij} + s_{ik} + s_{il} + s_{jk} + s_{jl} + s_{kl})$$
$$+ (S_{ijk} + s_{ijl} + s_{ikl} + s_{jkl}) + (S_{ijkl})$$
$$+ (t_{ij} + t_{kl} + t_{i.k} + t_{j.l} + t_{j.k} + t_{j.l})$$
$$+ (t_{ij.l} + t_{ij.k} + t_{ki.j} + t_{kl.j})$$
$$+ (t_{ij.kl})$$

where,

g_i = the average general effect of line 1.

s_{ij} = the 2 line interaction effect of lines i and j appearing together, irrespective of arrangement.

S_{ijk} = the 3 line interaction effect of lines i, j, and k appearing together, irrespective of arrangement.

S_{ijkl} = the 4 line interaction effect of lines i, j, k, and 1 appearing together, irrespective of arrangement.

t_{ij} = the 2-line interaction effect of lines i and j due to the particular arrangement (ij) (– –).

$t_{i.j}$ = the 2-line interaction of lines i and j due to the particular arrangement (i-j)(k-).

$t_{ij.k}$ = the 3-line interaction effect of lines i, j and k due to particular arrangement (ij) (k-).

$t_{ij.kl}$ = the 4-line interaction effect of lines i, j, k, and l due to the particular arrangement (ij) (kl).

The procedure for estimating general and specific line effects of various arrangements using the least square technique are given below.

i. Average effect of line i, $g_i = [(y_{i..}) / r P_1P_2P_3 / 2] \mu$

ii. The 2-line interaction effects of lines i and j appearing together irrespective of arrangement $S_{ij} = [(y_{ij..})/(3rP_2P_3/2)]-\mu-g_i-g_j$

iii. The 3-line interaction effects of lines i, j and k appearing together irrespective of arrangement $S_{ijk}=[(y_{ijk..})/3rP_3-\mu-g_i-g_j-g_k-s_{ij}-s_{ik}-s_{jk}]$

iv. The 4-line interaction effects of lines i, j, k and l appearing together irrespective of arrangement

$$S_{ijkl} = [(Y_{ijkl}../(3r)) - \mu - g_I - g_j - g_k - g_l - s_{ij} - s_{il} - s_{ik} - s_{jk} - s_{jl} - s_{kl} - s_{ijk} - s_{ijl} - s_{ikl} - s_{jkl}]$$

v. The 2-line interaction effects of lines i and j due to the particular arrangement (ij)(– –), $t_{ij} = [(y_{(ij)}(..)/(rP_2P_3/2)) - \mu - g_I - g_j - s_{ij}]$

vi. The 2-line interaction effects of lines i and j due to the particular arrangement (i–)(j–), $t_{i.j} = t_{(i-)(j-)} = [(y_{(i.)(j.)}/(rP_2P_3)) - \mu - g_i - g_j - s_{ij}]$

vii. The 3-line interaction effects of lines i, j and k due to the particular arrangement (ij)(k–),

$$t_{ijk} = t_{(ij)(k-)} = [(y_{(ij)(k-)}/(rP_3)) - \mu - g_i - g_j - g_k - s_{ij} - s_{ik} - s_{jk} - s_{ijk} - t_{i.j} - t_{j.k} - t_{i.k}]$$

viii. The four line interaction effects of lines i, j, k and l due to the particular arrangement (ij) (kl),

$$t_{ij.kl} = (y_{(ij)(kl)}/r) = \mu - g_i - g_j - g_k - g_l - s_{ij} - s_{ik} - s_{il} - s_{jk} - s_{jl} - s_{kl} - s_{ijk} - s_{ijl} - s_{ikl} - s_{jkl} - t_{ij} - t_{kl} - t_{i.k} - t_{i.l} - t_{j.k} - t_{j.l} - t_{ij.k} + t_{ij.l} + t_{ij.k} + t_{ki.j} + t_{kl.j}$$

where,

Pi denotes (P-i) for example, with P-6, P value are P=6-0=6, P_1=6-1=5 and so on.

The ANOVA for different effects would be then

Source	df	MS
Replications	(r-1)	R
Total	$3r^6\ C_4$-1	-
Hybrid	$3^6\ C_4$-1	H
Error	(r-1) (3^6C_4-1)	E
1 line general	P_1	G
2 line specific	$PP_3/2$	S_2
3 line specific *	$PP_1P_5/6$	S_3
4 line specific *	$PP_1P_2P_7/24$	S_4
2 line arrangement	$PP_3/2$	T_2
3 line arrangement	$PP_2P_4/3$	T_3
4 line arrangement	$PP_1P_4P_5/12$	T_4

* The minimum number of lines required for quadrallel is eight. If P=7, 3 and 4-line specific sum is treated as specific single sum with 14 df with P=6, only one 2-line specific sum of squares is available with 9 df and variances due to 3 and 4-line available with 9 df and variance due to 3 and 4-line specific effect cannot be estimated. The negative variances were however required in further calculation of these effects. With the help of mean sum of squares, estimates of components of variances are calculated.

3.4.10.1. Estimation of components of variances

$S^2t_4 = (T_4-E)/r$

$S^2t_3 = T_3-T_4/rP_3$

$S^2t_2 = (3/rP_1P_2)\ (T_2-(2P_2/P_3)T_3+(P_1/P_3)T_4)$

$S^2S_4 = (S_4-E)/3r$

$S^2S_4 = (S_4-E)/3r$

$S^2S_3 = (S_3-S_4)/3rP_6$

$S^2S_2 = (2/3rP_4P_5)\ (S_2-(2P_5/P_6)S_3+(P_4/P_6)S_4$

$S^2g = (2/rP_2P_3P_4)\ (G-3P_3/P_5)\ S_2+(3P_2/P_6)S_3-(P_2P_3P_5P_6)S_4$

where,

$C = Sy^2.../r\ PP_1P_2P_3. = y^2_{(ij)(kl)}m-C$

$R = (8\ \Sigma\ y^2...m)/(PP_1P_2P_3)-C$

$H = (\Sigma\ y^2_{(ij)(kl)}/r)-C$

$G = (2\ \Sigma\ y^2_i.../rP_2P_3P_4)-(4P_1/P_4)C$

$S_2 = (2\ \Sigma\ y^2_{ij}...\ /3r\ P_4P_5)-(6P_2P_3/P_4P_5)C-(3P_3/P_5)G$

$S_3 = (\Sigma\ y^2_{ijk}.\ /3r\ P_6)-(4P_3/P_6)C-(3P_4/P_6)G-(2P_5P_6)S_2$

$S_4 = (\Sigma\ y^2_{ijkl}/3r)-C-G-S_2-S_3$

$T_2 = (2\Sigma\ y^2_{(ij)(..)}/r\ P_1P_2)+\ (\Sigma\ y^2(i.)(j.)/r\ P_1P_2)-(2\ \Sigma\ y^2ij.../3r\ P_1P_2)$

$T_3 = (\Sigma\ y^2_{(ij)(k.)}/r\ P_3)-(\ \Sigma\ y^2\ ijk.../3r\ P_3)-(2P_2/P_3)T_2$

$T_4 = (\Sigma\ y^2_{(ij)(kl)}/r)-\ \Sigma\ y^2_{ijkl.}/3r)-T_2-T_3$

Using the estimates of components of variance, the genetic components of variances were estimated assuming a restricted genetic model. This has been done keeping in view that only the lower order components are generally of interest (Rawlings and Cockerham, 1962). Thus, a set of six estimates of genetic components of variances of the lowest order were derived using either a simple or weighted average of the two components which have the same genetic composition S^2s_4 and S^2t_4. If k be the simple average, then $k=S^2s_4+S^2t_4/2$. The six genetic variances were computed keeping F=1 as,

$$S^2_{10} = (4/3F)\ (6S^2g-3S^2s_2+2S^2s_3+(4/3)S^2t_2-2S^2t_3+2K)$$

$$S^2_{01} = (8/F_2)\ (2S^2t_2-4S^2t_3+3K)$$

$$S^2_{20} = (32F^2)\ (S^2s_2-S^2s_3-(4/9)\ S^2t_2+S^2t_3-K)$$

$$S^2_{11} = (128/F^3)\ (S^2t_3-K)$$

$$S^2_{02} = (128/F^4)K$$

$$S^2_{30} = (256/3F^3)\ (S^2s_3-S^2t_3+K)$$

where,

F_1 = 1, the inbreeding coefficient

S^2_{10} = Additive genetic variance

S^2_{01} = Variance due to dominance deviation

S^2_{20} = Additive × additive component of variance

S^2_{11} = Additive × dominance component of variance

S^2_{02} = Dominance × dominance component of variance and

S^2_{30} = Additive × additive × additive component of variance

The effects arising due to the arrangement of lines are exclusively the results of dominance effects or interactions involving dominance components.

3.4.10.2. Double cross prediction

The performance of double cross hybrids from the performance of single cross can be predicted using the formula given by Jenkin (1934).

$$\hat{D}_{ij.lm} = \left(\frac{1}{4}\right)\left(S_{il} + S_{im} + S_{jl} + S_{jm}\right)$$

$\hat{D}$ = Estimated value of double cross

S_{il} = the value of the single cross between i and l

S_{im} = the value of the single cross between i and m

S_{jl} = the value of the single cross between j and l

S_{jm} = the value of the single cross between j and m

EXPERIMENTAL RESULTS

CHAPTER IV

EXPERIMENTAL RESULTS

4.1. Evaluation of genotypes

4.1.1. Analysis of variance

The ANOVA for nine characters studied in 25 genotypes of sesame are presented in the Table 3. The genotypes differed significantly for all the nine characters studied.

4.1.2. Mean performance of the genotypes

The mean performance of 25 genotype for nine characters are presented in Table 4.

The exotic collection used in the present study were early flowering types. The mean number of days to first flowering ranged from 22.3 (EC 357015) to 34.9 (CO 1). Among the 25 genotypes 19 genotypes showed significantly less days to flowering compared to the grand mean (26.38).

The plant height ranged from 60.5 (EC 357023) to 140.9cm (TMV 6). While comparing with the adapted cultivars the exotic cultures exhibited short stature. Eleven out of 25 genotypes showed a plant height above the grand mean (88.20cm).

The short statured exotic cultures revealed a low height to the first productive node. The lowest height was showed by EC 357016 (17.2cm) and the highest by TMV 3 (42.6cm). Nineteen out of 25 genotypes showed their height to the first productive node lower than the grand mean (23.04cm).

The adapted cultivars ***viz.,*** TMV 3, TMV 6 and CO 1 were rich in branches while the exotic cultivars were poorly branched or

Table 3. ANOVA for nine characters in 25 sesame genotypes

Source	df	Mean sum of squares								
		Days to first flowering	Plant height	Height to the first productive node	Number of branches plant^{-1}	Number of capsules plant^{-1}	Capsule length	1000 seed weight	Seed yield plant^{-1}	Oil content
Replication	2	0.21	15.41	5.72	0.84	49.38	3.17	9.16	9.08	0.76
Genotype	24	39.79**	2059.65**	151.05**	40.72**	9040.64**	0.39**	0.43**	228.98**	1.94**
Error	48	0.11	5.17	3.45	0.22	19.81	0.002	0.0007	0.30	0.02

** Significant at 1% level

Table 4. Mean performance of 25 sesame genotypes during summer

Genotypes	Days to first flowering	Plant height (cm)	Height to first productive node (cm)	Number of branches plant^{-1}	Number of capsule plant^{-1}	Capsule length (cm)	1000 seed weight (g)	Seed yield plant^{-1} (g)	Oil content (%)
EC 351879	25.2	93.8	20.4	3.5	70.9	3.1	2.8	13.5	51.5
EC 351880	24.8	89.3	19.6	1.4	60.7	2.8	2.6	11.7	51.8
EC 351903	26.7	91.8	19.9	0.0	59.3	3.9	2.8	12.4	52.2
EC 351904	25.7	91.1	22.0	3.3	66.1	2.7	2.7	12.8	51.8
EC 351905	24.5	98.5	21.4	0.0	84.2	3.2	2.8	15.6	52.8
EC 351906	26.1	103.3	23.3	0.8	76.4	3.0	2.9	16.2	52.8
EC 351907	23.5	80.3	25.8	2.0	55.6	3.2	2.4	9.7	51.5
EC 351908	24.9	81.1	19.4	0.7	55.2	3.2	2.7	10.3	52.8
EC 357015	22.3	60.6	17.6	0.0	27.6	2.7	2.6	5.1	50.2
EC 357016	22.9	70.7	17.2	0.0	37.2	2.8	2.6	7.4	52.0
EC 357017	22.7	68.0	20.2	0.0	41.3	2.8	2.6	7.6	51.8
EC 357018	23.6	63.4	21.9	1.0	39.9	2.7	2.7	8.2	52.8
EC 357019	23.4	69.1	17.9	2.4	38.3	2.8	2.6	6.9	52.5
EC 357020	24.6	71.9	20.3	1.6	43.1	2.7	2.6	8.3	51.8
EC 357021	24.7	71.8	19.9	0.0	46.2	2.6	2.5	8.5	51.7
EC 357022	25.8	66.8	19.5	0.0	31.7	2.8	2.7	6.3	51.2
EC 357023	26.1	60.5	18.8	0.0	36.9	2.6	2.9	8.3	52.2
EC 357024	26.3	70.4	20.3	2.4	47.9	2.5	2.7	9.4	52.1
EC 357025	25.2	68.3	18.6	2.0	40.4	3.5	3.0	8.9	51.1
EC 357026	26.1	70.1	19.8	1.7	43.3	2.8	2.8	8.7	53.4
TMV 3	32.9	135.8	42.6	10.0	195.3	2.5	3.2	31.3	51.8
TMV 4	33.7	140.7	39.9	10.5	171.4	2.4	3.2	27.4	52.7
TMV 6	33.9	140.9	37.2	9.9	194.4	2.4	3.1	30.1	52.8
CO 1	34.9	138.3	32.7	11.9	194.3	2.5	3.1	30.1	51.8
SVPR-1	29.0	108.4	19.7	3.6	131.3	3.1	4.3	31.5	54.1
Mean	26.38	88.20	23.04	4.04	75.56	2.85	2.84	13.85	52.13
SE	0.20	1.31	1.07	0.27	2.57	2.32	1.55	0.32	8.07

mono-stemmed types. The number of branches plant^{-1} ranged from 0.0 to 11.9.

Wide range of variation for capsule number was observed among the genotypes. The maximum number of capsules plant^{-1} was recorded by TMV 3 (195.3). The range for this character was 27.6 to 195.3. Among the exotic cultures, EC 351905 (84.2) and EC 351906 (76.4) recorded number of capsules more than the grand mean (75.56).

The mean length of capsule ranged from 2.4 to 3.9cm. EC 351903 recorded the maximum length of 3.9cm. Eight out of 25 genotypes showed a capsule length above the grand mean (2.85cm).

Weight of 1000 seed was high for SVPR 1 (4.3 g). The mean weight of 1000 seed ranged from 2.4 to 4.3g. Eight out of 25 genotypes recorded 1000 seed weight above the grand mean (2.84g).

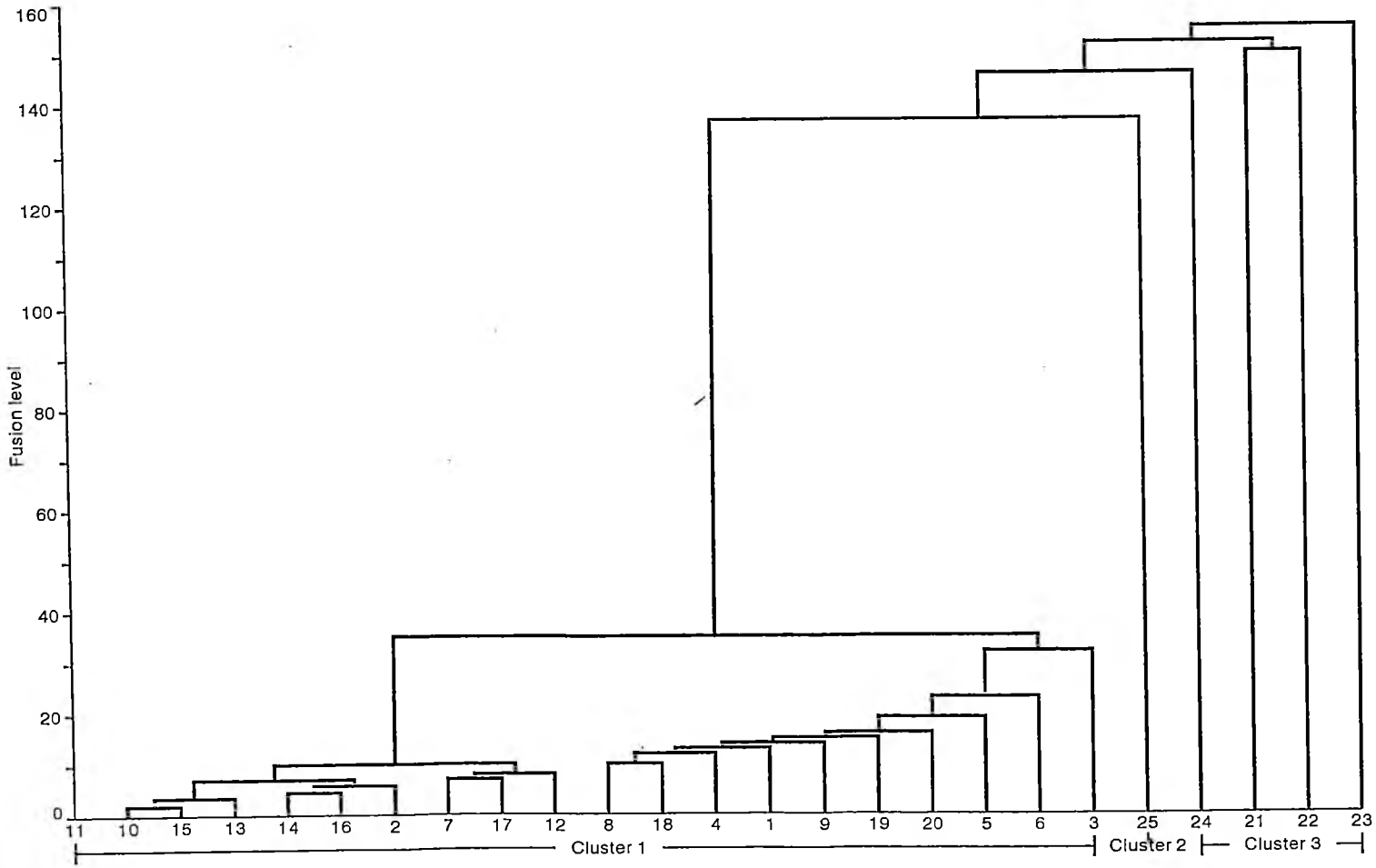
Among the 25 genotypes, SVPR 1 recorded maximum yield (31.5g) followed by TMV 3 (31.3g). The minimum seed yield was recorded by EC 357015 (5.1g). The mean seed yield plant^{-1} ranged from 5.1 to 31.5 g. Seven genotypes exhibited seed yield plant^{-1} above the grand mean (13.85 g).

The highest oil content was recorded by SVPR 1 (54.1%). The range for this character was low. Majority of the genotype recorded a oil content between 51 to 53 per cent.

4.1.3. Pattern analysis

Twenty five genotypes were evaluated for three seasons. The mean squares of pooled analysis over seasons for seed yield plant^{-1} are presented in Table 5. Genotypes and replication effects were considered as fixed effects and seasons assumed to be random.

Fig. 1. Dendrogram for seed yield for 25 sesame genotypes



Significant differences existed among the genotypes for seed yield. The genotype × environment (season) interaction was highly significant indicating that the differences existed among genotypes in their response to changes of environment.

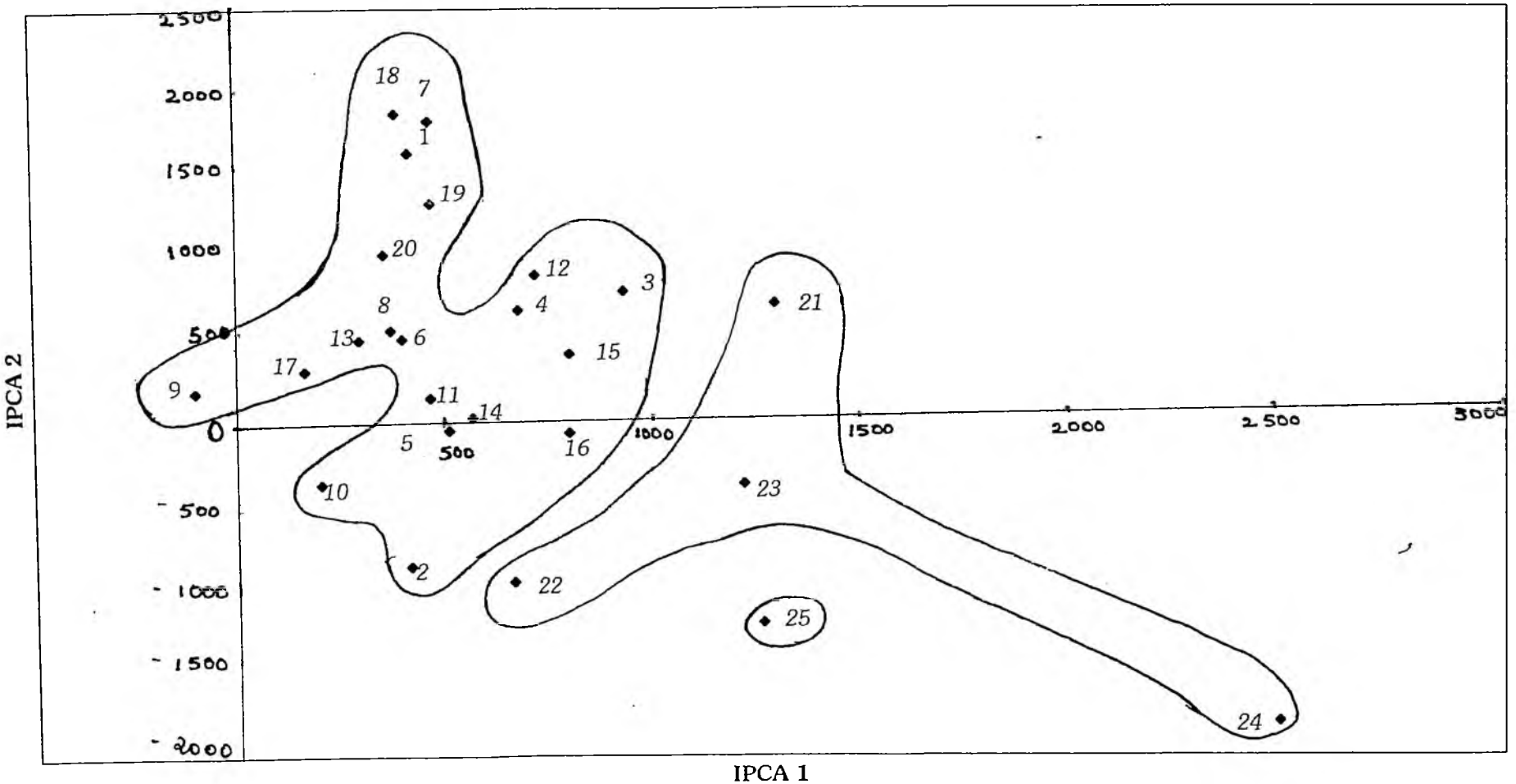
4.1.3.1. Classification

The delimination of 25 season genotypes into cluster was represented by dendrogram (Fig. 1). The number of clusters was done depending on the level at which the hierarchy is truncated. In the present study the hierarchy was truncated arbitarily at the three cluster level; that is fusion of individuals lower in hierarchy was not considered.

Dendrogram for seed yield was presented in Fig. 1. The values on the vertical axis of each dendrogram are unstandardised squared Euclidean distances between individual genotype basis. The positions of the clusters along the x axis of the dendrogram have no meaning since any two individuals may be rotated about their point of fusion. The dendrogram suggested that for seed yield there was a major discontinuity for performance of individual genotypes over environments (seasons). The major discontinuity in the classification based on yield suggested that mean yield was important in identifying clusters I, II and III.

Clusters which were closely related in classification generally had similar responses over environments. The relatively unrelated clusters were more inconsistent in their responses but exhibited both large differences in yield with similar responses and quite different responses over most of the environments. This classificatory procedure indicated that it was effective in the determination of groups of genotypes which differed in either mean performance or environmental response or both.

Fig. 2. Spatial arrangement of 25 sesame genotype for seed yield



4.1.3.2. Ordination

The first two vectors obtained by ordination procedure for yield accounted for nearly 100 per cent of the information contained in the matrices of inter individual distances. Thus a plot of vector 1 against vector 2 as Euclidean axes should provide a reasonable representation of the spatial arrangement of seed yield in the original eight-dimensional space.

Cluster boundaries were drawn around those genotypes which were grouped together in the classification procedure. The genotype with in the first cluster were in close proximity where as in cluster III it was more diffused. Genotypes in cluster I were predominantly of Akola types. Ordination diagram (Fig. 2) suggested that this group of genotype occupied substantially in the eight dimensional space.

4.1.4. Additive Main effects and Multiplicative Interaction effects (AMMI)

The ANOVA for AMMI is presented in Table 5. The G × E interactions and IPCA were significant. The genotype sum of square was large nearly 80 times as large as G × E interaction sum of square. The IPCA axis 1 and 2 were significant. The residual was zero.

The ANOVA main effects with 26 degrees of freedom contained 98.79%. The first PCA axis of the interactions captured 66.85% of the interaction sum of square. Partitioning of interactions sum of square by AMMI is quite effective because the MS for the first PCA axis was being very large over the MS for the residual. The remaining interaction effects were captured by IPCA 2.

The scores of IPCA 1 and IPCA 2 for the 25 genotypes are presented in Table 6. The IPCA scores and the mean values of

Table 5. AMMI analysis of variance for seed yield plant^{-1} of 25 sesame genotypes

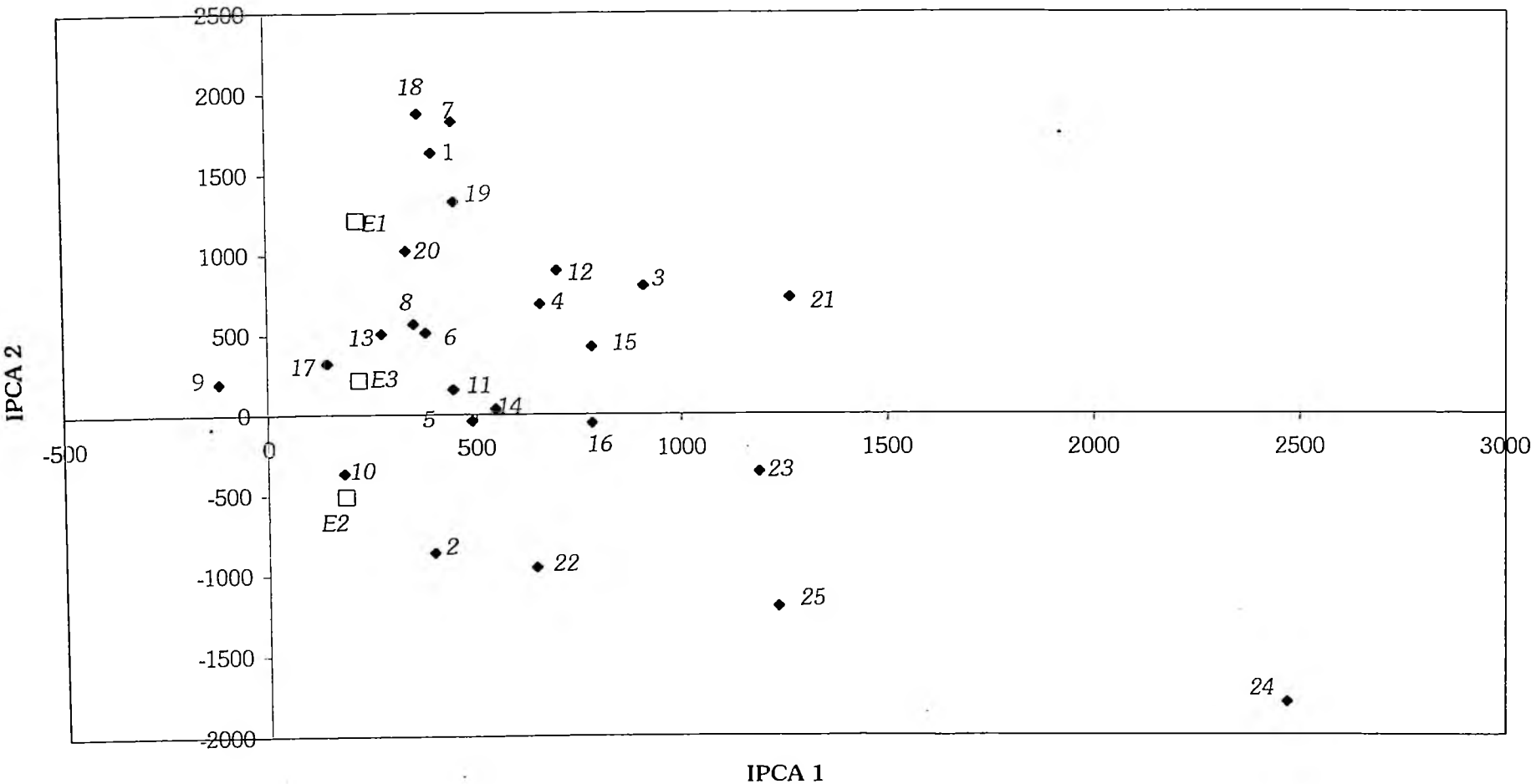
Source	df	SS	MS
Genotype	24	14755.82	614.83**
Environment	2	143.97	71.98**
G × E	48	175.53	3.66**
I PCA 1	25	117.34	4.69**
I PCA 2	23	58.88	2.56**
Residual	0	–	–
Error	144	58.40	0.41

** Significant at 1% level

Table 6. Mean and IPCA scores of 25 genotypes

Genotypes	Mean (x)	IPCA 1 ($\times 10^4$)	IPCA 2 ($\times 10^4$)
EC 351879	12.32	395.6	1636.2
EC 351880	10.75	398.0	861.5
EC 351903	10.67	905.8	803.0
EC 351904	11.55	650.0	690.7
EC 351905	14.82	488.3	-41.1
EC 351906	15.39	379.3	513.6
EC 351907	8.41	444.3	1827.6
EC 351908	9.70	351.3	56.6
EC 357015	5.25	-117.8	197.8
EC 357016	7.23	184.0	-367.5
EC 357017	6.86	445.2	15.7
EC 357018	6.75	694.2	902.5
EC 357019	6.30	274.4	505.4
EC 357020	7.38	544.5	37.2
EC 357021	7.22	716.3	423.3
EC 357022	6.07	146.0	-55.0
EC 357023	6.97	778.0	320.2
EC 357024	8.22	363.3	1874.3
EC 357025	7.77	448.2	1332.7
EC 357026	7.84	3350	1024.3
TMV 3	29.03	1265.1	732.0
TMV 4	26.65	642.5	-953.7
TMV 6	28.33	1189.4	-661.4
CO 1	26.58	2466.2	-1797.8
SVPR 1	29.84	1236.8	-1199.4
Environment 1	12.12	2172.8	12102.0
Environment 2	12.18	1883.7	-5129.3
Environment 3	13.85	2203.8	2146.8

Fig. 3. Biplot of the 1st and 2nd principal components for seed yield of 25 sesame genotypes



genotypes and the environment were marked in the biplot graph which demonstrated the main and interaction effects (Fig. 3).

4.2. Diallel analysis

The recorded data on the expression of nine traits studied in six parents and 15 hybrids from a 6 × 6 diallel design were statistically analysed and the results are presented below (Table 2a).

4.2.1. Analysis of variance

All the nine traits studied shown highly significant differences among the genotypes (Table 7).

4.2.2. Mean performance of parents and hybrids

Mean performance of parents and hybrids for nine traits studied are furnished in Table 8.

4.2.2.1. Parents

Among the six parents, parent 5 was the earliest to flower, while parents 2 and 1 were the late flowering types. The range among the parents was wide for this trait.

Parents 5, 4 and 6 exhibited short stature whereas parents 1 and 2 were tall. Parents 3 had medium height. There was wide range of variation for this traits among the parents.

The short statured parents ***viz.***, 3, 4, 5 and 6 had their fruiting points very near to their ground level where as the parents 1 and 2 had the substantial distance from the ground.

The parents 5 and 6 were mono-stemmed type whereas 1 and 2 were rich in branches. Parents 3 and 4 had poor number of branches.

Table 7. Analysis of variance for parents and hybrids

Source	df	Mean sum of squares								
		Days to first flowering	Plant height	Height to the first productive node	Number of branches plant^{-1}	Number of capsules plant^{-1}	Capsule length	1000 seed weight	Seed yield plant^{-1}	Oil content
Replication	2	0.0743	37.810	0.6500	0.0344	21.2078	0.0015	0.0001	0.2520	0.0720
Genotypes	20	49.4589**	1137.6000**	671.6400**	38.6865**	4571.6604**	0.3353**	0.5149**	130.2930**	2.7340**
Error	40	0.0843	9.6300	3.2700	0.2426	16.7923	0.0017	0.0006	0.4204	0.0690
Total	62									

** Significant at 1% level

Table 8. Mean performance of parents and hybrids

Entry	Days to first flowering	Plant height (cm)	Height to first productive node (cm)	No. of branches plant^{-1}	No. of capsule plant^{-1}	Capsule length (cm)	1000 seed weight (g)	Seed yield plant^{-1} (g)	Oil content (%)
Parents									
1	36.00	135.13	42.60	10.00	195.83	2.50	3.24	31.32	51.40
2	36.40	140.97	37.17	9.93	194.40	2.41	3.14	30.09	52.48
3	29.87	108.53	19.70	3.63	131.33	3.10	4.33	31.52	53.63
4	25.20	89.17	20.43	3.50	70.97	3.09	2.77	13.39	51.04
5	24.53	83.50	20.23	0.00	80.83	3.20	2.80	15.61	52.40
6	26.13	92.07	23.27	0.00	79.77	3.00	2.93	16.17	52.53
Mean	29.70	108.23	27.23	6.77	125.52	2.88	3.20	23.02	52.25
Hybrids									
1 × 2	39.20	114.47	82.93	12.10	146.90	2.51	3.82	32.79	52.47
1 × 3	39.20	111.27	43.40	12.20	150.50	2.75	3.25	31.95	52.65
1 × 4	32.20	130.67	24.00	7.43	238.37	3.26	3.63	52.01	54.29
1 × 5	32.40	127.20	27.63	3.87	214.40	3.40	2.91	42.00	53.32
1 × 6	32.33	136.13	30.67	5.07	239.77	3.78	3.46	50.69	54.00
2 × 3	32.20	114.67	51.30	12.43	211.00	3.20	2.77	40.46	54.09
2 × 4	31.20	128.00	30.53	4.97	199.83	2.94	2.74	38.39	52.02
2 × 5	32.80	128.07	30.67	5.73	208.00	3.20	3.07	41.75	53.27
2 × 6	31.93	124.07	30.07	6.53	226.00	3.58	2.66	41.97	52.52
3 × 4	29.80	81.77	17.37	6.73	192.10	3.00	3.55	41.42	52.64
3 × 5	29.13	80.80	18.30	4.33	188.77	3.28	3.14	38.57	53.06
3 × 6	29.73	101.00	21.47	4.33	180.00	3.04	3.61	39.28	52.94
4 × 5	27.83	121.27	29.90	5.97	187.80	3.16	3.23	38.94	51.13
4 × 6	28.40	97.80	28.90	4.60	185.20	3.01	3.13	37.96	51.26
5 × 6	28.27	93.50	19.97	3.07	192.57	3.13	3.15	39.40	53.52
$\bar{X}$	31.78	112.71	32.47	6.62	197.41	3.15	3.21	40.50	52.88
SE	0.24	2.53	1.48	0.40	3.35	0.03	0.02	0.53	0.21
CD	0.48	5.12	2.98	0.81	6.76	0.07	0.04	1.07	0.43

The branched types ***viz.***, 1 and 2 had more number of capsules than the mono or poorly branched types ***viz.***, 5, 6, 3 and 4. Wide range for capsule number was noticed for mono-stemmed, poorly branched and richly branched types.

Adapted cultivars ***viz.***, 1 and 2 produced small sized capsule while the exotic parents 3 to 6 produced lengthy capsules. However the range for capsule length was narrow.

Parent 3 produced heavy seeds followed by parents 1 and 2. Parents 4, 5 and 6 had light seeds. However, the range was narrow for this character.

For seed yield the adapted cultivars expressed more or less equal performance where as the exotic cultivars ***viz.***, 4, 5 and 6 produced substantially low yield.

All the cultivars behaved almost in the same manner with regard to expression of oil content. However, parent 3 had the edge over the remaining parents.

4.2.2.2. Hybrids

Most of the hybrids were intermediary in nature with their parents for days to first flowering however transgression for earliness was noticed in the combinations ***viz.***, 1 × 2 and 1 × 3. None of the combinations exhibited earliness than the early flowering parents. The cross combinations among early flowering parents also showed transgression for this character. Except the two combinations ***viz.***, 1 × 2 and 1 × 3, the remaining hybrids showed narrow range (Table 8).

Majority of the hybrids had medium stature. The tall statured parents 1 and 2 when combined with each other and with parents 3 produced short statured hybrids (1 × 2, 1 × 3 and 2 × 3). However,

three combinations ***viz.***, 1 × 6, 4 × 5, and 5 × 6 exhibited heterosis for tallness. Wide range for plant height was noticed among the hybrids.

The distance between the ground to the fruiting point was substantially increased in case of 1 × 2, 1 × 3 and 2 × 3 combinations while considerable reduction was noticed in combinations ***viz.***, 3 × 4, 3 × 5 and 3 × 6. In the remaining cases it was intermediate when compared with their parents. However, the range was wide for this trait.

Five cross combinations ***viz.***, 2 × 3, 1 × 3, 1 × 2, 1 × 4 and 3 × 4 recorded more branches than mean number of branches. Mono-stemmed genotype when crossed with branch type and among themselves produced less number of branche. The cross combinations varied among themselves for number branches. Three cross combinations ***viz.***, 1 × 2, 1 × 3, and 2 × produced substantially high number of branches.

The parents 1 and 2 with more number of capsules when crossed re ited hybrids with reduced number of capsules. Number of capsul produced by most hybrids were intermediate to that of their parents. In certain crosses ***viz.***, 4 × 5, 4 × 6 and 5 × 6 a slight increase in mber of capsules were noticed. Only seven combinations ***viz.***, 1 × 4, 1 × 5, 1 × 6, 2 × 3, 2 × 4, 2 × 5 and 2 × 6 had number of capsules above the mean. Wide variation was observed for this traits.

Except the cross combinations ***viz.***, 1 × 2, 2 × 3, 1 × 4 and 2 × 4 all other combinations recorded a capsule length more than 3.0cm. Variation for capsule length among the cross combinations was very low.

Wherever the heavy seeded genotypes ***viz.***, 1, 2 and 3 are involved as parents, the resultant hybrids had heavy seeds whereas when one of the parents involved was light seeded, the hybrids produced had an intermediate seed weight.

Significant increase in seed yield was observed among the hybrids. Notably cross combinations ***viz.***, 1 × 4, 1 × 6, 1 × 5, 2 × 6, 2 × 5 and 3 × 4 had higher level of seed yield plant^{-1} above the mean. There was wide range of variation among the hybrids for this traits.

High oil content (> 54%) was recorded in combinations ***viz.***, 1 × 4, 1 × 6 and 2 × 3. In the remaining combinations slight increase for oil content was observed. However the variation for oil content among the hybrids was limited.

4.2.3. Genetical analysis

4.2.3.1. Validity of the hypothesis

The estimates of t^2 value, deviations $(b-o)/SE_{(b)}$ and $1-b/SE_{(b)}$, regression, Wr+Vr and Wr–Vr estimates are presented in Tables 9 and 10.

The t^2 estimates were significant for the height to first productive node alone, whereas for the remaining eight characters it was not significant.

The deviations or the regression slope of Wr on Vr from unity as well as from zero were tested. These results showed that traits like number of branches alone satisfied both the tests ***viz.***, (1)significant deviation from zero and (2) non significant deviation from unity.

Table 9. Tests of goodness of fit of the data to the diallel model

Character	t^2 value	b–0 /SE(b)	1–b /SE(b)	Joint regression	
				b–0 /SE(b)	1–b /SE(b)
Days to first flowering	2.0488	-3.2181*	3.7891*	3.2857*	3.8571*
Plant height	0.1118	2.4871	0.1773	2.4474	0.1842
Height to the first productive node	17.0796**	4.1333*	11.5188**	4.5000*	12.1700**
Number of branches plant^{-1}	0.0604	7.2029**	0.7097	45.5000*	4.500*
Number of capsules plant^{-1}	1.0298	1.8310	6.8201**	5.6250**	6.8750**
Capsule length	0.1149	1.7557	1.5568	1.6774	1.5484
1000 seed weight	0.0237	1.5206	0.7391	1.5111	0.9333
Seed yield plant^{-1}	0.0657	2.5545	6.2731**	-0.0047	2.3256
Oil content	0.9358	2.7701	8.2510**	-0.7286	2.1268

* Significant at 5% level

** Significant at 1% level

Table 10. ANOVA of Wr + Vr and Wr – Vr

Item	df	Mean sum of squares								
		Days to first flowering	Plant height	Height to first Productive node	Number of branches plant^{-1}	Number of Capsule plant^{-1}	Capsule length	1000 seed weight	Seed yield plant^{-1}	Oil content
Wr + Vr										
Between arrays	1	4392.80**	4000158.00**	1697686.00**	3448.58**	42253950.00*	0.51**	0.71**	25913.8**	16.57**
Within arrays	16	249.10**	140517.20*	42454.94	144.80**	1111737.00*	0.01**	0.03**	1250.18	1.01**
Wr – Vr										
Between arrays	1	89.76**	293807.50**	610005.10**	152.74**	36087107.00*	0.26**	0.14**	52048.07*	13.69**
Within arrays	16	5.82**	20016.61**	38883.16**	10.46**	2261721.00*	0.02**	0.01**	3259.63*	15.28**

* Significant at 5% level

** Significant at 1% level

The rest of the characters satisfied with anyone of the tests. Joint regression and Wr + Vr test showed none of the nine characters satisfied the assumption.

4.2.3.2. Estimates of genetic parameters and genetic ratios

The estimates of genetic parameters and ratios for the nine traits are presented in Tables 11 and 12.

The salient features of the diallel analysis are presented separately for each of the nine characters under study.

4.2.3.2.1. Days to first flowering

The additive component of variation (D) and dominance components H_1, H_2 and h^2 were significant. The rates of $(Hi/D)^{\frac{1}{2}}$ was less than unity. The estimates for $H_2/4H_1$ was 0.2282 and K_d/K_r ratio was more than unity. The ratio of h^2/H_2 was 1.1760. The heritability estimates was 84.39%.

4.2.3.2.2. Plant height

The additive component (D) and dominance component (H_1 and H_2) were highly significant and positive. The parameters F and h^2 were non significant. $(H_1/D)^{\frac{1}{2}}$ and K_d/K_r ratio were more than unity. $H_2/4H_1$ and h^2/H_2 were 0.1927 and 0.0814 respectively. The heritability estimates was moderate.

4.2.3.2.3. Height to the first productive node

Both estimates of additive and non-additive components for this trait were non significant. The mean degree of dominance was more than unity. $H_2/4H_1$ ratio was 0.2160. K_d/K_r ratio is less than unity. Heritability estimates was found to be moderate (55%).

Table 11. Estimates of genetic parameters

Characters	D	F	H_1	H_2	h^2	E
Days to first flowering	28.8265** ± 1..5797	1.6868 ± 1.5797	11.2758** ± 4.0103	10.2930** ± 3.5825	12.1052** ± 2.4113	0.0279 ± 0.5970
Plant height	602.7045** ± 96.5326	329.4774 ± 235.8293	856.2957** ± 245.0569	660.2097** ± 218.9155	53.8025 ± 147.3446	3.6600 ± 36.4859
Height to the first productive node	99.4579 ± 118.3225	-135.1534 ± 289.0620	565.1671 ± 300.3724	488.4025 ± 268.3302	75.6887 ± 180.6039	1.0500 ± 44.7217
Number of branches $plant^{-1}$	20.3267** ± 1.1285	3.8429 ± 2.7571	17.8074** ± 2.8650	15.7427** ± 2.5594	12.3630** ± 1.7226	0.0776 ± 0.4265
Number of capsules $plant^{-1}$	3352.0416* ± 1332.9807	4816.9585 ± 3256.4734	6577.6095 ± 3383.8930	4727.8180 ± 30.2291	2191.6004 ± 2034.6221	5.6675 ± 503.8193
Capsule length	0.1145 ± 0.0650	0.1238 ± 0.1588	0.4419** ± 0.1650	0.3819** ± 0.1474	0.1994* ± 0.0992	0.0060 ± 0.0245
1000 seed weight	0.3419** ± 0.0618	0.3840* ± 0.1510	0.6134** ± 0.1569	0.4558 ± 0.1401	0.0001 ± 0.0943	0.0002 ± 0.0233
Seed yield $plant^{-1}$	77.0237 ± 41.3692	126.3604 ± 101.0649	212.0652* ± 105.0194	155.3267 ± 93.8164	56.4732 ± 63.1446	0.1375 ± 15.6360
Oil content	0.8242 ± 0.5152	0.6975 ± 1.2587	3.3499* ± 1.3079	2.9080* ± 1.1684	1.0940 ± 0.7864	0.0230 ± 0.1947

* Significant at 5% level
** Significant at 1% level

Table 12. Ratios of genetic parameters

Character	$(H_1/D)^{\frac{1}{2}}$	$(H_2/4H_1)$	K_d/K_r	h^2/H_2	Heritability % (narrow sense)
Days to first flowering	0.6254	0.2282	1.0980	1.1760	84.39
Plant height	1.1919	0.1927	1.5951	0.0814	58.17
Height to first productive node	2.3838	0.2160	0.5564	0.1549	55.83
Number of branches plant^{-1}	0.9359	0.2210	1.2246	0.7853	69.79
Number of capsules plant^{-1}	1.4008	0.1797	3.1061	0.4636	13.94
Capsule length	1.9643	0.2160	1.7588	0.5220	20.93
1000 seed weight	1.3394	0.1858	2.444	0.0002	33.58
Seed yield plant^{-1}	1.6592	0.1831	2.955	0.3636	8.67
Oil content	2.0159	0.2170	1.5313	0.3762	27.48

4.2.3.2.4. Number of branches plant^{-1}

Both the estimates of additive and non additive component for this trait was non significant. Mean degree of dominance was near to unity. $H_2/4H_1$ ratio was 0.2210. The estimates of K_d/K_r was more than unity. The ratio of h^2/H_2 was less than 1. Heritability for this trait was high (69.79%)

4.2.3.2.5. Number of capsules plant^{-1}

The additive component alone was significant for this trait. Dominance and F component estimates were non-significant. Both mean degree of dominance and K_d/K_r ratio were more than unity. $H_2/4H_1$ and h^2/H_2 ratio were very low. Heritability also was low in magnitude (13.94%).

4.2.3.2.6. Capsule length

Additive and F components were non significant and dominance component was significant for this character. Mean degree of dominance and K_d/K_r were more than unity. $H_2/4H_1$ was 0.2160. h^2/H_2 was less than 1. Estimates of heritability was also low (20%).

4.2.3.2.7. 1000 seed weight

Additive, dominance and F components were significant except h^2. Both mean degree of dominance and K_d/K_r ratio were more than unity. $H_2/4H_1$ was 0.1858. h^2/H_2 was very low. Heritability was moderate (33.58%).

4.2.3.2.8. Seed yield plant^{-1}

Dominance component alone was significant. Rest of the components were non significant. Both $(H_1/D)^{\frac{1}{2}}$ and K_d/K_r were more

than unity. $H_2/4H_1$ was 0.1831. h^2/H_2 was less than one. Heritability estimate was low.

4.2.3.2.9. Oil content

Dominance component H_1 and H_2 were significant. Remaining components were non significant. Mean degree of dominance and K_d/K_r were more than unity. $H_2/4H_1$ was 0.2170. h^2/H_2 was less than one. Heritability was moderate.

4.2.4. Graphic analysis

The estimated values of the variance of progeny family means within an array around and the array mean (Vr) and covariance of the offspring in each parental array with the non recurring parents (Wr) were plotted in Wr, Vr and standardised deviation graphs and are presented in Figures 4 to 12.

4.2.4.1. Days of first flowering

The Wr-Vr graph for this trait revealed the following conclusions. The linear regression line of unit slope intercepted Wr axis above the origin. The parents 6 and 4 were near the origin and 3 was far away from the point of origin. Parent 5, 2 and 1 occupied middle position (Fig. 4a).

Parents 1 and 2 occupied the recessive-positive quadrant of the standardised deviation graph. While parents 4 and 6 occupied the dominant negative quadrant. Parent 5 was in the recessive negative quadrant while parent 3 was a border line case (Fig. 4b).

4.2.4.2. Plant height

The linear regression line of unit slope crossed the Wr this below the origin. The parent 2 occupied a position near the origin.

Fig. 4(a). Wr-Vr Graph for days to first flowering

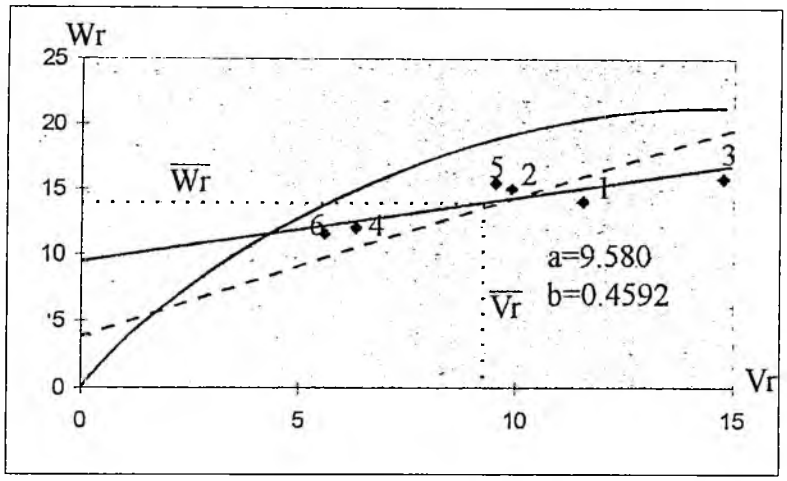
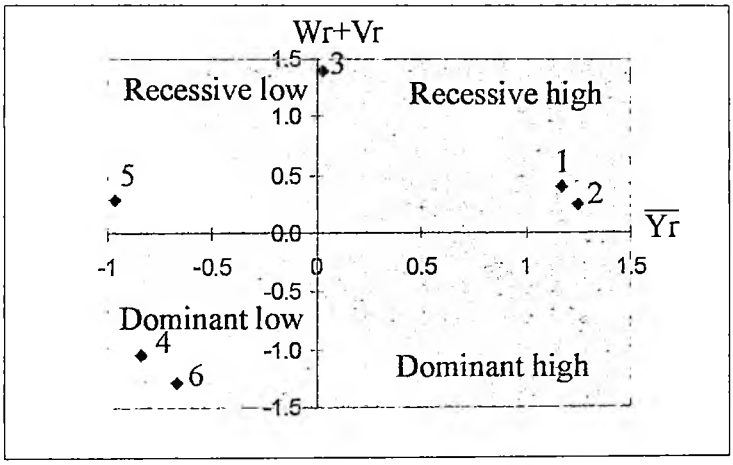


Fig.4(b). Standardised deviation graph for days to first flowering



1- TMV 3, 2- TMV6, 3- SVPR 1, 4- EC 351879, 5- EC 351905, 6- EC 351906

Fig. 5(a). Wr-Vr Graph for plant height

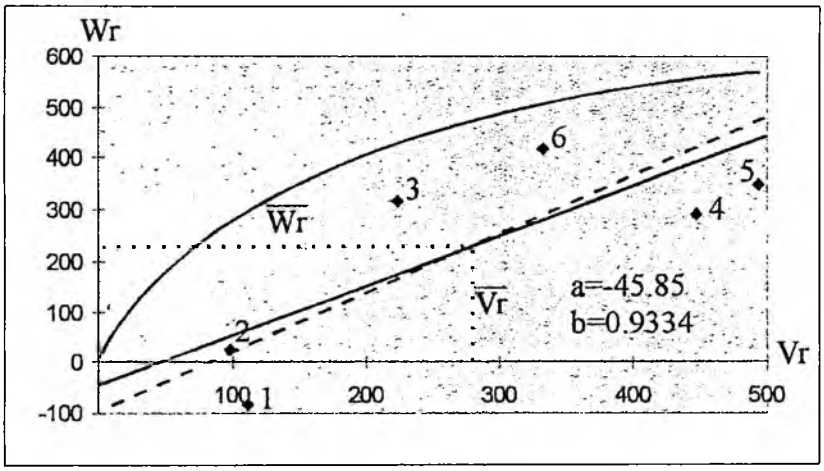
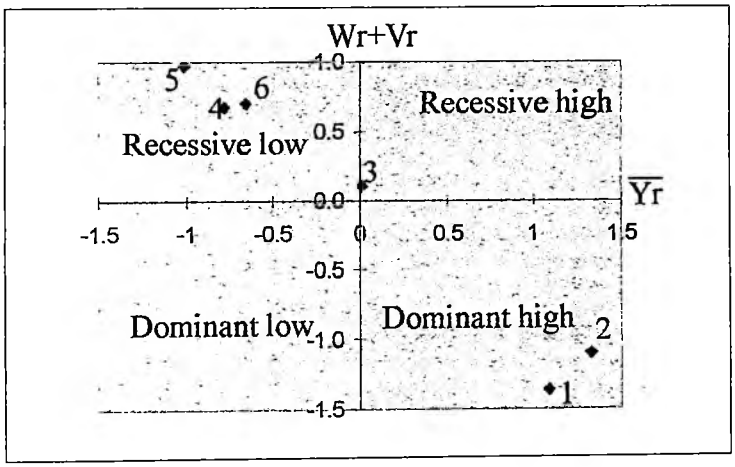


Fig.5(b). Standardised deviation graph for plant height



1- TMV 3, 2- TMV6, 3- SVPR 1, 4- EC 351879, 5- EC 351905, 6- EC 351906

The parents 4 and 5 were at the extreme position parent 3 and 6 occupied middle position from the point of origin (Fig. 5a).

Parents 1 and 2 occupied the dominant positive quadrant of the standardised deviation graph while parents 4, 5 and 6 occupied the recessive-negative quadrant and parent 3 was a border line case (Fig. 5b).

4.2.4.3. Height to the first productive node

The linear regression line crossed the Wr axis above the point of origin. The parents 4, 5 and 6 were near the origin, while parents 2 and 1 were at the extreme position. Parent 3 occupied middle position (Fig. 6a).

Standardised deviation graph revealed that parents 1 and 2 occupied recessive-positive quadrant while parent 3 was in the recessive-negative quadrant. However, parents 4, 5 and 6 occupied dominant-negative quadrant of the standardised deviation graph (Fig. 6b).

4.2.4.4. Number of branches plant^{-1}

The linear regression line of unit slop intercepted the Wr axis above the origin. Parents 4, 5 and 6 were near the point of origin while parent 3 at the extreme position. Parents 2 and 1 occupied the middle position (Fig. 7a).

Parents 1 and 2 occupied the recessive-positive quadrant of the standardised deviation graph while parent 3 was in the recessive-negative quadrant. Parents 4, 5 and 6 occupied the dominant negative quadrant (Fig. 7b).

Fig. 6(a). Wr-Vr Graph for height to first productive node

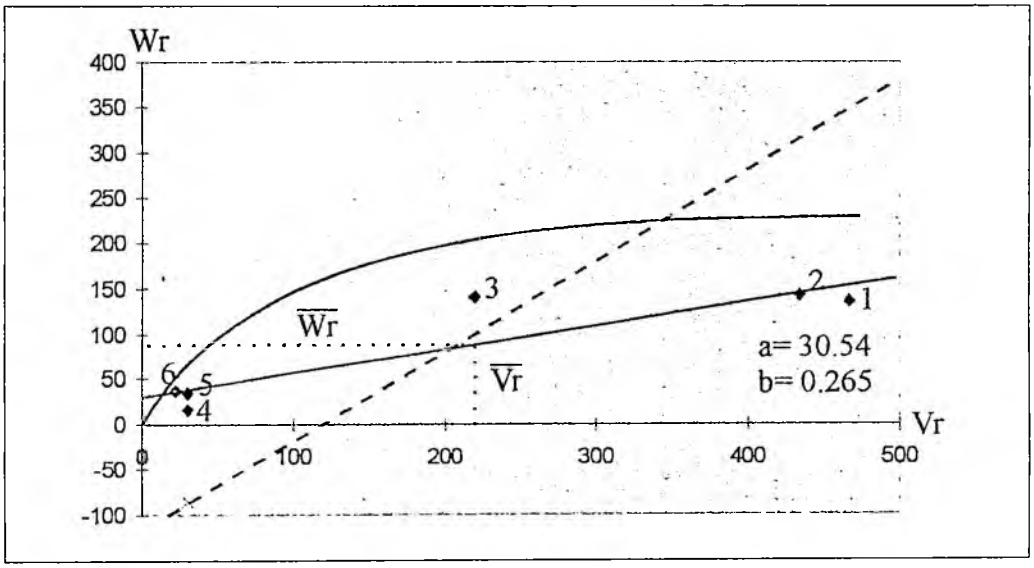
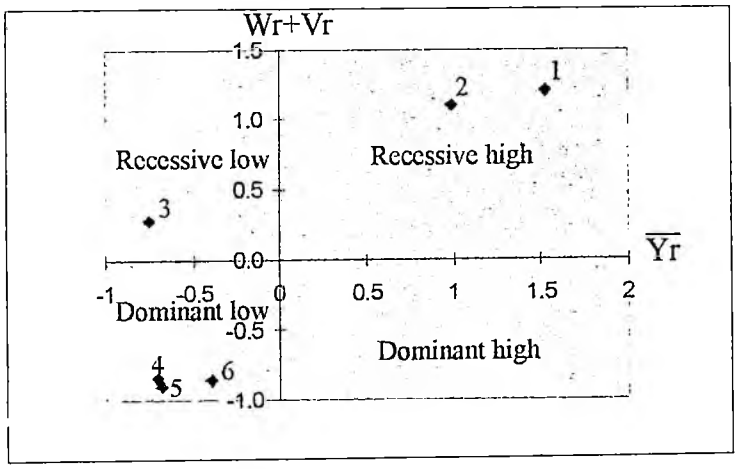


Fig.6(b). Standardised deviation graph for height to first productive node



1- TMV 3, 2- TMV6, 3- SVPR 1, 4- EC 351879, 5- EC 351905, 6- EC 351906

Fig. 7(a). Wr-Vr graph for number of branches plant^{-1}

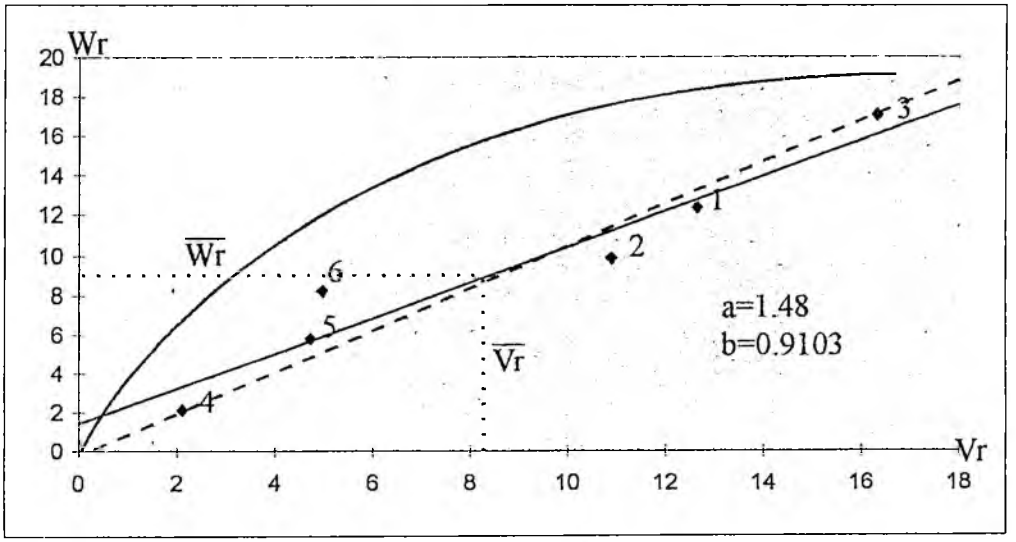
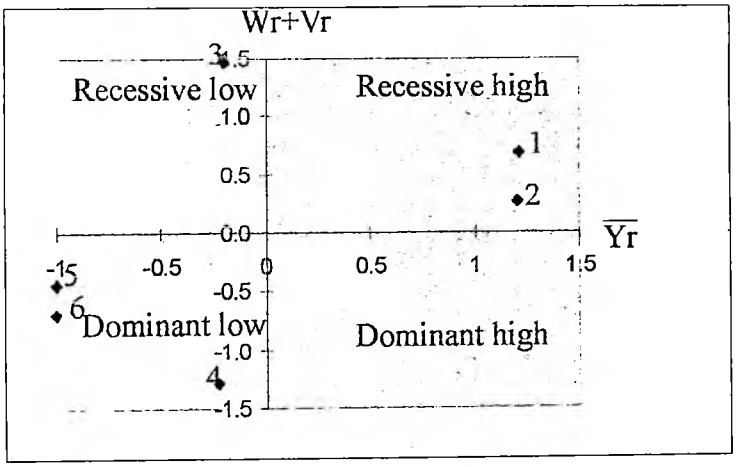


Fig.7(b). Standardised deviation graph for number of branches plant^{-1}



1- TMV 3, 2- TMV6, 3- SVPR 1, 4- EC 351879, 5- EC 351905, 6- EC 351906

Fig. 8(a). Wr-Vr Graph for number of capsules plant^{-1}

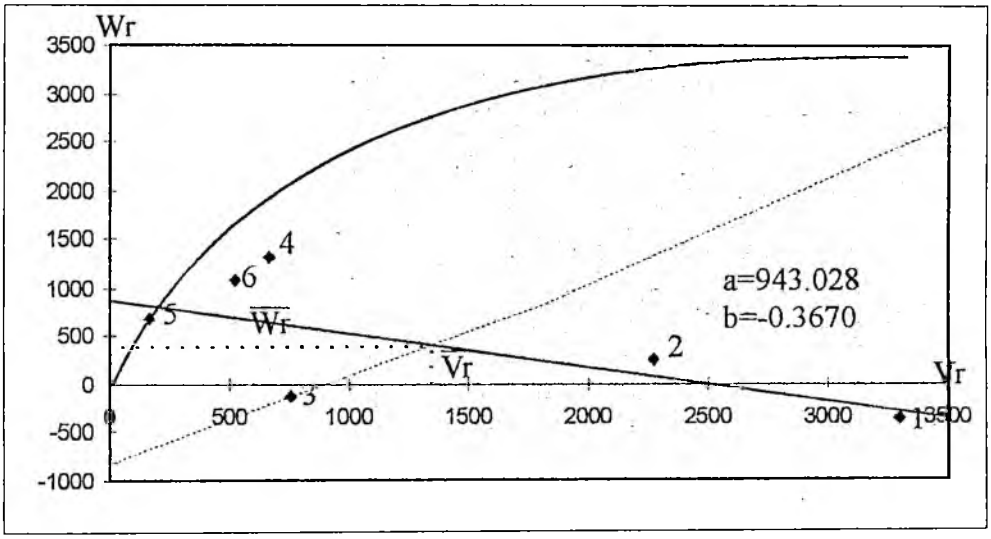
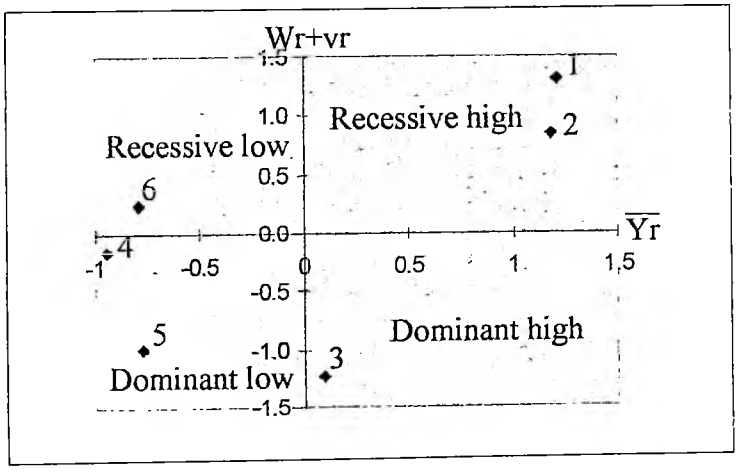


Fig. 8(b). Standardised deviation graph for number of capsules plant^{-1}



1- TMV 3, 2- TMV6, 3- SVPR 1, 4- EC 351879, 5- EC 351905, 6- EC 351906

4.2.4.5. Number of capsule plant^{-1}

The Wr-Vr and standardised deviation graph are presented in Fig.8a and 8b. The regression line crossed the y ordinate above the point of origin. Parents 5, 6, 4 and 3 occupied their position near the origin while parent 1 was far away from the origin. Parent 2 occupied middle position.

Parent 3 occupied dominant-positive quadrant of the standardised deviation graph. While parents 4 and 5 occupied dominant-negative quadrant. Parents 1 and 2 where in the recessive-positive quadrant and parent 6 occupied recessive negative quadrant (Fig. 8b).

4.2.4.6. Capsule length

The linear regression line intercepted the Wr- axis below the origin. Parents 3, 4 and 5 were near the point of origin. Parent 1 was far away and parents 2 and 6 occupied middle position (Fig. 9a).

Parents 3, 4, 5 and 6 occupied the dominant positive quadrant of the standardised deviation graph while parents 1 and 2 occupied recessive-negative quadrant (Fig. 9b).

4.2.4.7. 1000 seed weight

The linear regression line of unit slope cut the Wr axis below the origin. Parent 6 alone was near the origin. Parents 3 was far away from the origin while parents 1, 2, 5 and 4 occupied middle position (Fig. 10a).

Parent 3 occupied recessive-positive quadrant while parents 4 and 6 occupied recessive-negative quadrant. Parent 1 occupied

Fig. 9(a). Wr-Vr Graph for capsule length

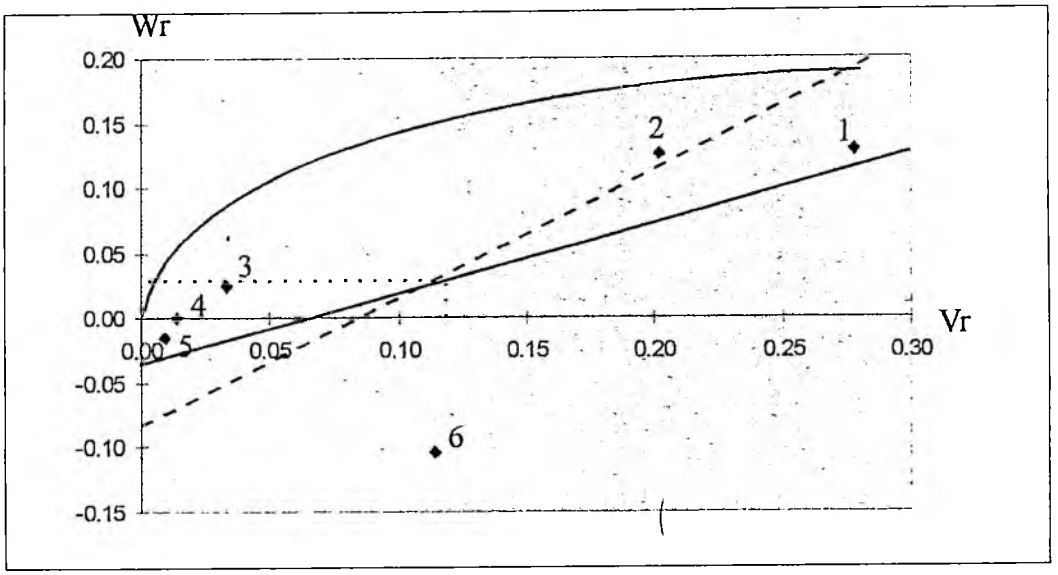
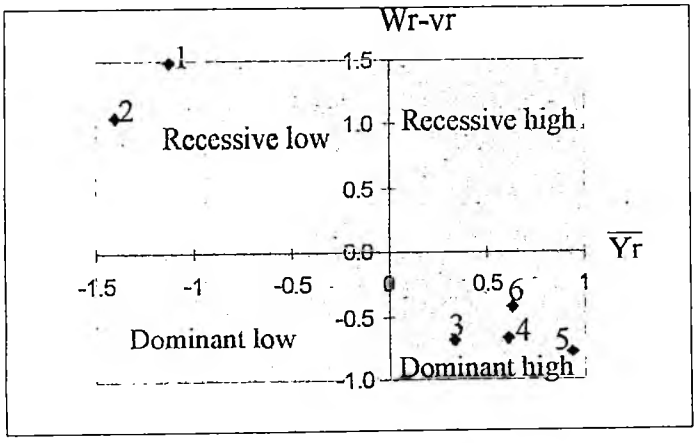


Fig.9(b). Standardised deviation graph for capsule length



1- TMV 3, 2- TMV6, 3- SVPR 1, 4- EC 351879, 5- EC 351905, 6- EC 351906

Fig. 10(a). Wr-Vr Graph for 1000 seed weight

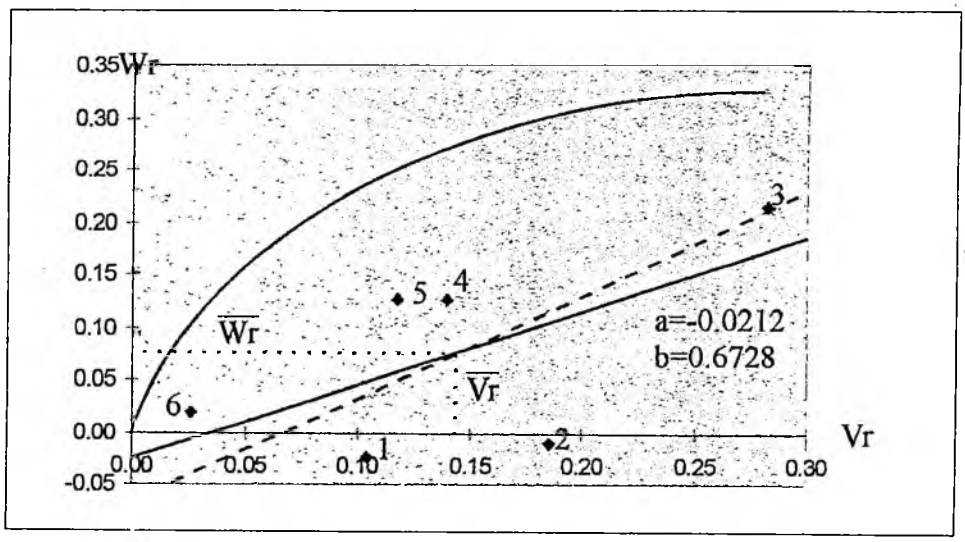
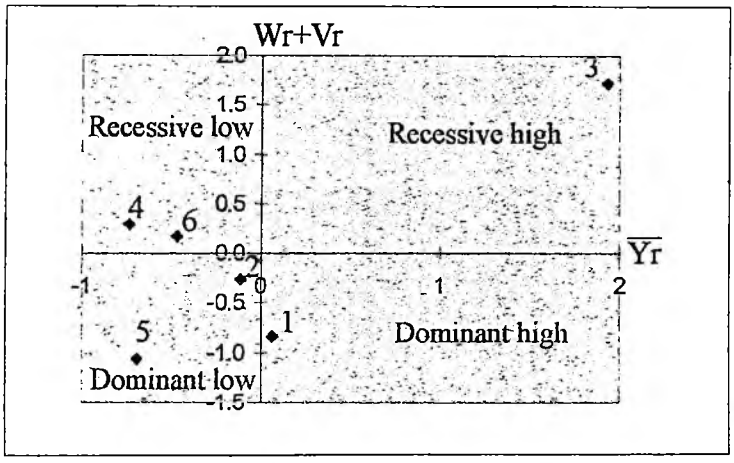


Fig. 10(b). Standardised deviation graph for 1000 seed weight



1- TMV 3, 2- TMV6, 3- SVPR 1, 4- EC 351879, 5- EC 351905, 6- EC 351906

Fig. 11(a). Wr-Vr Graph for seed yield plant^{-1}

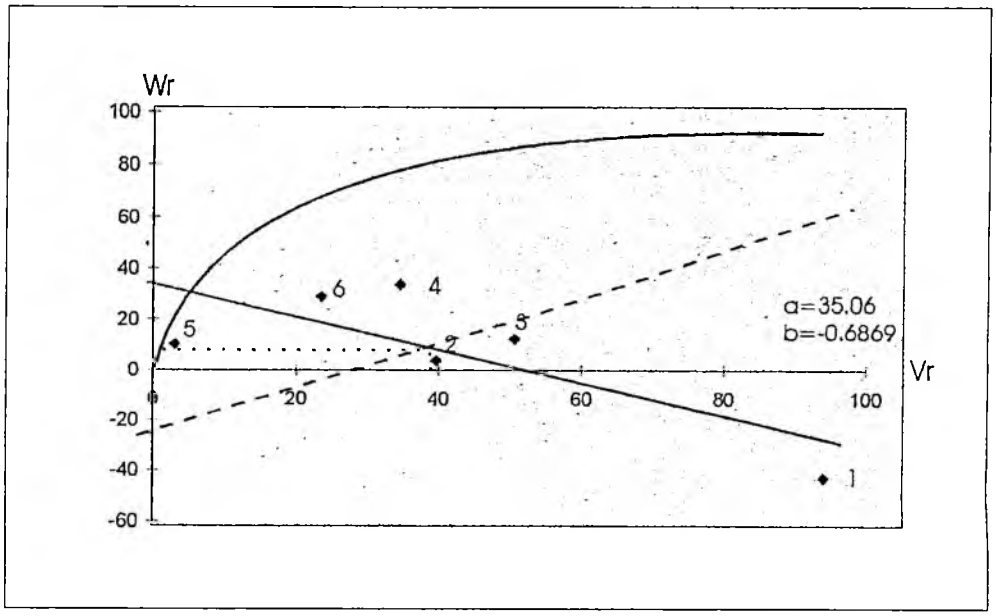
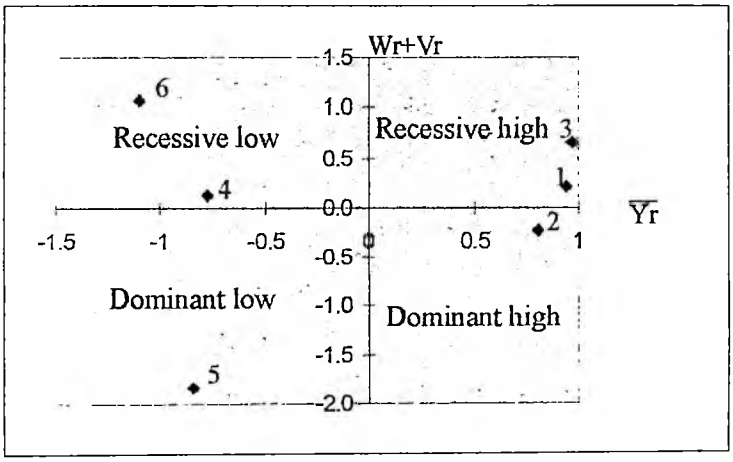


Fig. 11(b). Standardised deviation graph for seed yield plant^{-1}



1- TMV 3, 2- TMV6, 3- SVPR 1, 4- EC 351879, 5- EC 351905, 6- EC 351906

Fig. 12(a). Wr-Vr Graph for oil content

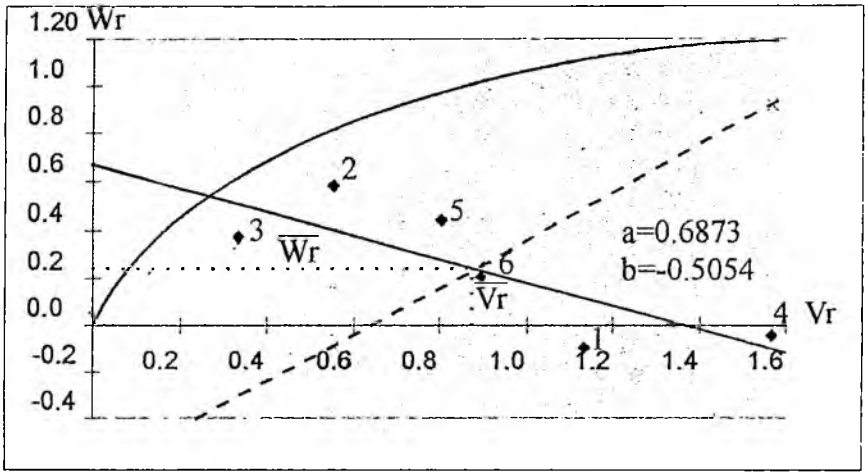
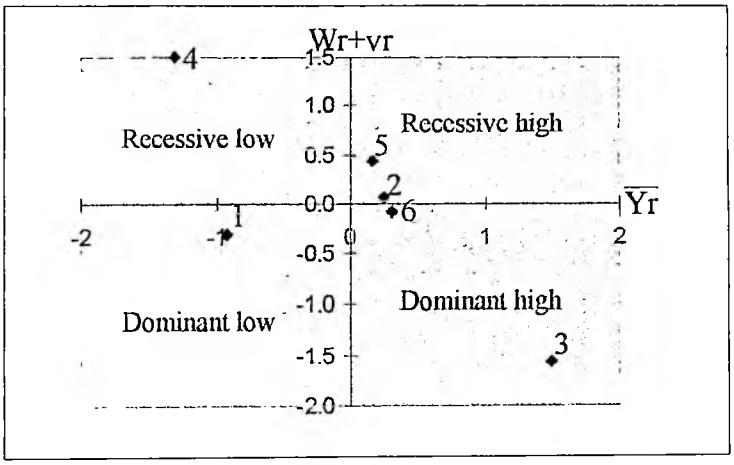


Fig. 12(b). Standardised deviation graph for oil content



1- TMV 3, 2- TMV6, 3- SVPR 1, 4- EC 351879, 5- EC 351905, 6- EC 351906

dominant positive quadrant while parent 2 and 5 occupied dominant negative quadrant in the standardised deviation graph (Fig. 10b).

4.2.4.8. Seed yield plant^{-1}

The linear regression line of unit slope intercept the Wr axis above the point of origin. Parents 5 and 6 were near the origin while parents 2, 4and 3 occupied middle position. Parent 1 was at the extreme end (Fig. 11a).

Parent 2 occupied the dominant-positive quadrant while parent 5 occupied the dominant-negative quadrant. Parent 1 and 3 occupied recessive-negative quadrant while parents 4 and 6 occupied recessive-negative quadrant of the standardised deviation graph (Fig. 11b).

4.2.4.9. Oil content

The linear regression line of unit slope intercepted the Wr axis above the point of origin. Parents 3 and 2 were almost near the origin. Parents 5, 6 and 1 occupied middle position while parents 4 was at the extreme position (Fig. 12a).

Parent 3 occupied dominant positive quadrant while parent 1 occupied dominant-negative quadrant. Parent 5 occupied recessive-positive quadrant and parent 4 occupied recessive-negative quadrant. Parents 2 and 6 were border line case 3 in the standardised deviation graph (Fig. 12b).

4.2.5. Combining ability analysis

4.2.5.1. Analysis of variance

The estimates of general and specific combining ability variances for nine traits are presented in Table 13. The variances due to general and specific combining ability were highly significant

Table 13. Analysis of variance for combining ability

Source	df	Mean sum of squares								
		Days to first flowering	Plant height	Height to the first productive node	Number of branches plant^{-1}	Number of capsules plant^{-1}	Capsule length	1000 seed weight	Seed yield plant^{-1}	Oil content
GCA	5	1842.7622**	23750.18**	2251.9184**	103.8757**	21994.2122**	17.4655*	19.1636*	784.3696*	5103.8029**
SCA	15	3.2319**	194.089**	135.5765**	4.7707**	1510.5452**	0.1119*	0.1338*	48.4277*	0.8431**
Error	40	0.0281	3.21	1.09	0.0809	5.5974	0.0006	0.0002	0.1401	0.023
GCA:SCA		71.8972:1	15.5510:1	2.0921:1	2.7665:1	1.8264:1	19.6139:1	17.9339:1	1.9369:1	777.8952:1

** Significant at 1% level

for all the traits. The ratio of general to specific combining ability variances ranged from 1.82: 1 to 777. 89:1.

4.2.5.2. General combining ability effects

The estimates of ***gca*** effects for the six parents under study are presented in Table 14.

Parents 4, 5 and 6 exhibited significant and negative ***gca*** effects while the remaining three displayed positive ***gca*** effects for days to first flowering.

Plant height of four parents 3, 4, 5 and 6 showed significant negative ***gca*** effects while 1 and 2 showed significant positive ***gca*** effects. The ***gca*** effects of the character height to the first capsule was also in the similar manner.

In case of number of branches parents 4, 5 and 6 had significant negative ***gca*** effects and 1, 2 and 3 exhibited significant positive ***gca*** effects.

The adapted cultivar 1 and 2 had significant positive ***gca*** effects while the remaining four parents showed significant negative ***gca*** effects for number of capsules.

None of the parents showed significant ***gca*** effects for capsule length.

With regard to 1000 seed weight parents 2, 3, 5 and 6 had significant negative ***gca*** effects while 1 and 3 had positive significant ***gca*** effects.

Three parents 1, 2 and 3 showed significant positive ***gca*** effects for seed yield plant^{-1} while parents 4, 5 and 6 had negative significant ***gca*** effects.

Table 14. General combining ability effects of parents

Parents	Days to first flowering	Plant height	Height to the first productive node	Number of branches plant^{-1}	Number of capsule plant^{-1}	Capsule length	1000 seed weight	Seed yield plant^{-1}	Oil content
1	3.6333**	13.7486**	9.6250**	2.3153**	17.9361**	-0.1015	0.1386**	2.9400**	0.0797
2	2.7333**	13.8986**	10.3750**	2.4361**	17.8028**	-0.1590	-0.1366**	0.8736**	0.0560
3	0.1917**	-9.1810**	-3.2000**	0.6444**	-6.6347**	-0.0057	0.3173**	0.7716**	0.4685**
4	-2.3000**	-5.2722**	-5.6583**	-0.6805**	-11.6097**	0.0056	-0.0782**	-1.6318**	-0.6824**
5	-2.3417**	-7.7722**	-6.2375**	-2.3972**	-10.6139**	0.1318	-0.1680**	-2.0887**	0.0276
6	-1.9170**	-5.422**	-4.9042**	-2.3181**	-6.8806**	0.1290	-0.0731**	-0.8646**	0.0510
SE (gi)	0.0541	0.5800	0.3400	0.0918	0.7636	0.0076	0.0046	0.1208	0.049

** Significant at 1% level

Only one parent 3 showed positive and significant ***gca*** effects for oil content. The remaining parents had non-significant ***gca*** effects for this trait.

4.2.5.3. Specific combining ability effects

The specific combining ability effects of 15 hybrids are presented in Table 15.

Out of the 15 hybrids eight hybrids ***viz.***, 1 × 2, 1 × 3, 2 × 5, 3 × 4, 3 × 6, 4 × 5, 4 × 6 and 5 × 6 showed significant positive ***sca*** effects for days to first flowering. Significant negative effects were recorded by five hybrids ***viz.***, , 1 × 4, 1 × 6, 2 × 3, 2 × 4, and 2 × 6.

The highest ***sca*** effects for plant height was observed in the hybrid 4 × 5 while the lowest effects were recorded by the hybrid 1 × 2. Eight out 15 cross combinations ***viz.***, 1 × 4, 1 × 5, 1 × 6, 2 × 4, 2 × 5, 2 × 6, 3 × 6 and 4 × 5 recorded significant positive ***sca*** effects. However, six hybrids ***viz.***, 1 × 2, 1 × 3, 3 × 4, 3 × 5, 4 × 6 and 5 × 6 registered significant negative effects.

In the case of height to the first capsule five hybrids ***viz.***, 1 × 2, 1 × 3, 2 × 3, 4 × 5 and 4 × 6 recorded significant positive ***sca*** effects. Eight hybrids 1 × 4, 1 × 5, 1 × 6, 2 × 4, 2 × 5, 2 × 6, 3 × 4 and 3 × 5 recorded significant negative ***sca*** effects.

With regard to number of branches six out of 15 hybrids ***viz.***, 1 × 2, 1 × 3, 2 × 3, 3 × 4, 4 × 6 and 5 × 6 showed significant positive ***sca*** effects while three cross combinations 1 × 5, 1 × 6, and 2 × 4 showed significant negative ***sca*** effects.

The highest ***sca*** effects for capsule number was recorded by the hybrid 1 × 4 while the lowest ***sca*** effects was showed by the cross combination 1 × 2 which involved the adapted parents 1 and

Table 15. Specific combining ability effects of hybrids

Parents	Days to first flowering	Plant height	Height to the first productive node	Number of branches plant^{-1}	Number of capsule plant^{-1}	Capsule length	1000 seed weight	Seed yield plant^{-1}	Oil content
1 × 2	1.6524**	-24.6107**	31.9571**	1.3280**	-94.2833**	-0.3060**	0.6157**	-12.8169**	-0.3627**
1 × 3	4.1940**	-4.7315**	5.9988**	3.2196**	-66.2458**	-0.2160**	-0.4146**	-13.5585**	-0.5985**
1 × 4	-0.3143*	10.7601**	-10.9429**	-0.2220	26.5958**	0.2861**	0.3616**	8.9093**	2.1923**
1 × 5	-0.0726	9.7935**	-6.7304**	-2.0720**	1.6333	0.2932**	-0.2676**	-0.6569*	0.5157**
1 × 6	-0.5643**	16.3768**	-5.0304**	-0.9512**	23.2667**	0.6828**	0.1872**	6.8248**	1.1594**
2 × 3	-1.9060**	-1.4815	13.1488**	3.3321**	-5.6125**	0.2882**	-0.6147**	-2.9781**	0.8652**
2 × 4	-0.4143**	7.9435**	-5.1595**	-2.8095**	-11.8042**	0.0203	-0.2528**	-2.6413**	-0.0473
2 × 5	1.2274**	10.5101**	-4.4470**	-0.3262	-4.6333**	0.1574**	0.1723**	1.1672**	0.4927**
2 × 6	-0.0643	4.1601**	-6.3804**	0.3946	9.6333**	0.5370**	-0.3316**	0.1701	-0.2835*
3 × 4	0.7274**	-15.2107**	-4.7512**	0.7488**	4.9000**	-0.0697**	0.1006**	0.4901	0.1569
3 × 5	0.1024	-13.6774**	-3.2387**	0.0655	0.5708	0.0807**	-0.2146**	-1.9028**	-0.1364
3 × 6	0.2774*	4.1726**	-1.4054	-0.0137	-11.9292**	-0.1530**	0.1572**	-2.4168**	-0.2793*
4 × 5	1.3274**	22.8810**	10.8196**	3.0238	4.5792**	-0.0539**	0.2719**	0.8623**	-0.9089**
4 × 6	1.4357**	-2.9357*	8.4863**	1.5780**	-1.7542	-0.1943**	0.0737**	-1.3380**	-0.8085**
5 × 6	1.3440**	-4.7357**	0.1321	1.7613**	4.6167**	-0.2039**	0.1815**	0.5485*	0.7482**
SE (gi)	0.1227	1.3100	0.7600	0.2081	1.7317	0.0173	0.0105	0.2740	0.1100

* Significant at 5% level
** Significant at 1% level

2. Six out of 15 hybrids ***viz.***, 1 × 2, 1 × 3, 2 × 3, 2 × 4, 2 × 5 and 3 × 6 recorded significant negative ***sca*** effects.

Cross combinations 1 × 4, 1 × 5, 1 × 6, 2 × 3, 2 × 5, 2 × 6, and 3x5 showed significant positive ***sca*** effects for capsule length. Seven combinations ***viz.***, 1 × 2, 1 × 3, 3 × 4, 3 × 6, 4 × 5, 4 × 6 and 5 × 6 had significant negative effects.

All the hybrids exhibited significant ***sca*** effects with regard to 1000 seed weight. It was positively significant for eight hybrids ***viz.,*** 1 × 2, 1 × 4, 1 × 6, 3 × 4, 3 × 6, 4 × 5, 4 × 6 and 5 × 6 and negatively significant for six hybrids ***viz.,*** 1 × 3, 1 × 5, 2 × 3, 2 × 4, 2 × 6 and 3 × 5.

The highest ***sca*** effects for seed yield plant^{-1} as expressed by the hybrid 1 × 4. Five hybrids ***viz.***, 1 × 4, 1 × 6, 2 × 5, 4 × 5, and 5 × 6 had significant positive ***sca*** effects while eight hybrids ***viz.,*** 1 × 2, 1 × 3, 1 × 5, 2 × 3, 2 × 4, 3 × 5, 3 × 6 and 4 × 6 had significant negative ***sca*** effects.

With regard to oil per cent six cross combinations ***viz.***, 1 × 4, 1 × 5, 1 × 6, 2 × 3, 2 × 5 and 5 × 6 recorded significant positive ***sca*** effects. Six hybrids ***viz.***, 1 × 2, 1 × 3, 2 × 6, 3 × 6, 4 × 5 and 4 × 6 had significant negative ***sca*** effects.

4.3. Component analysis

The results of component analysis are presented in Tables 16 and 17.

i) The component character x_2 (b/a) exhibited significant and high positive correlation with b, c, and y. (number of capsules plant^{-1}, number of seed per capsules and yield). y has established high correlation with b and c. The coefficient of determinations r^2 (y, a...y) showed high value with b and c.

Table 16. Coefficients of correlation (r) between the components (x_1, ... x_4) of the complex character y and the primary characters (a, ..., y) and complementary determination (cd) derived from the r^2 (y, a, ..., y)

	a	b	c	y
x_1 = a	1.000**	0.210	0.003	-0.370
x_2 = b/a	**-0.243**	0.999**	0.917**	0.909**
x_3 = c/b	0.505	**-0.666****	0.340	-0.531
x_4 = y/c	-0.864**	0.289	**0.1357**	0.563
y	0.370	0.906**	0.894**	1.000**
r^2 (y, a.....y)	0.137	0.821	0.799	1.000
cd (y, x_1,....., x_4)	0.137	0.684	-0.022	0.201

* Significant at 5% level

** Significant at 1% level

Table 17. Estimates of coefficient of variation (v%) of yield, standard deviation (σ) of log yield and 'c_i' coefficient for yield components of sesame (all parameters except v% multiplied by 10^2)

Genotype	Yield			Plants/ m^2	Capsule /plant	Seeds/ plant	Seed wt./seed
	V%	$\hat{\sigma}$ ($\times 10^2$)	$\hat{\sigma}^2$ ($\times 10^2$)	$\hat{c}_1$ ($\times 10^2$)	$\hat{c}_2$ ($\times 10^2$)	$\hat{c}_3$ ($\times 10^2$)	$\hat{c}_4$ ($\times 10^2$)
EC 351879	14.0	18.7	3.5	1.2	2.4	0.4	0.4
EC 351880	31.0	35.7	12.7	0.7	3.1	9.6	-0.6
EC 351903	39.1	34.8	12.1	3.4	5.4	2.4	0.9
EC 351904	23.2	31.4	1.0	5.4	3.5	0.3	0.7
EC 351905	9.4	21.0	4.3	0.6	1.0	1.8	0.9
EC 351906	14.7	27.5	7.5	1.2	1.6	4.6	0.1
EC 351907	35.4	30.0	9.0	1.0	9.6	-0.8	-0.9
EC 351908	30.4	27.5	7.5	3.0	3.7	-0.02	0.9
EC 357015	59.0	23.2	5.4	1.3	4.2	-0.4	0.2
EC 357016	53.1	31.1	9.6	0.6	9.7	0.01	-0.7
EC 357017	45.1	27.3	7.5	2.5	4.4	1.6	-1.0
EC 357018	45.0	22.3	5.0	0.9	4.9	-0.7	-0.2
EC 357019	44.0	22.0	4.7	2.9	2.8	-1.6	0.7
EC 357020	42.5	22.2	4.9	3.2	2.2	-1.0	0.6
EC 357021	21.5	13.6	1.9	1.0	2.8	-2.3	0.4
EC 357022	30.4	18.7	3.5	-0.1	2.7	-0.5	1.4
EC 357023	33.0	19.7	3.9	1.8	3.0	-1.4	0.5
EC 357024	74.0	44.1	19.4	3.4	13.5	1.1	1.4
EC 357025	35.0	30.0	9.0	1.3	6.6	0.9	0.1
EC 357026	43.0	36.4	13.2	1.9	6.0	5.3	0.1
TMV 3	4.3	17.6	3.1	0.8	2.1	0.4	-0.01
TMV 4	2.5	8.5	0.7	0.8	0.6	-0.5	-0.2
TMV 6	3.4	11.8	1.4	0.5	1.1	-0.3	0.04
CO 1	10.0	33.0	10.8	1.2	7.4	1.6	0.7
SVPR-1	4.5	15.4	2.4	0.1	1.4	0.5	0.4

Table 18. Predicted progeny value for seed yield for 15 single cross hybrids

Hybrid	Predicted yield	Predicted Mid Parent Value
1 × 2	420.27	420.98
1 × 3	436.42	423.86
1 × 4	302.81	307.91
1 × 5	389.74	359.95
1 × 6	360.62	345.45
2 × 3	395.84	381.42
2 × 4	273.46	265.47
2 × 5	355.57	317.51
2 × 6	327.78	303.01
3 × 4	260.84	268.35
3 × 5	340.52	320.39
3 × 6	313.23	305.89
4 × 5	201.26	204.44
4 × 6	187.57	189.94
5 × 6	242.56	241.98

Complementary determination (cd) showed high value for component x_2. This was followed by x_4 while x_3 showed negative value. The correlation between each component and its preceding primary character (bold figure) illustrated x_4 with c alone positively correlated and x_2 and x_3 showed negative relationship with a and b respectively.

ii) The component analysis as per Piepho (1995) was presented in Table 17 illustrated the following results. The agreement between the coefficient of variation for yield (v%) and the deviation of the log yield (σ) were rather close in most of the cases. For all the genotypes the yield components namely, number of capsules per plant had the highest 'c_i' values except for genotypes 4, 13, 14 and 22 which had the 'c_i' values for plants/m^2. The genotype 2, 5, 6 and 20 also showed high 'c_i' values for seeds/capsule (Table 17).

4.3.1. Recombinative heterosis

The predicted progeny values for recombinative heterosis was presented in Table 18. The high predicted progeny values in comparison with their midparental values were noticed in hybrids ***viz.,*** 1 × 3, 1 × 5, 1 × 6, 2 × 3, 2 × 4, 2 × 5, 2 × 6, 3 × 5, 3 × 6 and 5 × 6. The remaining hybrids showed lesser values than their midparent values.

4.3.2. The effects of multiplicative characters of heterosis

The hybrid factor (HF) and multiplication factor (MF) estimates were presented in Table 19. The hybrid factor was high for cross 1 × 4. All the hybrid factors for sub characters were equally high. Multiplicative factor for xy and xz were high while it was low for yz. The multiplicative factor for three characters were high for cross 1 × 4.

Table 19. The effects of multiplicative characters of heterosis

Cross combinations	Hybrid factor (HF)				Multiplication factor (MF)			
	HF_u	HF_x	HF_y	HF_z	MF_{xyz}	MF_{xy}	MF_{xz}	MF_{yz}
1 × 4	2.66	1.79	1.23	1.24	0.98	1.02	1.00	0.96
1 × 6	2.01	1.72	1.13	1.13	0.91	1.05	1.06	0.83

1 TMV 3

4 EC 351879

6 EC 351906

4.4. Estimates of heterosis through Probability of Net Gain (PNG) of favourable alleles

Predicted three way hybrid means were less than 50 gm plant^{-1} for all the three way cross hybrid except for (4 × 6) 1. Generally three way hybrid means were greater than their corresponding single cross hybrids except in few cases (Table 20).

The estimate of the merits of inbred [illegible] line as donors for enhancing inbred lines of superior hybrids for seed yield were presented in table 20. Parents 1, 2 and 3 as donors introduces negatives alleles at class D or F loci along with positive alleles at class G loci. Highest number of positive alleles were noticed in 4 × 5 and 4 × 6 with parent as donor.

Fewer negative alleles are introduced at class D than at class F loci. In crosses (1 × 4) 5, (1 × 4) 6, (1 × 6) 5, (2 × 3) 1, (2 × 5) 1, (2 × 6) 1, (3 × 4) 2, (4 × 5) 2, (4 × 5) 6 and (5 × 6) 4, parents 4 and 1 were potential donor of favourable allele.

4.5. Best Linear Unbiased Predictions (BLUP)

Best linear unbiased prediction (BLUP) by mixed and random models for 25 sesame genotypes based on their performance in three environments are presented in Table 21.

Both models predicted more or less same values for 25 genotypes. The highest prediction values were recorded by five genotypes ***viz.***, SVPR 1, TMV 3, TMV 6, TMV 4 and CO 1 for seed yield while the exotic types recorded low values.

Fifteen crosses involving six parents were considered for the BLUP analysis. The actual yield of 15 cross combinations and the differences of actual and predicted yields of both midparent value

Table 20. Estimates of number of favourable alleles present in a donor inbred line (P_D) which are not present in either parent (P_1 or P_2) of a single cross hybrid ($P_1 \times P_2$) (μ_G), the net merit of a donor inbred line crossed to P_1 (N_1), the net merit of a donor inbred line crossed to P_2 (N_2) the probability of a net gain favourable alleles from $P_1 \times P_D$ (PNG_1) the probability of a net favourable alleles from $P_2 \times P_D$ (PNG_2), and predicted three way hybrid mean (PTC) for seed yield plant^{-1} for sesame donor inbred (P_D) and single cross hybrids ($P_1 \times P_2$)

$P_1 \times P_2$	P_D	$\bar{\mu}_G$	N_1	N_2	PNG_1	PNG_2	PTC
1 × 2	3	-0.05	-0.42	3.83	0.87	0.48	36.21
	4	9.98	9.61	2.80	0.84	-1.31	45.20
	5	4.97	4.61	4.48	0.88	0.90	41.87
	6	9.32	8.95	4.59	0.89	3.33	46.33
1 × 3	2	0.58	0.42	4.25	0.98	0.53	36.63
	4	10.18	10.03	4.73	0.98	-14.04	46.72
	5	5.18	5.03	3.31	0.97	1.89	40.28
	6	9.32	8.95	4.59	0.89	3.33	45.00
1 × 4	2	-4.44	-9.61	-6.81	0.23	0.19	35.59
	3	-4.86	-10.03	-5.30	0.31	0.23	36.68
	5	0.17	-5.00	-6.54	0.24	0.28	40.47
	6	4.51	-0.66	-7.03	0.21	0.44	44.32
1 × 5	2	-1.94	-4.61	-0.13	0.50	0.37	37.27
	3	-2.36	-5.03	-1.72	0.42	0.33	35.26
	4	7.67	5.00	-1.53	0.43	0.99	45.47
	6	7.02	4.35	-1.30	0.44	0.85	45.05
1 × 6	2	-4.11	-8.95	-4.36	0.33	0.24	37.38
	3	-4.53	-9.37	-5.71	0.25	0.19	35.62
	4	5.50	0.66	-6.37	0.21	0.58	44.98
	5	0.50	-4.35	-5.64	0.26	0.29	40.70
2 × 3	1	-1.24	-3.83	-4.25	-9.40	9.85	32.37
	4	1.56	-1.04	0.48	0.55	0.42	39.91
	5	3.24	0.64	-0.94	0.37	0.67	40.16
	6	3.35	0.76	-0.59	0.42	0.65	40.63

Contd...

Table . Contd...

2 × 4	1	-0.72	-2.80	6.81	0.68	0.45	42.40
	3	3.11	1.04	1.51	0.55	0.54	40.94
	5	3.76	1.68	0.27	0.51	0.57	40.35
	6	7.04	1.79	-0.21	0.49	0.59	39.96
2 × 5	1	-1.57	-4.48	0.13	0.50	0.37	37.39
	3	2.27	-0.65	-1.59	0.43	0.47	39.52
	4	1.24	-1.68	-1.41	0.39	0.43	38.66
	6	3.03	0.11	-1.17	0.45	0.51	40.68
2 × 6	1	-1.62	-4.59	4.36	0.63	0.41	41.74
	3	2.21	-0.76	-1.35	0.44	0.47	39.87
	4	1.18	-1.79	-2.01	0.41	0.42	38.17
	5	2.86	-0.11	-1.29	0.44	0.49	40.57
3 × 4	2	2.00	-0.48	-1.51	0.43	0.48	41.98
	5	1.05	-1.42	-1.24	0.45	0.44	39.43
	6	1.41	-1.07	-1.73	0.43	0.45	38.76
3 × 5	1	-1.55	-3.31	1.72	0.56	0.41	38.62
	2	2.71	0.94	1.59	0.56	0.53	36.97
	4	3.19	1.42	0.18	0.51	0.57	41.11
	6	2.11	0.35	0.42	0.57	0.51	40.18
3 × 6	1	-1.72	-3.66	5.71	0.67	0.43	39.34
	2	2.53	0.59	1.35	0.55	0.52	41.32
	4	3.01	1.07	-0.66	0.47	0.56	39.69
	5	1.59	-0.35	0.06	0.50	0.49	38.98
4 × 5	1	12.90	6.53	1.53	0.56	0.90	47.00
	2	6.11	-0.27	1.41	0.55	0.49	40.07
	3	7.62	1.24	-0.18	0.49	0.56	40.00
	6	5.90	-0.49	5.23	0.65	0.49	43.68
4 × 6	1	13.17	7.03	6.37	0.68	0.71	51.35
	2	6.36	0.22	2.01	0.58	0.51	40.18
	3	7.87	1.73	0.66	0.53	0.58	40.35
	5	6.63	0.49	0.72	0.53	0.52	39.17
5 × 6	1	7.25	1.30	5.64	0.66	0.53	46.35
	2	7.12	1.17	1.29	0.55	0.55	41.86
	3	5.53	-0.42	-0.06	0.50	0.48	38.93
	4	5.72	-0.23	-0.72	0.47	0.49	38.45

Table 21. Best linear unbiased predictions of mixed and random model for single plant yield in 25 sesame genotypes

Genotype	Mixed model	Random model
EC 351879	28.21	28.21
EC 351880	27.03	27.03
EC 351903	26.70	26.65
EC 351904	27.70	27.70
EC 351905	31.21	31.21
EC 351906	31.60	31.60
EC 351907	24.40	24.40
EC 351908	26.38	26.38
EC 357015	22.42	22.42
EC 357016	24.33	24.33
EC 357017	23.65	23.65
EC 357018	23.03	23.03
EC 357019	23.03	23.03
EC 357020	24.10	24.10
EC 357021	23.70	23.66
EC 357022	23.13	23.13
EC 357023	23.42	23.42
EC 357024	24.24	24.24
EC 357025	24.00	23.98
EC 357026	24.24	24.24
TMV 3	43.90	43.90
TMV 4	42.72	42.72
TMV 6	43.85	43.87
CO 1	41.80	41.83
SVPR 1	45.50	45.46

Table 22. Actual yield, predicted differences and standard errors (SE) of the difference of seed yield of 15 sesame crosses

Cross	Actual yield	Differences between actual and predicted value	
		MPV	BLUP
1 × 2	32.79	-2.08	11.06
1 × 3	31.95	-0.53	12.75
1 × 4	52.01	-29.65	-15.96
1 × 5	42.00	-18.53	-4.45
1 × 6	50.69	-26.94	-12.94
2 × 3	40.46	-9.65	4.19
2 × 4	38.39	-16.65	-2.39
2 × 5	41.75	-18.90	-4.25
2 × 6	41.97	-18.84	-4.27
3 × 4	41.42	-18.96	-4.57
3 × 5	38.57	-15.01	-0.22
3 × 6	39.28	-15.43	-0.73
4 × 5	38.94	-24.44	-9.24
4 × 6	37.96	-23.18	-8.06
5 × 6	39.40	-23.51	-8.00
$\bar{X}$	40.51	-17.50	-3.14
SE	1.37	2.14	2.04

MPV = Mid Parent Value

BLUP = Best Linear Unbiased Prediction

Table 23. Genetic variance/covariance coefficients for 6 sesame genotypes

Genotype	1	2	3	4	5	6
1	1	0.148	0.060	0.045	0.013	0.050
2		1	0.126	0.111	0.078	0.115
3			1	0.023	-0.009	0.027
4				1	-0.024	0.013
5					1	-0.020
6						1

1 – TMV 3; 2 – TMV 6; 3 – SVPR 1; 4 – EC 351879; 5 – EC 351905; 6 – EC 351906

(MPV) and best linear unbiased prediction (BLUP) are furnished in Table 22. Mean yields were predicted for all the 15 crosses.

The highest yielding crosses ***viz.***, 1 × 4 and 1 × 6 did not recorded the highest predictions while the crosses involving the high yielding genotypes 1, 2 and 3 ***viz.***, 1 × 2 and 1 × 3 recorded the highest predictions values. When the midparent value was used for prediction, cross 1 × 3 recorded lowest difference while 1 × 4 recorded highest differences.

With regard to BLUP prediction, three crosses ***viz.***, 1 × 2, 1 × 3 and 2 × 3 exceeded the prediction value in their actual yield. The cross 3 × 5 recorded the least difference while 1 × 4 recorded the highest difference. The lowest standard error of the differences was observed in BLUP prediction (Table 22).

When predictions from BLUP and MPV were compared except for four cross combinations ***viz.,*** 1 × 5, 1 × 6, 2 × 6 and 3 × 5 all the remaining showed no difference. The comparison revealed that the standard error of difference for BULP predictions was lower than for MPV prediction.

The genetic variance and covariance coefficients for 6 parents are given in Table 23. Examinations of genetic variance and covariance matrix among the six parents which were involved in the 15 crosses revealed that the parents of cross 1 × 4 and 1 × 6 recorded low value of variance/covariance matrix with 3, 4, 5 and 6. While 1 with 2, 2 with 3 and 4 with 6 shared high valued of covariance coefficients (Table 23).

The high yielding parents 1 and 3 recorded low covariance coefficient in comparison with 2 and with their remaining parents. Other exotic genotypes in combinations with themselves recorded very low variance/covariance coefficients.

Table 24. Prediction for single plant yield in F_2 generation

Single cross combination	Predicted F_2 yield (g)
1 × 2	31.75
1 × 3	31.68
1 × 4	37.18
1 × 5	32.73
1 × 6	37.22
2 × 3	35.63
2 × 4	30.06
2 × 5	32.30
2 × 6	32.55
3 × 4	31.94
3 × 5	31.06
3 × 6	31.56
4 × 5	26.72
4 × 6	26.37
5 × 6	27.64

Table 25. Estimated yield potential per metre square (a), tolerance to density (b^{-1}) and crop yield potential (y_{max}) of 2 cross combinations of sesame in 3 densities

Cross combinations	Density of planting (cm)	Potential Yield g/m^2 (a)	Density tolerance (b^{-1})	Maximum crop yield (y_{max})
1 × 4	30 × 15	408.35	19.08	433.67
	30 × 30	272.91	11.77	313.42
	30 × 45	166.34	7.68	223.65
1 × 6	30 × 15	372.30	17.80	467.97
	30 × 30	201.90	10.91	280.87
	30 × 45	152.10	7.40	155.54

1 TMV 3

4 EC 351879

6 EC 351906

T2
27/6/2000

4.6. Prediction of seed yield for F_2 generation

Predicted seed yield plant^{-1} of F_2 plants for 15 cross combinations were computed and presented in Table 24. Three combinations ***viz.***, 1 × 6, 1 × 4 and 2 × 3 recorded high predicted single plant yield of more than 35 g for the F_2 generation . While combinations 4 × 5, 4 × 6 and 5 × 6 exhibited low predicted seed yield plant^{-1} ≤ 27.64 g.

4.7. Relation between crop yield potential and single plant yield potential

The results obtained for two cross combinations ***viz.***, 1 × 4 and 1 × 6 in three density of planting ***viz.***, 30 × 15cm, 30 × 30cm and 30 × 45cm are furnished in Table 25.

In both cross combinations the plants of 30 × 15cm density registered high yield. The wider spacing recorded low yield.

4.8. Double cross hybrid analysis

4.8.1. Analysis of variance

The analysis of variance for double cross hybrid is presented in Table 26. All the double cross hybrids exhibited significant differences among themselves for all the characters except for height of the plant. All the interaction effects such as 1-line general, 2-line specific, 2-line arrangement, 3-line arrangement and 4-line arrangement showed significant differences except for 1-line general effect with regard to capsule length and 4-line arrangement for seed yield plant^{-1}.

4.8.2. Performance of double cross hybrids

The mean performance of 45 double cross for nine biometrical traits are presented in Table 27.

Table 26. Analysis of variance for double crosses

Source	df	Days to first flowering	Height to first productive node	Plant height	Number of branches plant-1	Number of capsules plant-1	Capsule length	1000 seed weight	Seed yield plant-1	Oil content
Replication	1	0.0053	65.8901	254.0500	0.0003	1829.1600	0.3413	0.0150	35.2010	0.2290
Hybrids	44	5.0042**	111.4600**	174.6200	2.7710**	414.2900**	0.0333*	0.0900**	10.7900**	4.6300**
Error	44	0.1519	8.6870	15.1600	0.2828	43.3700	0.0130	0.0048	1.9750	0.1612
1-line general	5	5.8681**	584.5200**	798.9100**	11.2250**	617.0000**	0.0255	0.4403**	30.4100**	8.7540**
2-line specific	9	146095.77**	261313.64**	1882838.7**	3081.88**	1812889.8**	1272.81**	1620.53**	42944.69**	494641.46**
2-line arrangement	9	7.6800**	90.5700**	165.7700**	3.3106**	852.6700**	0.0716*	0.0262**	19.5300**	1.1600**
3-line arrangement	16	4.6500**	39.8400**	71.8900**	1.1154**	219.1900**	0.0200	0.0242**	5.4600**	4.5600**
4-line arrangement	5	1.5500**	36.3800**	74.2800**	0.8413**	257.3200**	0.0300*	0.0723**	2.1500	4.6100**

** Significant at 1% level

Table 27. Mean performance of double cross hybrids

Cross combinations	Days to first flowering	Height to first productive node (cm)	Plant height (cm)	Number of branches plant^{-1}	Number of capsules plant^{-1}	Capsule length (cm)	1000 seed weight (g)	Seed yield plant^{-1} (g)	Oil content (%)
(1 × 2) (3 × 4)	28.24	111.36	52.05	6.44	129.74	3.16	3.05	28.59	52.83
(1 × 2) (3 × 5)	30.15	113.87	57.70	5.55	88.47	2.71	3.15	23.69	52.89
(1 × 2) (3 × 6)	30.24	115.29	47.24	5.29	108.79	2.92	3.34	28.51	52.17
(1 × 2) (4 × 5)	32.13	105.78	41.36	6.48	107.25	2.68	3.17	28.03	51.69
(1 × 2) (4 × 6)	27.55	116.00	46.41	5.40	126.32	2.66	3.19	28.85	53.66
(1 × 2) (5 × 6)	29.53	112.92	43.42	3.43	105.65	2.70	2.93	25.24	51.03
(1 × 3) (2 × 4)	28.05	117.13	51.50	5.50	88.45	2.53	3.35	26.38	50.62
(1 × 3) (2 × 5)	28.08	114.70	54.36	6.75	98.37	2.48	2.98	25.37	50.82
(1 × 3) (2 × 6)	31.10	109.18	52.18	5.42	101.82	2.54	3.11	25.95	53.48
(1 × 3) (4 × 5)	27.56	98.93	37.59	5.41	104.64	2.62	3.35	28.12	50.54
(1 × 3) (4 × 6)	29.57	100.63	31.28	3.64	95.58	2.67	3.16	24.68	54.97
(1 × 3) (5 × 6)	28.80	109.25	42.48	3.47	92.44	2.73	3.12	27.61	53.19
(1 × 4) (2 × 3)	28.21	106.95	45.14	4.04	102.32	2.59	3.29	23.85	51.24
(1 × 4) (2 × 5)	27.67	96.00	38.72	2.97	84.96	2.48	3.04	24.12	52.67
(1 × 4) (2 × 6)	27.56	101.86	37.75	4.48	93.36	2.56	3.01	23.92	51.78

Contd...

Contd...

(1 × 4) (3 × 5)	27.67	108.37	45.31	4.70	95.65	2.80	2.96	24.86	52.21
(1 × 4) (3 × 6)	27.40	102.95	36.55	5.11	257.75	2.68	3.09	54.86	52.27
(1 × 4) (5 × 6)	27.23	84.36	30.45	2.24	70.29	2.73	2.73	19.98	51.23
(1 × 5) (2 × 3)	26.68	104.65	33.77	4.48	219.93	2.60	3.14	45.74	53.75
(1 × 5) (2 × 4)	27.24	98.89	37.73	2.60	72.36	2.59	3.07	22.12	51.74
(1 × 5) (2 × 6)	26.31	95.56	35.28	3.70	86.46	2.55	3.04	24.00	52.35
(1 × 5) (3 × 4)	28.08	100.33	36.95	5.95	112.50	2.56	3.13	28.57	51.87
(1 × 5) (3 × 6)	-26.32	98.68	32.96	3.41	91.94	2.70	3.00	24.94	50.29
(1 × 5) (4 × 6)	26.87	93.71	33.12	2.88	91.37	2.65	2.90	24.07	51.29
(1 × 6) (2 × 3)	31.28	102.23	38.25	5.23	239.01	2.59	3.26	51.62	52.43
(1 × 6) (2 × 4)	28.63	113.69	39.04	5.14	249.52	2.56	3.01	53.22	50.75
(1 × 6) (2 × 5)	27.96	100.87	39.46	3.91	88.65	2.37	2.94	23.81	52.71
(1 × 6) (3 × 4)	27.43	109.13	32.84	5.31	243.80	2.63	2.95	51.44	53.00
(1 × 6) (3 × 5)	27.32	93.62	31.56	3.74	96.21	2.86	2.96	24.98	52.55
(1 × 6) (4 × 5)	30.50	101.45	35.25	5.16	254.65	2.79	3.02	54.11	50.45

Contd...

Contd...

(2 × 3) (4 × 5)	27.80	107.53	38.14	5.19	110.67	2.69	3.05	27.93	52.36
(2 × 3) (4 × 6)	32.27	106.91	34.45	4.41	124.18	2.78	2.71	25.76	51.49
(2 × 3) (5 × 6)	29.38	107.88	32.81	3.20	104.47	2.61	2.93	26.05	53.43
(2 × 4) (3 × 5)	30.64	92.20	31.24	3.85	98.03	2.62	3.12	24.72	53.22
(2 × 4) (3 × 6)	29.18	110.65	33.85	3.95	105.12	2.72	2.65	24.36	53.35
(2 × 4) (5 × 6)	31.77	104.17	32.18	3.20	107.50	2.76	2.62	24.71	52.40
(2 × 5) (3 × 4)	28.67	103.52	31.50	4.09	119.91	2.65	2.98	28.61	53.30
(2 × 5) (3 × 6)	29.68	109.90	44.41	3.74	212.55	2.68	2.98	45.40	51.90
(2 × 5) (4 × 6)	27.82	91.98	31.67	3.52	113.83	2.73	2.43	23.42	50.59
(2 × 6) (3 × 4)	27.24	94.49	30.42	3.50	85.50	2.66	3.01	23.20	55.68
(2 × 6) (3 × 5)	27.15	90.15	33.11	3.80	89.82	2.56	2.61	22.03	51.21
(2 × 6) (4 × 5)	27.00	92.38	32.21	3.54	89.79	2.53	2.44	21.87	51.41
(3 × 4) (5 × 6)	27.19	84.81	28.44	3.81	212.00	2.69	2.93	45.55	52.26
(3 × 5) (4 × 6)	27.46	85.12	28.97	3.60	86.14	2.57	3.00	24.64	57.23
(3 × 6) (4 × 5)	27.35	79.85	28.66	3.13	66.53	2.71	3.10	20.46	56.54
Mean	28.48	102.22	37.99	4.32	122.76	2.66	3.00	29.57	52.42
SE	0.39	3.89	2.94	0.53	6.50	0.11	0.07	1.41	0.40

The range for days to first flowering was very narrow (Table 27). The double cross hybrid (1 × 5) (2 × 6) was the earliest to come to first flowering, with a mean of 26.30 days whereas the maximum number of days (32.27) was taken by (2 × 3) (4 × 6) combination. Most of the double cross hybrids flowered at about 28.48 days.

All the double cross hybrids were medium in height. The shortest hybrids (3 × 6) (4 × 5) recorded a height of 79.85cm whereas the tallest hybrid (1 × 3) (2 × 4) recorded 117.13cm height.

Wide range of variation for the height at which first productive node arise (28.65 - 57.70cm) was noticed. The combination (3 × 6) (4 × 5) recorded the least height while the gap between ground and first node was high in (1 × 2) (3 × 4).

The number of branches in double cross hybrids had a range from 2.13 to 6.75. The number of branches was restricted to 3 to 5 in most of the hybrids.

Considerable variation (70.30 - 257.75) was exhibited by the double cross hybrids towards number of capsules per plant. High number of capsules were recorded by the double cross hybrids which had 4 × 6 and 4 × 5 as pollen parent. The hybrid (1 × 4) (3 × 6) produced the highest number of capsules.

Except one (1 × 2) (3 × 4) all the double cross hybrids recorded capsule length > 2cm but < 3cm. Generally double cross hybrids displayed less variation for this trait.

Majority of the double cross hybrids exhibited 1000 seed weight around 3.0gm. Variability for this trait among double cross hybrids was minimum.

Enormous variation was noticed for seed yield plant^{-1}. High seed yield was recorded by the hybrid (1 × 4) (3 × 6) (54.86g). Whereas the minimum seed yield was produced by (1 × 4) (5 × 6) (9.98g). Most of the hybrids recorded a seed yield of 23 to 25 g per plant.

Increased oil content was noticed in double cross hybrids to a considerable level. The highest oil content was recorded in the hybrid (3 × 5) (4 × 6) (57.23%) and the lowest by (1 × 5) (3 × 6) (50.29%).

4.8.3. Combining ability of double cross hybrids

4.8.3.1. Days to first flowering

The 1-line general effects was positive and significant for parent 2 alone. It was negative and significant for parents 1, 4 and 5. Positive and significant 2-line interaction effect of particular arrangement with t_{2ij} was noticed in four combinations ***viz.***, 1 × 2, 1 × 6, 2 × 4 and 5 × 6 whereas negative and significant 2-line interaction effect was provided by 1 × 4, 1 × 5, 2 × 6 and 3 × 4 cross combinations. In the arrangement $t_{2i.j}$, the 2-line interaction effects were positive and significant for 1 × 5 and 2 × 6. The combinations 1 × 2 and 5 × 6 were negative and significant under $t_{2i.j}$ arrangement. 2-line specific interaction effect $S_{2i.j}$ between hybrids 1 × 4 and between 1 × 5 was negative (Table 28).

The 3-line interaction effect of lines i, j and k in $t_{3ij.k}$ arrangement showed positive and significant showed positive and significant effect in the combinations ***viz.***, (1 × 2)5, (1 × 3)6, (1 × 4)2, (1 × 5)3, (1 × 5)6, (2 × 5)3, (2 × 6)1, (3 × 4)5, (3 × 6)5, (4 × 5)1, (4 × 6)3 and (1 × 5) 6. The other combinations under $t_{3ij.k}$ arrangement ***viz.***, (1 × 2)6, (1 × 3)4, (1 × 3)5, (1 × 4)5, (1 × 6)3, (2 × 3)5, (3 × 4)6, (3 × 5)6, (4 × 5)3, (4 × 6)1 and (5 × 6)1, showed

Table 28. Estimates of 1 and 2-line general and 2-line arrangement effects for days to first flowering in double crosses

2-line interaction effect of line i and j due to the particular arrangement (ij) (- -) i.e. t_{2ij} above the diagonal and (i-) (j-) i.e. $t_{2i.j}$ below the diagonal; values in bracket correspond to S_{2ij} i.e. effect of i and j irrespective of arrangement

line	1 line general effect	1	2	3	4	5	6
1	-0.1091**		0.9372** (-0.0307)	0.4066 (-0.0240)	-0.5755* (-0.0904)*	-1.1991** (0.0408)*	0.4309* (0.0288)
2	0.3522**	**-0.4686***		0.1561 (-0.2213)	0.4932* (-0.0079)	-0.3321 (0.0286)	-1.2543** (0.1251)
3	0.0516	**-0.2033**	**-0.0780**		-0.5259* (-0.1174)	0.2873 (-0.2086)	-0.3240 (0.1322)
4	-0.0886**	**0.2878**	**-0.2466**	**0.2630**		0.3524 (0.1910)	0.2559 (-0.0798)
5	-0.2211**	**0.5995****	**0.1661**	**-0.1436**	**-0.1762**		0.8916** (-0.1913)
6	0.0150	**-0.2154**	**0.6272****	**0.1620**	**-0.1279**	**-0.4458***	

SE (gi) = 0.0311
SE (t_{2ij}) = 0.2043
SE ($t_{2i.j}$) = 0.1997
SE (S_{2ij}) = 0.0106

* Significant at 5% level
** Significant at 1% level

Table 29. Estimates of 3-line interaction effect of line ij and k due to the particular arrangement (ij) (k -) i.e. $t_{3ij.k}$ in double crosses. Values in bracket correspond to $S_{3ij.k}$ i.e. 3-line effect irrespective of arrangement for days to first flowering

	Parental line					
	1	**2**	**3**	**4**	**5**	**6**
1 × 2			-0.2286 (0.1164)**	-0.0405 (-0.1647)**	0.4812* (-0.0503)	-1.1493** (0.0371)
1 × 3		0.1039		-0.5867** (-0.1350)**	-0.5663** (-0.1325)**	0.6426** (0.1992)**
1 × 4		0.7421**	0.2525		-0.6514** (0.1994)*	0.2324 (-0.0805)*
1 × 5		-0.1714	0.7225**	0.0961		0.4898* (-0.0983)*
1 × 6		-0.2060	-0.5431*	0.1813	0.1370	
2 × 3	0.1247			0.3319 (0.0068)	-0.9183** (-0.0195)	0.3057 (0.3390)**
2 × 4	-0.7016		-0.3094		0.4285 (0.2133)**	0.0894 (-0.0396)
2 × 5	-0.3098		0.6749**	-0.1600		0.1270 (-0.0863)*
2 × 6	1.3553**		-0.0589	0.1152	-0.1574	
3 × 4	0.3343	-0.0225			0.7806** (-0.0489)	-0.5665* (-0.0576)
3 × 5	-0.1562	0.2434		0.1693		-0.5437* (-0.2162)
3 × 6	-0.0995	-0.2468		-0.1774	0.8477**	
4 × 5	0.4932*	-0.2684	-0.9499**			0.3727 (0.0181)
4 × 6	-0.4136*	-0.2046	0.7439**		-0.3815	
5 × 6	-0.6268**	0.0997	-0.3039	0.0088		

SE (t3ij.k) = 0.2004
SE (S3ij.k) = 0.0306

* Significant at 5% level
** Significant at 1% level

Table 30. Estimates of 4-line effects of lines i, j, k and l for days to first flowering due to the particular arrangement (ij) (kl) i.e. $t_{4ij.kl}$ in double crosses. Figures in brackets are 4-line effects irrespective of their arrangement i.e. S_{4ijkl}

	2 × 3	2 × 4	2 × 5	2 × 6	3 × 4	3 × 5	3 × 6	4 × 5	4 × 6	5 × 6
1 × 2					-0.1428 (-0.3678)**	-0.2071 (-0.1657)*	0.3498** (0.8827)**	0.3498** (0.3300)**	-0.2071 (-0.4562)**	-0.2122 (-0.3151)**
1 × 3		0.4753**	-0.1072	-0.3681**				-0.3681** (0.0081)	-0 1072 (-0.0453)	0.4753** (-0.2399)**
1 × 4	-0.3325**		0.2400*	0.0925		0.0925	0.2400**			-0.3325** (0.2602)**
1 × 5	0.3143**	-0.5278**		0.2756	0.3377**		-0.5899**		0.3764**	
1 × 6	0.0183	0.1146	-0.1329		-0.1329	0.1146		0.0183		
2 × 3								0.0183 (0.1805)*	0.7492** (0.2078)**	-0.4020** (-0.0734)
2 × 4						0.1146	-0.5899**			0.4059** (0.1295)*
2 × 5					-0.1329		0.2400*		-0.1072	
2 × 6					0.2756*	0.0925		-0.3681**		
3 × 4										-0.1428 (-0.3353)**
3 × 5									-0.2071	
3 × 6								0.3498**		

SE ($t_{4ij.kl}$) = 0.1014
SE (S_{4ijkl}) = 0.0783

* Significant at 5% level
** Significant at 1% level

negative and significant 3-line interaction effect. 3-line specific interaction effect under S_{3ijk} arrangement exhibited positive and significant effect in the combinations ***viz.***, (1 × 2)3, (1 × 3)6, (1 × 4)5, (2 × 3)6 and (2 × 4)5. The negative and significant specific interaction effect was revealed by combinations ***viz.***, (1 × 2)4, (1 × 3)4, (1 × 3)5, (1 × 5)6 and (2 × 5)6 (Table 29).

The 4-line interaction effect of lines i, j, k and l in the particular arrangement (ij) (kl) showed positive and significant effects in crosses (1 × 2) (3 × 6), (1 × 2) (4 × 5), (1 × 3) (2 × 4), (1 × 3) (5 × 6), (1 × 4) (2 × 5), (1 × 4) (3 × 6), (1 × 5) (2 × 3), (1 × 5) (3 × 4), (1 × 5) (4 × 6), (2 × 3) (4 × 6), (2 × 4) (5 × 6), (2 × 5) (3 × 6), and negative and significant in crosses (1 × 3) (2 × 6), (1 × 3) (4 × 5), (1 × 4) (2 × 3), (1 × 4) (5 × 6), (1 × 5) (2 × 4), (1 × 5) (3 × 6), (2 × 3) (5 × 6), (2 × 4) (3 × 6) and (2 × 6) (4 × 5). Considering the 4-line specific interaction effect of lines under S_{4ijkl}, (1 × 2) (3 × 6) alone displayed positive and significant effect while combinations (1 × 2) (4 × 6) expressed negative significant effect (Table 30).

4.8.3.2. Plant height

Positive and significant 1-line general effect was observed for lines 1 and 2 while it was negative and significant for lines 4, 5 and 6. 2-line interaction effect of lines i and j due to the particular arrangement (***i.e.***, t_{2ij}) was positive and significant for 1 × 2, 1 × 3, 2 × 4, 3 × 6, 4 × 5 and 5 × 6 whereas the same was negative and significant for 1 × 4, 1 × 5, 2 × 3, 2 × 6, 3 × 4 and 3 × 5. 2-line interaction effect of lines i and j due to particular arrangement (i–) (j–) ***i.e.***, $t_{2i,j}$ was positive and significant only for the cross combination 2 × 6. All the other crosses were non significant for this effect. The 2-line specific effect S_{2ij} was negative and significant for

Table 31. Estimates of 1 and 2-line general and 2-line arrangement effects for plant height in double crosses

2-line interaction effect of line i and j due to the particular arrangement (ij) (- -) i.e. t_{2ij} above the diagonal and (i-) (j-) i.e. $t_{2i.j}$ below the diagonal; values in bracket correspond to S_{2ij} i.e. effect of i and j irrespective of arrangement

line	1 line general effect	1	2	3	4	5	6
1	2.3912**		4.9280**	1.7902**	-3.6691**	-3.1384**	0.0893
			(0.2588)	(1.1139)	(0.6544)	(0.0013)	(0.3628)
2	2.7370**	**-2.4640**		-0.5629*	2.1501**	0.4438	-6.9590**
				(0.8429)	(0.5308)	(0.2686)	(0.8359)
3	0.7894	**-0.8951**	**0.2815**		-0.5520*	-2.9669**	2.2916**
					(-0.3353)	(0.0168)	(-0.8489)
4	-1.5159**	**1.8345**	**-1.0751**	**0.2760**		1.5771**	0.4938*
						(-1.7888*)	(-0.5771)
5	-2.8383**	**1.5692**	**-0.2219**	**1.4834**	**-0.7886**		4.0844**
							(-1.3361)
6	-1.5633**	**-0.0446**	**3.4795***	**-1.1458**	**-0.2469**	**-2.0422**	

SE (gi) = 0.5104
SE (t_{2ij}) = 0.2387
SE ($t_{2i.j}$) = 1.5732
SE (S_{2ij}) = 0.8913

* Significant at 5% level
** Significant at 1% level

Table 32. Estimates of 3-line interaction effect of line ij and k due to the particular arrangement (ij) (k -) i.e. $t_{3ij.k}$ in double crosses. Values in bracket correspond to $S_{3ij.k}$ i.e. 3-line effect of irrespective arrangement for plant height

	Parental line					
	1	2	3	4	5	6
1 × 2			-1.4042 (0.2431)	-2.1604 (0.2399)	-0.2250 (-0.2347)	-1.1385 (0.2692)
1 × 3		3.4680		-4.5337 (0.8781)	-1.9259 (1.0179)	1.2014 (0.0887)
1 × 4		1.2936	4.1803*		0.4872 (-0.4788)	-2.2920 (0.6695)
1 × 5		0.7202	-0.9430	1.1087		2.2737 (-0.3018)
1 × 6		-3.0179	-0.9379	3.7720	0.0945	
2 × 3	-2.0638			2.8545 (0.3683)	1.0555 (0.8989)	-1.2833 (0.1756)
2 × 4	0.8667		-1.6868		-1.8818 (-0.4504)	0.5518 (0.9038)
2 × 5	-0.4952		2.2338	-0.5728		-1.6095 (0.3233)
2 × 6	4.1563*		0.5757	0.9537	1.2733	
3 × 4	0.3534	-1.1678			0.4479 (-0.9191)	0.9184 (-0.9980)
3 × 5	2.869	-3.2892		3.0779		0.3092 (-0.9642)
3 × 6	-0.2635	0.7076		-1.6748	-1.0609	
4 × 5	-1.5747	2.4546	-3.5258			1.0687 (-1.7295)
4 × 6	-1.4799	-1.5054	0.7563		1.7353	
5 × 6	-2.3682	0.6035	0.7516	-2.8040		

SE ($t_{3ij.k}$) = 2.0090 SE (S_{3ijk}) = 1.3823 * Significant at 5% level ** Significant at 1% level

Table 33. Estimates of 4-line effects of lines i, j, k and l for plant height due to the particulars arrangement (ij) (kl) i.e. $t_{4ij.kl}$ in double crosses. Figures in brackets are 4-line effects irrespective of their arrangement i.e. S_{4ijkl}

	2 × 3	2 × 4	2 × 5	2 × 6	3 × 4	3 × 5	3 × 6	4 × 5	4 × 6	5 × 6
1 × 2					-0.5978 (0.3934)	2.1498 (1.3481)	-1.5520 (-1.0122)	-1.5220 (-1.7728)	2.1498 (2.0992)*	-0.8650 (-0.2793)
1 × 3		3.3355**	-2.7531	-0.5824				-0.5824 (1.3341)	-2.7531* (0.9070)	3.3355** (0.3714)
1 × 4	-2.7377*		1.0497	1.6880		1.6880	1.0497			-2.7377* (-0.9976)
1 × 5	0.6033	0.4811		-1.1056	-1.1268		0.5023		0.5821	
1 × 6	2.1344	-3.8378**	1.7034		1.7034	-3.8378*		2.1344		
2 × 3								2.1344 (0.2606)	-3.6692** (0.4510)	-3.0050* (1.0879)
2 × 4						-3.8378**	0.5023			3.0682* (0.1611)
2 × 5					1.7034		1.0497		-2.7531*	
2 × 6					-1.1056	1.6880		-0.5824		
3 × 4										-0.5978 (-4.3519)**
3 × 5									2.1498	
3 × 6								-1.5520		

SE (t_{4ijkl}) = 1.2967 SE (S_{4ijkl}) 1.2100 * Significant at 5% level ** Significant at 1% level

cross 4 × 5 while it was non significant for the rest of the cross combinations (Table 31).

The estimates for 3-line interaction effect of lines i, j and k ($t_{3ij.k}$) due the particular arrangement (ij) (k–) was positive and significant in crosses (1 × 4)3 and (2 × 6)1. It was non significant in rest of the crosses. The 3-line specific effect S_{3ijk} was non significant for plant height (Table 32).

The 4-line interaction effects with particular arrangement (ij) (kl) ***i.e.***, $t_{4ij.kl}$ was positive and significant in three out of 45 double crosses ***viz.***, (1 × 3) (2 × 4), (1 × 3) (5 × 6) and (2 × 4) (5 × 6). It was negative and significant for (1 × 3) (4 × 6), (1 × 4) (2 × 3), (1 × 4) (5 × 6), (1 × 6) (2 × 4), (1 × 6) (3 × 5), (2 × 3) (4 × 6), (2 × 3) (5 × 6), (2 × 4) (3 × 5) and (2 × 5) (4 × 6). The 4-line specific effects S_{4ijkl} was positive and significant for (1 × 2) (4 × 6) and negative and significant for the cross (3 × 4) (5 × 6) (Table 33).

4.8.3.3. Height to first productive node

The 1-line general effect was positive and significant in parents 1 and 2 and negative and significant for 4, 5 and 6 (Table 34). 2-line interaction effect with particular arrangement t_{2ij} was positive and significant only in one cross ***viz.,*** 1 × 2. Negative and significant effects were observed in three crosses ***viz.,*** 1 × 5, 2 × 3, and 2 × 5. In the arrangement $t_{2i.j}$ the 2-line interaction effects were positive and significant in crosses ***viz.,*** 1 × 5 and 2 × 3. Negative and significant effect was noticed only in one cross ***viz.,*** 1 × 2. The two time specific arrangement $S_{2i.j}$ was positive and significant in cross ***viz.,*** 1 × 2 alone. The rest of the cross combinations exhibited non-significant effect for this trait.

Table 34. Estimates of 1 and 2-line general and 2-line arrangement effects for height to first productive node in double crosses

2-line interaction effect of line i and j due to the particular arrangement (ij) (- -) i.e. t_{2ij} above the diagonal and (i-) (j-) i.e. $t_{2i.j}$ below the diagonal; values in bracket correspond to S_{2ij} i.e. effect of i and j irrespective of arrangement

line	1 line general effect	1	2	3	4	5	6
1	2.5948**		4.0649* (1.4570)*	2.6936 (1.0873)	-0.4030 (0.4363)	-4.3377* (0.0150)	-2.0178 (-0.4008)
2	1.9171**	**-2.0324****		-4.1362* (0.7884)	-0.4863 (-0.2000)	1.7397 (-0.3291)	-1.1820 (0.2007)
3	0.5289	**-1.3468**	**2.0681****		-1.0167 (-0.5060)	0.7634 (-0.0029)	1.6960 (-0.8380)
4	-1.6356**	**0.2015**	**0.2431**	**0.5084**		1.1184 (-0.6418)	0.7876 (-0:7242)
5	-1.3008*	**2.1688****	**-0.8698**	**-0.3817**	**-0.5592**		0.7162 (-0.3421)
6	-2.1043**	**1.0089**	**0.5910**	**-0.8480**	**-0.3938**	**-0.3581**	

SE (gi) = 0.6236
SE (t_{2ij}) = 1.9739
SE ($t_{2i.j}$) = 0.7177
SE (S_{2ij}) = 0.7033

* Significant at 5% level
** Significant at 1% level

Table 35. Estimates of 3-line interaction effect of line ij and k due to the particular arrangement (ij) (k -) i.e. $t_{3ij.k}$ in double crosses. Values in bracket correspond to S_{3ijk} i.e. 3-line effect irrespective of arrangement for height to first productive node

	Parental line					
	1	2	3	4	5	6
1 × 2			-0.4779 (1.6525)**	-1.2031 (0.7346)*	-0.2935 (0.0725)	-2.0904 (0.4544)
1 × 3		1.9316		-4.3042** (0.5216)	-1.0768 (0.4918)	0.7559 (-0.4913)
1 × 4		-0.5699	2.5537*		-0.4312 (-0.0766)	-1.1495 (-0.3070)
1 × 5		0.4084	-0.7864	1.1240		1.4752 (-0.4577)
1 × 6		0.2624	0.0574	2.0653	-0.3673	
2 × 3	-1.4537			3.9308** (-0.1876)	0.6217 (0.0747)	1.0375 (0.0373)
2 × 4	1.7730		-1.9270		0.6596 (-0.8311)*	-0.0193 (-0.1158)
2 × 5	-0.1149		0.3270	-2.4330*		0.4812 (0.0256)
2 × 6	1.8281		0.0097	-0.5378	-0.1180	
3 × 4	1.7505	-2.0037			0.1622 (-0.3482)	1.1078 (-0.9978)
3 × 5	1.8632	-0.9487		0.3753		-2.0531 (-0.2242)
3 × 6	-0.8133	-1.0472		-0.5102	0.6747	
4 × 5	-2.8092*	1.7734	-0.5374			0.4548 (-0.0278)
4 × 6	-0.9158	0.5571	-0.5976		0.1687	
5 × 6	-1.1079	-0.7074	1.3785	-0.6235		

SE ($t_{3ij.k}$) = 1.1413 SE (S_{3ijk}) = 0.3247 * Significant at 5% level ** Significant at 1% level

Table 36. Estimates of 4-line effects of lines i, j, k and l for height of the first productive node due to the particular arrangement (ij) (kl) i.e. $t_{4ij.kl}$ in double crosses. Figures in brackets are 4-line effects irrespective of their arrangement i.e. S_{4ijkl}

	2 × 3	2 × 4	2 × 5	2 × 6	3 × 4	3 × 5	3 × 6	4 × 5	4 × 6	5 × 6
1 × 2					0.2053 (2.3790)**	2.0972** (1.5673)**	-2.3025* (1.0111)**	-2.3025* (-0.9385)**	2.0972* (0.7632)**	0.5494 (-0.4112)**
1 × 3		1.5091	-1.5675	0.0585				0.0585 (0.7895)**	-1.5675 (-1.6035)**	1.5091 (-0.8813)**
1 × 4	-1.7144		1.8428	-0.1285		-0.1285	1.8428			-1.7144 (-0.0807)
1 × 5	-0.5297	2.5762*		0.0700	2.1864**		0.4597		1.5867	
1 × 6	2.2441*	-1.9688	-0.2753		-0.2753	-1.9688		2.2441*		
2 × 3								2.2441* (-0.1629)**	-2.7984* (-1.2489)**	-1.3702 (0.3498)**
2 × 4						-1.9688	0.4597			1.8532 (0.1383)
2 × 5					-0.2753		1.8428		-1.5675	
2 × 6					0.0700	-0.1285		0.0585		
3 × 4										0.2053 (-0.1410)**
3 × 5									2.0972*	
3 × 6								-2.3025*		

SE ($t_{i4ij.kl}$) = 1.0231 SE (S_{4ijkl}) = 0.0416 * Significant at 5% level ** Significant at 1% level

The 3-line interaction effect with particular arrangement $t_{3ij.k}$ was positive and significant in crosses (1 × 4)3, and (2 × 3)4. In crosses ***viz.***, (1 × 3)4, (2 × 5)4 and (4 × 5)1 the effect was negative and significant. The 3-line specific interaction effect was positive and significant in crosses ***viz.***, (1 × 2)3, (1 × 2)4, and negative and significant in the cross (2 × 4)5 (Table 35).

The 4-line interaction effect with particular arrangement t_{4ijkl} was positive and significant in (1 × 2) (3 × 5), (1 × 2) (4 × 6), (1 × 5) (2 × 4), (1 × 5) (3 × 4), (1 × 6) (2 × 3), (1 × 6) (4 × 5), (2 × 3) (4 × 5) and (3 × 5) (4 × 6). Negative and significant 4-line interaction effect was shown by the cross combinations ***viz.,*** (1 × 2) (3 × 6), (1 × 2) (4 × 5), (2 × 3) (4 × 6) and (3 × 6) (4 × 5). The 4-line specific interaction effect (S_{4ijkl}) was non significant (Table 36).

4.8.3.4. Number of branches plant^{-1}

The 1-line general effect, was positive and significant in parent 1 alone whereas it was negative and significant in parent 6. The 2-line arrangement effects t_{2ij} was positive and significant in two crosses ***viz.***, 1 × 2 and 4 × 5. While it was negative and significant for crosses 14 alone. The 2-line interaction effect with particular arrangement $t_{2i.j}$ was positive and significant for cross 1 × 4 while the effect was negative and significant for the cross combination 1 × 2. None of the single crosses had significant 2-line specific interaction effect (S_{2ij}) (Table 37).

The 3-line interaction effects was positive and significant in crosses ***viz.***, (1 × 3)2, (1 × 4)3, (1 × 4)6, (1 × 5)6 and (2 × 6)1. Negative and significant 3-line interaction effect ($t_{3ij.k}$) was observed in the crosses ***viz.,*** (1 × 3)4, (3 × 4)2 and (4 × 6)1 (Table 38).

Table 37. Estimates of 1 and 2-line general and 2-line arrangement effects for number of branches plant^{-1} in double crosses

2-line interaction effect of line i and j due to the particular arrangement (ij) (- -) i.e. t_{2ij} above the diagonal and (i-) (j-) i.e. $t_{2i.j}$ below the diagonal; values in bracket correspond to S_{2ij} i.e. effect of i and j irrespective of arrangement

line	1 line general effect	1	2	3	4	5	6
1	0.3423*		0.6671* (0.0993)	0.2834 (0.1477)	-0.8796** (0.0862)	-0.5433 (0.0208)	0.4724 (0.0116)
2	0.2080	**-0.3335***		-0.4876 (0.1147)	-0.2013 (-0.0097)	0.2187 (-0.1128)	-0.1969 (0.1166)
3	0.1376	**-0.1417**	**0.2438**		0.3709 (-0.0332)	-0.0077 (0.0604)	-0.1591 (-0.1519)
4	-0.0777	**0.4398****	**0.1007**	**-0.1855**		0.5794* (-0.0325)	0.1306 (-0.0884)
5	-0.2696	**0.2716**	**-0.1093**	**0.0038**	**-0.2897**		-0.2471 (-0.2054)
6	-0.3407*	**-0.2362**	**0.0984**	**0.0796**	**-0.0653**	**0.1235**	

SE (gi) = 0.1638
SE (t_{2ij}) = 0.2356
SE ($t_{2i.j}$) = 0.1405
SE (S_{2ij}) = 0.1047

* Significant at 5% level
** Significant at 1% level

Table 38. Estimates of 3-line interaction effect of line ij and k due to the particular arrangement (ij)(k -)i.e.$t_{3ij.k}$ in double crosses. Values in bracket correspond to S_{3ijk} i.e. 3-line effect of irrespective of arrangement for number of branches plnant^{-1}

	Parental line					
	1	2	3	4	5	6
1 × 2			-0.3073 (0.1323)*	0.1194 (0.0182)	0.0071 (-0.0864)	-0.4863 (0.1344)*
1 × 3		0.3938*		-0.4776** (0.0666)	-0.0674 (0.1588)**	-0.1322 (-0.0623)
1 × 4		0.1592	0.3680*		-0.0649 (0.0761)	0.4173* (0.0115)
1 × 5		-0.0737	0.2447	0.2656		0..4373* (-0.1069)
1 × 6		-0.1458	-0.1637	-0.0166	-0.1464	
2 × 3	-0.0865			0.3454 (-0.0176)	-0.0779 (0.0369)	0.3065 (0.0777)
2 × 4	-0.2787		0.1348		0.0988 (-0.1087)	0.2464 (0.0886)
2 × 5	0.0666		0.0978	-0.2180		-0.1652 (-0.0675)
2 × 6	0.6320**		-0.1690	-0.3475	0.0814	
3 × 4	0.1096	-0.4801*			0.2280 (0.0645)	-0.2283 (-0.1800)
3 × 5	-0.1772	-0.0199		0.2305		-0.0256 (-0.1393)
3 × 6	0.2950	-0.1375		0.0872	-0.0865	
4 × 5	0.1300	0.1192	-0.4584			-0.3701 (-0.0970)
4 × 6	-0.4007*	0.1011	0.1411		0.0279	
5 × 6	-0.2910	-0.0499	0.1121	0.3422		

SE ($t_{3ij.k}$) = 0.1673 SE (S_{3ijk}) = 0.0471 * Significant at 5% level ** Significant at 1% level

Table 39. Estimates of 4-line effects of lines i, j, k and l for number of branches plant^{-1} due to the particular arrangement (ij) (kl) i.e. $t_{4ij.kl}$ in double crosses. Figures in brackets are 4-line effects irrespective of their arrangement i.e. S_{4ijkl}

	2 × 3	2 × 4	2 × 5	2 × 6	3 × 4	3 × 5	3 × 6	4 × 5	4 × 6	5 × 6
1 × 2					-0.0076 (-0.0058)	-0.1345 (0.1532)	0.1421 (0.2496)*	-0.1421 (-0.2527)*	0.1345 (0.3131)**	-0.1260 (-0.1597)
1 × 3		0.1526	0.3087*	-0.4613**				-0.4613** (0.4825)**	0.3087 (-0.2770)*	0.1526 (-0.1594)
1 × 4	-0.1450		-0.0771	0.2221		0.2221	-0.0771			-0.1450 (-0.0016)
1 × 5	-0.1743	-0.3956**	0.2392		-0.0914		-0.0649		-0.5049**	
1 × 6	0.3193*	-0.0876	-0.2316		-0.2316	-0.0876		0.3193		
2 × 3								0.3193 (-0.0365)	0.3188 (-0.0105)	-0.0114 (-0.0061)
2 × 4						-0.0876	-0.0649			0.2862 (-0.0368)
2 × 5					-0.2316		-0.0771		0.3087	
2 × 6					0.2392	0.2221		-0.4613**		
3 × 4										-0.0076 (-0.2525)*
3 × 5									-0.1345	
3 × 6								0.1421		

SE ($t_{4ij.kl}$) = 0.1535 SE (S_{4ijkl}) = 0.1113 * Significant at 5% level ** Significant at 1% level

The 3-line specific interaction effects S_{3ijk} was significant and positive for (1 × 2)3, (1 × 2)6, and (1 × 3)5. The remaining combinations showed either negative or non significant interaction effect.

Two double crosses ***viz.***, (1 × 3) (2 × 5) and (1 × 6) (2 × 3) revealed positive and significant 4-line interaction effect with particular arrangement $t_{4ij.kl}$ and crosses ***viz.***, (1 × 3) (2 × 6), (1 × 3) (4 × 5, (1 × 5) (2 × 4), (1 × 5) (4 × 6) and (2 × 6) (4 × 5) showed negative and significant 4-line interaction effect. Positive and significant 4-line specific interaction effect S_{4ijkl} was shown by crosses ***viz.,*** (1 × 2) (3 × 6), (1 × 2) (4 × 6) and (1 × 3) (4 × 5), while it was negative and significant for (1 × 2) (4 × 5), (1 × 3) (4 × 6) and (3 × 4) (5 × 6) (Table 39).

4.8.3.5. Number of capsules plant^{-1}

The 1-line general effect was positive and significant in parents 2 and 3 whereas, it was negative and significant in parent 5. (Table 40).

The 2-line interaction effects t_{2ij} was positive and significant in crosses ***viz.***, 1 × 2, 2 × 3, 2 × 6, 3 × 4 and 4 × 6 while the effect was negative and significant in crosses ***viz.***, 1 × 3, 1 × 4, and 2 × 4. The 2-line specific effects S_{2ij} were positively significant for the crosses ***viz.***, 1 × 3, 2 × 3, 2 × 4 and 2 × 6 while it was negatively significant for 1 × 2, 1 × 5, 3 × 6, 4 × 5 and 5 × 6. (Table40).

The 3-line interaction effects for the arrangement $t_{3ij.k}$ was positive and significant for the combinations such as (1 × 3)2, (1 × 4)3, (2 × 4)6, (2 × 6)1, (3 × 5)4, and (4 × 5)1 and negative and significant for (1 × 2)3, (1 × 6)2, (2 × 3)6, (2 × 4)1, (2 × 6)4, (3 × 4)2, (4 × 5)3 and (4 × 6)1. The combinations (1 × 2)6, (1 × 3)4,

Table 40. Estimates of 1 and 2-line general and 2-line arrangement effects for number of capsule plant^{-1} in double crosses

2-line interaction effect of line i and j due to the particular arrangement (ij) (- -) i.e. t_{2ij} above the diagonal and (i-) (j-) i.e. $t_{2i.j}$ below the diagonal; values in bracket correspond to S_{2ij} i.e. effect of i and j irrespective of arrangement

line	1 line general effect	1	2	3	4	5	6
1	-0.3757		9.8467**	-6.3053*	-9.8614**	0.6599	5.6601
			(-1.1935)**	(1.4878)**	(0.3029)	(-1.6258)**	(0.6259)
2	2.4428**	**-4.9223****		6.3665*	-6.9941*	3.1186	12.3376**
				(0.8775)*	(0.7324)*	(0.3829)	(1.6526)**
3	1.7597**	**3.1526**	**-3.1832**		9.5465**	-7.0726	-2.5351
					(0.2772)	(0.5982)	(-1.4809)**
4	0.3391	**4.9307****	**3.4971***	**-4.7732****		0.6953	6.6138*
						(-0.8811)*	(-0.0833)
5	-3.2164**	**-0.3300**	**-1.5593**	**3.5363***	**-0.3476**		2.5988
							(-1.6907)**
6	-0.9494	**-2.8301**	**6.1688****	**1.2676**	**-3.3069**	**-1.2994**	

SE (gi) = 0.6321
SE (t_{2ij}) = 0.3016
SE ($t_{2i.j}$) = 1.0842
SE (S_{2ij}) = 0.3436

* Significant at 5% level
** Significant at 1% level

Table 41. Estimates of 3-line interaction effect of line ij and k due to the particular arrangement (ij)(k -)i.e.$t_{3ij.k}$ in double crosses. Values in bracket correspond to S_{3ijk} i.e. 3-line effect of irrespective of arrangement for number of capsules plnant^{-1}

	Parental line					
	1	2	3	4	5	6
1 × 2			-6.0255** (-0.1039)	1.2409 (-0.9693)**	-2.1783 (-2.0532)**	-2.8838 (0.7394)**
1 × 3		5.4124*		-3.2300 (1.4935)**	1.5672 (1.0710)**	2.5556 (0.5150)*
1 × 4		3.2490	4.4514*		0.4326 (-1.1196)**	1.7284 (1.2012)**
1 × 5		4.0609	0.7566	-0.7130		1.4299 (-1.1497)**
1 × 6		-7.7990**	-2.3352	3.9656	0.5085	
2 × 3	0.6131			0.1980 (0.3641)	-1.3447 (1.5299)**	-5.8328** (-0.0352)
2 × 4	-4.4900*		5.0463		1.0516 (0.3701)	5.3862* (1.6818)**
2 × 5	-1.8826		2.1143	-0.5119		-2.8385 (0.9191)**
2 × 6	10.6828**		2.0481	-4.4241*	4.0308	
3 × 4	-1.2214	-5.2443*			-0.8278 (0.3668)	-2.2530 (-1.6701)**
3 × 5	-2.3238	-0.7696		5.9034**		4.2627 (-1.7714)**
3 × 6	-0.2204	3.7847		1.9019		-2.9310
4 × 5	6.4747**	-0.5397	-5.0756*			-1.5547 (-1.3795)**
4 × 6	-5.6940**	-0.9621	0.3511			-0.3088
5 × 6	-1.9383	0.8164	-1.3317	1.8635		

SE ($t_{3ij.k}$) = 2.1531 SE (S_{3ijk}) = 0.2127 * Significant at 5% level ** Significant at 1% level

Table 42. Estimates of 4-line effects of lines i, j, k and l for number of capsules plant^{-1} due to the particulars arrangement (ij) (kl) i.e. $t_{4ij.kl}$ in double crosses. Figures in brackets are 4-line effects irrespective of their arrangement i.e. S_{4ijkl}

	2 × 3	2 × 4	2 × 5	2 × 6	3 × 4	3 × 5	3 × 6	4 × 5	4 × 6	5 × 6
1 × 2					6.3650** (-0.9063)	-3.3446 (0.3605)	-3.0204 (0.2342)	-3.0204 (-5.2529)	-3.3446 (3.2513)	4.6563* (-1.2673)
1 × 3		0.1220	-3.0098	2.8878				2.8878 (3.4643)	-3.0098 (1.9225)	0.1220 (-0.6118)
1 × 4	-6.4870**		4.3320*	2.1551		2.1551	4.3320*			-6.4870** (-1.5701)
1 × 5	6.3544**	-7.5059**		-5.0429**	-11.2372**		-1.3116		0.1601	
1 × 6	0.1326	1.1896	-1.3222		-1.3222	-1.1896		0.1326		
2 × 3								0.1326 (3.2839)	7.8378** (-1.2851)	-8.4957** (0.9453)
2 × 4						1.1896	-1.3116			-1.8867 (3.0793)
2 × 5					-1.3222		4.3320			-3.0098
2 × 6					-5.0429**	2.1551		2.8878		
3 × 4										6.3650** (-5.6476)
3 × 5									-3.3446	
3 × 6								-3.0204		

SE ($t_{4ij.kl}$) = 2.1102 SE (S_{4inkl}) = 0.8924 * Significant at 5% level ** Significant at 1% level

(1 × 3)5, (1 × 3)6, (1 × 4)6, (2 × 3)5, (2 × 4)6, and (2 × 5)6, showed positive and significant 3-line specific interaction effect S_{3ijk} irrespective of the arrangement while combinations (1 × 2)4, (1 × 2)5, (1 × 4)5, (1 × 5)6, (3 × 4)6, (3 × 5)6 and (4 × 5)6 showed negative and significant effect (Table 41).

The 4-line interaction effect t_{4ijkl} was positive and significant for cross combinations (1 × 2) (3 × 4), (1 × 2) (5 × 6), (1 × 4) (2 × 5), (1 × 4) (3 × 6), (1 × 5) (2 × 3), (2 × 3) (4 × 6) and (3 × 4) (5 × 6). Negative and significant interaction effect was observed with regard to cross combinations (1 × 4) (2 × 3), (1 × 4) (5 × 6), (1 × 5) (2 × 4), (1 × 5) (2 × 6), (1 × 5) (3 × 4), (2 × 3) (5 × 6) and (2 × 6) (3 × 4). The 4-line specific effect S_{4ijkl} was not significant for all the double cross hybrids (Table 42).

4.8.3.6. Capsule length

Parent 3 possessed positive and significant 1-line general effect while parent 2 and 5 had significant but negative general effect (Table 43). The 2-line interaction effect for the particular arrangement t_{2ij} was significant for hybrids such as 1 × 2, 3 × 4, 3 × 5, and 3 × 6 in the positive direction while it was negative for 1 × 3, 1 × 4, 1 × 5, 1 × 6, 2 × 3, 2 × 4, 2 × 5 and 2 × 6 combinations. The interaction effect for the arrangement $t_{2i.j}$ was positive and significant for hybrids 1 × 3, and 2 × 6 and negatively significant for 1 × 2 and 3 × 4 (Table 43). Specific effects due to 2-line arrangement was positive and significant for hybrids 1 × 3, 2 × 3, and 2 × 6. Negative and significant specific effects were shown by the hybrids 1 × 2, 2 × 5, and 3 × 5 (Table 43).

The 3-line interaction effects due to the particular arrangement $t_{3ij.k}$ was positive and significant for (1 × 3)5, (1 × 3)6,

Table 43. Estimates of 1 and 2-line general and 2-line arrangement effects for capsule length in double crosses

2-line interaction effect of line i and j due to the particular arrangement (ij) (- -) i.e. t_{2ij} above the diagonal and (i-) (j-) i.e. $t_{2i.j}$ below the diagonal; values in bracket correspond to S_{2ij} i.e. effect of i and j irrespective of arrangement

line	1 line general effect	1	2	3	4	5	6
1	-0.0031		0.1797** (-0.0133)**	-0.0925** (0.01270)**	-0.0248** (-0.0024)	-0.0364** (0.0001)	-0.0260* (-0.0002)
2	-0.0166**	**-0.0899****		-0.0288** (0.0111)**	-0.0336** (0.0125)**	-0.0457** (-0.0191)**	-0.0716** (-0.0078)
3	0.0180**	**0.0463****	**0.0144**		0.0417** (-0.0015)	0.0288** (-0.0068)**	0.0507** (0.0024)
4	0.0094	**0.0124**	**0.0168**	**-2.0209****		0.0115 (0.0026)	0.0052 (-0.0018)
5	-0.0118*	**0.0182**	**0.0228**	**-0.0144**	**-0.0057**		0.0418** (0.0114)**
6	0.0040	**0.0130**	**0.0358***	**-0.0254**	**-0.0026**	**-0.0209**	

SE (gi) = 0.0061
SE (t_{2ij}) = 0.0102
SE ($t_{2i.j}$) = 0.0132
SE (S_{2ij}) = 0.0016

* Significant at 5% level
** Significant at 1% level

Table 44. Estimates of 3-line interaction effect of line ij and k due to the particular arrangement (ij)(k -)i.e.$t_{3ij.k}$ in double crosses. Values in bracket correspond to S_{3ijk} i.e. 3-line effect of irrespective of arrangement for capsules length

	Parental line					
	1	2	3	4	5	6
1 × 2			0.0113 (0.0111)	-0.0200* (0.0002)	-0.0967** (-0.0218)	-0.0743** (-0.0161)
1 × 3		0.0028		0.0144 (0.0007)	0.0245* (0.0050)	0.0508** (0.0086)
1 × 4		-0.0061	-0.0060		0.0266* (0.0021)	0.0102 (-0.0078)
1 × 5		0.1094**	-0.0476*	-0.0075		0.0003 (0.0150)
1 × 6		-0.0163	-0.0040	0.0188	0.0275*	
2 × 3	-0.0142			0.0074 (0.0186)	0.0372** (-0.0113)	0.0053 (0.0039)
2 × 4	0.0261**		-0.0492**		0.0382** (0.0023)	0.0184* (0.0040)
2 × 5	-0.0127		0.0261**	0.0175*		0.0147 (-0.0074)
2 × 6	0.0906**		-0.0027	-0.0216	0.0054	
3 × 4	-0.0085	0.0148**			-0.0437** (-0.0109)	-0.0314* (-0.0114)
3 × 5	0.0232**	-0.0564**		0.0037		0.0006 (0.0036)
3 × 6	-0.0468**	-0.0026		-0.0047	0.0034	
4 × 5	-0.0010	-0.0557**	0.0399**			0.0053 (0.0116)
4 × 6	-0.0290**	0.0032	0.0361**		-0.0154	
5 × 6	-0.0277**	-0.0393**	-0.0040	0.0101		

SE ($t_{3ij.k}$) = 0.0079 SE (S_{3ijk}) = 0.1123 * Significant at 5% level ** Significant at 1% level

Table 45. Estimates of 4-line effects of lines i, j, k and l for capsules length due to the particulars arrangement (ij) (kl) i.e. $t_{4ij.kl}$ in double crosses. Figures in brackets are 4-line effects irrespective of their arrangement i.e. S_{4ijkl}

	2 × 3	2 × 4	2 × 5	2 × 6	3 × 4	3 × 5	3 × 6	4 × 5	4 × 6	5 × 6
1 × 2					0.0698** (0.0419)**	-0.0733* (-0.0188)*	0.0075 (0.0100)	0.0075 (-0.0148)	-0.0773** (-0.0265)**	0.0890** (-0.0318)**
1 × 3		-0.0177	0.0494**	-0.0317*				-0.0317 (-0.0108)	0.0494* (-0.0290)**	-0.0177 (0.0448)**
1 × 4	-0.0520**		0.0025	0.0495**		0.0495*	0.0025			-0.0520** (0.0319)**
1 × 5	0.0278*	-0.0282*		-0.0178	-0.0359*		-0.0101		0.0097	
1 × 6	0.0242	0.0278*	-0.0520*		-0.0520*	0.0278*		0.0242		
2 × 3								0.0242 (-0.0015)	0.1175** (0.0152)*	-0.0328* (-0.0136)
2 × 4						0.0278*	-0.0101			0.0015 (0.0233)**
2 × 5					-0.0520*		0.0025		0.0494**	
2 × 6					-0.0174	0.0495*		-0.0317*		
3 × 4										0.0698** (-0.0204)**
3 × 5									-0.0773**	
3 × 6								0.0075		

SE ($t_{4ij.kl}$) = 0.0118 SE (S_{4ijkl}) = 0.0057 * Significant at 5% level ** Significant at 1% level

(1 × 4)5, (1 × 5)2, (1 × 6)5, (2 × 3)5, (2 × 4)1, (2 × 4)5, (2 × 4)6, (2 × 5)4, (2 × 6)1, (3 × 4)2, (3 × 5)1, (4 × 5)3 and (4 × 6)3 and negative and significant for (1 × 2)4, (1 × 2)5, (1 × 2)6, (1 × 5)3, (2 × 4)3, (3 × 4)5, (3 × 4)6, (3 × 5)2, (3 × 6)1, (4 × 5)2, (4 × 6)1, (5 × 6)1 and (5 × 6)2. The specific effect due to 3-line arrangement was not significant for any of the hybrid combination (Table 44).

The 4-line interaction effect due to the particular arrangement $t_{4ij.kl}$ was positive and significant for the hybrids (1 × 2) (3 × 4), (1 × 2) (5 × 6), (1 × 3) (2 × 5), (1 × 3) (4 × 6), (1 × 4) (2 × 6), (1 × 4) (3 × 5), (1 × 5) (2 × 3), (1 × 6) (2 × 4), (1 × 6) (3 × 5), (2 × 3) (4 × 6), (2 × 4) (3 × 5), (2 × 5) (4 × 6), (2 × 6) (3 × 5), and (3 × 4) (5 × 6). It was negative and significant for (1 × 2) (3 × 5), (1 × 2) (4 × 6), (1 × 3) (2 × 6), (1 × 4) (2 × 3), (1 × 4) (5 × 6), (1 × 5) (2 × 4), (1 × 5) (3 × 4), (1 × 6) (2 × 5), (1 × 6) (3 × 4), (2 × 3) (5 × 6), (2 × 5) (3 × 4), (2 × 6) (4 × 5) and (3 × 5) (4 × 6). Positive and significant 4-line specific interaction effect was shown by the hybrids (1 × 2) (3 × 4), (1 × 3) (4 × 6), (1 × 4) (5 × 6), (2 × 3) (4 × 6), (2 × 4) (5 × 6). Whereas it was negative and significant for (1 × 2) (3 × 5), (1 × 2) (4 × 6), (1 × 2) (5 × 6), (1 × 3) (4 × 6), and (3 × 4) (5 × 6) (Table 45).

4.8.3.7. 1000 seed weight

1-line general effect was positive and significant for the parents 1 and 3 and it was negative and significant for parents 5 and 6. (Table 46). The 2-line interaction effect due to particular arrangement t_{2ij} was positive and significant for the hybrids 1 × 2, 1 × 3, 2 × 3, 3 × 6 and 4 × 5. Negative and significant for the hybrids 1 × 4, 1 × 6, 2 × 5, 2 × 6, 3 × 4, and 3 × 5. The 2-line interaction effect due to the particular arrangement $t_{2i.j}$ was positive and significant for the hybrids 1 × 4, 3 × 4 and 3 × 5. The 2-line

Table 46. Estimates of 1 and 2-line general and 2-line arrangement effects for 1000 seed weight in double crosses

2-line interaction effect of line i and j due to the particular arrangement (ij) (- -) i.e. t_{2ij} above the diagonal and (i-) (j-) i.e. $t_{2i.j}$ below the diagonal; values in bracket correspond to S_{2ij} i.e. effect of i and j irrespective of arrangement

line	1 line general effect	1	2	3	4	5	6
1	-0.0813**		0.0215* (0.0468)**	0.0451* (0.0027)	-0.0611** (0.0168)*	0.0140 (-0.0068)	-0.0194* (0.0217)**
2	-0.0130	**-0.0108**		0.0251* (0.0044)	0.0148 (-0.0151)*	-0.0314** (-0.0242)*	-0.0300** (-0.0250)**
3	0.0486**	**-0.0225****	**-0.0126**		-0.0402* (0.0161)*	-0.0624** (0.0180)**	0.0324* (0.0073)
4	-0.0166	**0.0306****	**-0.0074**	**0.0201***		0.0746* (0.0021)	0.0119 (-0.0366)**
5	-0.0393**	**-0.0070**	**0.0157**	**0.0312****	**-0.0373****		0.0052 (-0.0284)*
6	-0.0610**	**0.0097**	**0.0150**	**-0.0162***	**-0.0059**	**-0.0026**	

SE (gi) = 0.0112
SE (t_{2ij}) = 0.0102
SE ($t_{2i.j}$) = 0.0103
SE (S_{2ij}) = 0.0057

* Significant at 5% level
** Significant at 1% level

Table 47. Estimates of 3-line interaction effect of line ij and k due to the particular arrangement (ij)(k -)i.e.$t_{3ij.k}$ in double crosses. Values in bracket correspond to S_{3ijk} i.e. 3-line effect irrespective of arrangement for 1000 seed weight

	Parental line					
	1	**2**	**3**	**4**	**5**	**6**
1 × 2			0.0074 (0.0150)	-0.0408** (0.0314)*	-0.0012 (0.0062)	0.0132 (0.0411)**
1 × 3		-0.0612		0.0415** (-0.0021)	-0.0074 (-0.0162)	-0.0180 (0.0088)
1 × 4		0.0635**	0.0298**		-0.0268* (0.0037)	-0.0053 (0.0007)
1 × 5		0.0159	-0.0175	0.0222		0.0004 (-0.0072)
1 × 6		-0.0074	0.0028	-0.0184	0.0424**	
2 × 3	0.0538**			0.0423** (-0.0009)	-0.0231 (-0.0005)	-0.0135 (-0.0048)
2 × 4	-0.0227		-0.0081		0.0644** (-0.0142)	-0.0484** (-0.0465)**
2 × 5	-0.0146		-0.0010	0.0134		0.0337* (-0.0399)**
2 × 6	-0.0058		0.0144	0.0771**	-0.0557**	
3 × 4	-0.0713**	0.0504**			-0.0084 (0.0387)**	0.0694** (-0.0035)
3 × 5	0.0249	0.0242		0.0351*		-0.0218 (0.0141)
3 × 6	0.0151	-0.0008		-0.0544**	0.0078	
4 × 5	0.0396**	-0.0777**	-0.0267*			-0.0098 (-0.0240)
4 × 6	0.0238	-0.0288*	-0.0150		0.0081	
5 × 6	-0.0429**	0.0046	0.0140	0.0017		

SE ($t_{i3ij.k}$) = 0.0131 SE (S_{3ijk}) = 0.0123 * Significant at 5% level ** Significant at 1% level

Table 48. Estimates of 4-line effects of lines i, j, k and l for 1000 seed weight due to the particular arrangement (ij) (kl) i.e. $t_{4ij.kl}$ in double crosses. Figures in brackets are 4-line effects irrespective of their arrangement i.e. S_{4ijkl}

	2 × 3	2 × 4	2 × 5	2 × 6	3 × 4	3 × 5	3 × 6	4 × 5	4 × 6	5 × 6
1 × 2					-0.0945** (0.0149)	0.0694* (-0.0322)	0.0251 (0.0622)	0.0251 (0.0344)	0.0694* (0.0448)	-0.0770* (0.0164)
1 × 3		0.0789*	-0.0397	-0.0393				-0.0393 (-0.0010)	-0.0397 (-0.0203)	0.0789* (-0.0155)
1 × 4	0.0155		0.0666*	-0.0821*		-0.0821*	0.0666*			0.0155 (-0.0224)
1 × 5	-0.0297	-0.1267**		0.1214	0.0863**		-0.0917**		-0.0647*	
1 × 6	0.0142	0.0127	-0.0269		-0.0269	0.0127		0.0142		
2 × 3								0.0142 (0.0449)	0.0140 (-0.0624)*	0.0329 (-0.0143)
2 × 4						0.0127	-0.0917**			0.0964** (-0.1218)
2 × 5					-0.0269		0.0666*		-0.0397	
2 × 6					0.1214**	-0.0821*		-0.0393		
3 × 4										-0.0945** (0.0722)**
3 × 5									0.0694*	
3 × 6								0.0251		

SE ($t_{4ij.kl}$) = 0.0139 SE (S_{4ijkl}) = 0.0307 * Significant at 5% level ** Significant at 1% level

specific interaction effect for 1 × 2, 1 × 4, 1 × 6, 3 × 4 and 3 × 5 while it was negative and significant for 2 × 4, 2 × 6, 4 × 6 and 5 × 6 (Table 46).

The 3-line interaction effect due to the particular arrangement $t_{3ij.k}$ was positively significant for the hybrids (1 × 3)4, (1 × 4)2, (1 × 4)3, (1 × 6)5, (2 × 3)1, (2 × 4)5, (2 × 5)6, (2 × 6)4, (3 × 4)2, (3 × 4)6, (3 × 5)4, and (4 × 5)1 and negatively significant for (1 × 2)4, (1 × 4)5, (2 × 3)4, (2 × 4)6, (2 × 6)5, (3 × 4)1, (3 × 6)4, (4 × 5)2, (4 × 5)3, (4 × 6)2 and (5 × 6)1. The specific interaction effect (S_{3ijk}) was positive and significant for the hybrids (1 × 2)4, (1 × 2)6, and (3 × 4)5 and negative and significant for (2 × 4)6 and (2 × 5)6 (Table 47).

The 4-line interaction effect due to particular arrangement with t_{4ijkl} was positive and significant for the hybrids (1 × 2) (3 × 5), (1 × 2)(4 × 6)(1 × 3) (2 × 4), (1 × 3)(5 × 6), (1 × 4)(2 × 5), (1 × 4) (3 × 6), (1 × 5)(3 × 4), (2 × 4)(5 × 6), (2 × 5)(3 × 6) (2 × 6)(3 × 4) and (3 × 5)(4 × 6) while negatively significant effects were observed in hybrids (1 × 2)(3 × 4), (1 × 2)(5 × 6), (1 × 4)(2 × 6), (1 × 4) (3 × 5), (1 × 5)(2 × 4), (1 × 5)(3 × 6), (1 × 5)(4 × 6), (2 × 4)(3 × 6) and (3 × 4)(5 × 6). 4-line specific interaction effect was positive and significant in the hybrids (1 × 2)(3 × 6) and (3 × 4)(5 × 6). Negative and significant specific interaction effect was exhibited by one hybrid (2 × 3)(4 × 6) alone (Table 48).

4.8.3.8. Seed yield plant^{-1}

Significant 1-line general effects was expressed by all the parents. It was positively significant for 1, 2 and 3 and negatively significant for 4, 5 and 6 (Table 49). 2-line interaction effect with the particular arrangement t2 ij was positively significant for the

Table 49. Estimates of 1 and 2-line general and 2-line arrangement effects for seed yield plant^{-1} in double crosses

2-line interaction effect of line i and j due to the particular arrangement (ij) (- -) i.e. t_{2ij} above the diagonal and (i-) (j-) i.e. $t_{2i.j}$ below the diagonal; values in bracket correspond to S_{2ij} i.e. effect of i and j irrespective of arrangement

line	1 line general effect	1	2	3	4	5	6
1	0.4249**		1.0068 (0.0997)	-0.6084 (0.2460)*	-1.8944** (0.1144)	0.3935 (-0.2656)*	1.1025* (0.2305)*
2	0.1955*	**-0.5034**		1.2538* (0.1021)	-0.7142 (0.0242)	0.0979 (-0.0717)	-1.6444** (0.0412)
3	0.4680**	**0.3042**	**-0.6269***		1.3282* (0.1195)	-1.4677** (0.1443)	-0.5060 (-0.1440)
4	-0.0189*	**0.9472****	**0.3571**	**-0.6641***		0.6043 (-0.0199)	0.6761 (-0.2571)**
5	-0.5765**	**-0.1968**	**-0.0490**	**0.7338***	**-0.3022**		0.3719 (-0.3636)**
6	-0.4930**	**-0.5515**	**0.8222****	**0.2530**	**-0.3380**	**-0.1859**	

SE (gi) = 0.0076
SE (t_{2ij}) = 0.5223
SE ($t_{2i.j}$) = 0.3101
SE (S_{2ij}) = 0.1056

* Significant at 5% level
** Significant at 1% level

Table 50. Estimates of 3-line interaction effect of line ij and k due to the particular arrangement (ij)(k -)i.e.$t_{3ij.k}$ in double crosses. Values in bracket correspond to S_{3ijk} i.e. 3-line effect of irrespective of arrangement for seed yield plant^{-1}

	Parental line					
	1	2	3	4	5	6
1 × 2			-0.8000* (0.0850)	-0.1240 (0.0377)	-0.0855 (-0.2522)**	0.0026 (0.3288)**
1 × 3		0.5846**		-0.0576 (0.1886)**	0.2354 (0.0192)	-0.1540 (0.1992)*
1 × 4		0.9260**	0.7426**		0.0023 (-0.1143)	0.2236 (0.1168)
1 × 5		0.1253	0.0950	0.1891		0.4790** (-0.1839)*
1 × 6		-1.1325**	-0.3418*	0.3272	0.0446	
2 × 3	0.2154			-0.2006 (0.0310)	-0.2047 (0.1458)	-1.0639** (-0.0575)
2 × 4	-0.8021**		0.8079*		-0.1152 (0.0659)	0.8235** (-0.0863)
2 × 5	-0.0398		0.4156*	0.1106		-0.5844** (-0.1027)
2 × 6	1.1299**		0.2033	-0.1431	0.4543**	
3 × 4	-0.6850**	-0.6073**			-0.0182 (0.2861)**	-0.0177 (-0.2669)
3 × 5	-0.3304*	-0.2109		1.0264**		0.9826** (-0.1628)
3 × 6	0.4958**	0.8606**		-0.1041	-0.7463**	
4 × 5	1.0906**	0.0046	-1.0082**			-0.6913* (-0.2778)**
4 × 6	-0.5508**	-0.6804**	0.1218		0.4333*	
5 × 6	-0.5237**	0.3240	-0.2363	0.2580		

SE ($t_{3ij.k}$) = 0.1412 SE (S_{3jk}) = 0.0738 * Significant at 5% level ** Significant at 1% level

Table 51. Estimates of 4-line effects of lines i, j, k and l for seed yield plant^{-1} due to the particulars arrangement (ij) (kl) i.e. $t_{4ij.kl}$ in double crosses. Figures in brackets are 4-line effects irrespective of their arrangement i.e. S_{4ijkl}

	2 × 3	2 × 4	2 × 5	2 × 6	3 × 4	3 × 5	3 × 6	4 × 5	4 × 6	5 × 6
1 × 2					-0.0327 (-0.0213)	0.2180 (-0.2594)	-0.1853 (0.5356)*	-0.1853 (-0.4069)	0.2180 (0.5414)*	-0.2266 (-0.0905)
1 × 3		0.4867*	-0.6576**	0.1708				0.1708 (0.4211)*	-0.6576** (0.1660)	0.4867* (-0.1041)
1 × 4	-0.4541*		0.6236**	-0.1695		-0.1695	0.6236**			-0.4541* (-0.3571)
1 × 5	0.4396*	-1.7203**		-0.0013	-1.2832**		-0.4383*		-0.8423**	
1 × 6	0.0145	-0.0484	0.0340		0.0340	-0.0484		0.0145		
2 × 3								0.0145 (0.7595)**	0.5678** (-0.6452)**	-0.6480** (-0.0627)
2 × 4						-0.0484	-0.4383*			0.2928 (-0.1550)
2 × 5					0.0340		0.6236**		-0.6576**	
2 × 6					-0.0013	-0.1695		0.1708		
3 × 4										-0.0327 (-0.3215)
3 × 5									0.2180	
3 × 6								-0.1853		

SE ($t_{4ij.kl}$) = 0.2036 SE (S_{4ijhkl}) = 0.2008 * Significant at 5% level ** Significant at 1% level

hybrids 1 × 6, 2 × 4, and 3 × 4 while negative and significant effect was expressed by 1 × 4, 2 × 6, and 3 × 5. 2-line interaction effect due to the particular arrangement t_{2ij} was positive and significant for hybrids 1 × 4, 2 × 6 and 3 × 5. Hybrids 2 × 3 and 3 × 4 exhibited negative and significant effect. 2-line specific interaction effect was positive and significant for the hybrid 1 × 3 alone while it was negatively significant for 1 × 5, 4 × 6 and 5 × 6. (Table 49).

The 3-line interaction effect due to the particular arrangement with $t_{3ij.k}$ was positive and significant for the hybrids (1 × 3)2, (1 × 4)2, (1 × 4)3, (1 × 5)6, (2 × 4)3, (2 × 4)6, (2 × 5)3, (2 × 6)1, (2 × 6)5, (3 × 5)4, (3 × 5)6, (3 × 6)1, (3 × 6)2, (4 × 5)1 and (4 × 6)5. Negative and significant arrangement effects were exhibited by (1 × 2)3, (1 × 6)2, (1 × 6)3, (2 × 3)6, (2 × 4)1, (2 × 5)6, (3 × 4)1, (3 × 4)2, (3 × 5)1, (3 × 6)5, (4 × 5)3, (4 × 5)6, (4 × 6)1, (4 × 6)2 and (5 × 6)1 (Table 50). 3-line specific interaction effect was positive and significant in hybrids (1 × 2)6, (1 × 3)4, (1 × 3)6, and (3 × 4)5 whereas it was negatively significant in (1 × 2)5, (1 × 5)6, and (4 × 5)6 (Table 50).

The 4-line interaction effect of lines i, j, k and l due to the particular arrangement t_{4ijkl} was positive and significant for seven double cross hybrids ***viz.***, (1 × 3)(2 × 4), (1 × 3)(5 × 6), (1 × 4) (2 × 5), (1 × 4)(3 × 6), (1 × 5)(2 × 3), (2 × 3)(4 × 6) and (2 × 5) (3 × 6). Negative and significant effects were observed in the case of (1 × 3)(2 × 5), (1 × 3)(4 × 6), (1 × 4)(2 × 3), (1 × 4)(5 × 6), (1 × 5)(2 × 4), (I × 5) (3 × 4), (1 × 5) (3 × 6), (1 × 5) (4 × 6), (2 × 3) (5 × 6), (2 × 4)(3 × 6 and (2 × 5)(4 × 6) (Table 51).

The double cross hybrids (1 × 2)(3 × 6), (1 × 2)(4 × 6), (1 × 3)(4 × 5) and (2 × 3) (4 × 5) exhibited positive and significant 4-line specific effect while hybrids (2 × 3)(4 × 6) alone showed negative and significant effect for this trait.

4.8.3.9. Oil content

The parents 1 and 3 showed significant 1-line general effect. It was negative for parent 1 and positive for parent 3 (Table 52).

The 2-line arrangement effect (t_{2ij}) was positively significant for the cross 2 × 6, 3 × 5 and 4 × 6; while it was negatively significant for the cross 3 × 6. The 2-line arrangement effect due to the particular arrangement t_{2ij} was negatively significant for the cross 3 × 5 alone. The rest of the combinations were non- significant for this effect. The 2-line specific interaction effect S_{2ij} was non-significant for all the cross combinations (Table 52).

The 3-line interaction effect due to the particular arrangement with $t_{3ij.k}$ was positive and significant for the hybrids (1 × 3)6, (2 × 3)5, (3 × 4)2, (3 × 6)4, and (5 × 6)2 while negatively significant arrangement effects was shown by (1 × 2)5, (2 × 3)4, (2 × 6)5, (3 × 4)5, (3 × 5)2 (3 × 6)1, and (4 × 6)2. The specific interaction effect S_{3ijk} was positive and significant for (1 × 2)5, (1 × 2)6, (3 × 4)5, (3 × 4)6 and (3 × 5)6 while it was negative and significant for (1 × 3)4, (1 × 3)5, (1 × 4)5, (1 × 5)6, (2 × 4)6 and (2 × 5) 6 (Table 53).

The 4-line interaction effect due to the particular arrangement t_{4ijkl} was positive and significant for the hybrids(1 × 2)(3 × 5), (1 × 2)(4 × 6), (1 × 3)(2 × 4), (1 × 3)(5 × 6), (1 × 5)(2 × 6), (1 × 5)(3 × 4), (2 × 6)(3 × 4) and (3 × 5)(4 × 6) (Table 54). Negative and significant 4-line interaction effect was exhibited by the hybrids (1 × 2)(3 × 4), (1 × 2)(5 × 6), (1 × 4)(2 × 6), (1 × 4)(3 × 5), (2 × 3)(4 × 6), (2 × 6)(3 × 5) and (3 × 4)(5 × 6). 4-line specific interaction effect was positive and significant in (1 × 2) (3 × 5), (1 × 2) (4 × 5), (1 × 2) (5 × 6), (1 × 3) (4 × 6) and (3 × 4)(5 × 6). Negative and significant specific effects were exhibited by (1 × 2)

Table 52. Estimates of 1 and 2-line general and 2-line arrangement effects for oil content in double crosses

2-line interaction effect of line i and j due to the particular arrangement (ij) (- -) i.e. t_{2ij} above the diagonal and (i-) (j-) i.e. $t_{2i.j}$ below the diagonal; values in bracket correspond to S_{2ij} i.e. effect of i and j irrespective of arrangement

line	1 line general effect	1	2	3	4	5	6
1	-0.3361*		0.2306 (0.1829)	-0.0128 (-0.1488)	-0.0342 (-0.2177)	0.0344 (-0.1193)	-0.2181 (-0.0332)
2	-0.1203	**-0.1153**		-0.1139 (-0.0843)	-0.2508 (-0.1019)	-0.1936 (0.0087)	0.3278* (-0.1257)
3	0.3514*	**0.0064**	**0.0569**		0.1025 (0.2156)	0.4625* (0.0984)	-0.4383* (0.2704)
4	0.0692	**0.0171**	**0.1254**	**-0.0513**		-0.2247 (0.0153)	0.4072* (0.1579)
5	-0.1153	**-0.0172**	**0.0968**	**-0.2313****	**0.1124**		-0.0786 (-0.1184)
6	0.1181	**0.1090**	**-0.1639**	**0.2192**	**-0.2036***	**0.0393**	

SE (gi) = 0.1217
SE (t_{2ij}) = 0.1372
SE ($t_{2i.j}$) = 0.1018
SE (S_{2ij}) = 0.2379

* Significant at 5% level
** Significant at 1% level

Table 53. Estimates of 3-line interaction effect of line ij and k due to the particular arrangement (ij)(k -)i.e.$t_{3ij.k}$ in double crosses. Values in bracket correspond to $S_{3ij.k}$ i.e. 3-line effect irrespective of arrangement for oil content

	Parental line					
	1	2	3	4	5	6
1 × 2			0.0844 (-0.0152)	0.4647 (-0.0077)	-0.6257* (0.2628)**	-0.1540 (0.1258)**
1 × 3		-0.5356		-0.0797 (-0.1791)**	-0.2332 (-0.1363)**	0.8613* (0.0331)
1 × 4		0.0351	-0.1876		0.4535 (-0.1943)**	-0.2668 (-0.0544)
1 × 5		0.4151	0.1510	-0.4740		-0.5494 (-0.1708)**
1 × 6		0.2006	-0.0542	-0.3510	0.4226	
2 × 3	0.4511			-0.9414** (-0.0707)	0.8867** (-0.0158)	-0.2825 (-0.0669)
2 × 4	-0.4999		-0.0326		0.3428 (-0.0224)	0.4406 (-0.1030)*
2 × 5	0.2106		-0.1671	-0.0097		0.1599 (-0.2072)**
2 × 6	-0.0465		0.0583	0.3610	-0.7006*	
3 × 4	0.2674	0.9740**			-0.7847* (0.2276)**	-0.5592 (0.4534)**
3 × 5	0.0822	-0.7196*		0.4136		-0.2388 (0.1214)**
3 × 6	-0.8071*	0.2242		0.6588*	0.3625	
4 × 5	-0.4024	-0.3331	0.3711			0.5890 (0.0198)
4 × 6	0.6178	-0.8015*	-0.0996		-0.1239	
5 × 6	0.1268	0.6688*	-0.1238	-0.4651		

SE ($t_{3ij.k}$) = 0.3112 SE (S_{4ijk}) = 0.0321 * Significant at 5% level ** Significant at 1% level

Table 54. Estimates of 4-line effects of lines i, j, k and l for oil content due to the particular arrangement (ij) (kl) i.e. $t_{4ij.kl}$ in double crosses. Figures in brackets are 4-line effects irrespective of their arrangement i.e. S_{4ijkl}

	2 × 3	2 × 4	2 × 5	2 × 6	3 × 4	3 × 5	3 × 6	4 × 5	4 × 6	5 × 6
1 × 2					-1.0661** (-0.3911)**	0.7410** (0.2534)*	0.3251 (0.0921)	0.3251 (0.3089)**	0.7410** (0.0592)	-1.1942** (0.2262)*
1 × 3		0.5622*	-0.4282	-0.1340				-0.1340 (-0.4078)**	-0.4282 (0.2617)*	0.5622* (-0.2546)*
1 × 4	0.5039		0.0697	-0.5736*		-0.5736**	0.0697			0.5039 (-0.4841)**
1 × 5	-0.3128	0.0280		0.7076**	1.1305**		-0.3949		0.1104	
1 × 6	-0.1911	-0.1674	0.3585		0.3585	-0.1674		-0.1911		
2 × 3								-0.1911 (0.0856)	-1.4699** (0.0934)	0.3758 (-0.3863)**
2 × 4						-0.1674	-0.3949			0.4342 (-0.4616)**
2 × 5					0.3585		0.0697		-0.4282	
2 × 6					0.7076**	-0.5736*		-0.1340		
3 × 4										-1.0661** (1.0051)**
3 × 5									-0.7410**	
3 × 6								0.3251		

SE ($t_{4ij.kl}$) = 0.2663 SE (S_{4ijkl}) = 0.1054 * Significant at 5% level ** Significant at 1% level

(3 × 4), (1 × 3)(4 × 5), (1 × 3)(5 × 6), (1 × 4)(5 × 6), (2 × 3)(5 × 6) and (2 × 4) (5 × 6) (Table 54).

4.8.4. Genetic components of variance

The estimates of genetic components of variance were presented in Table 55. The estimates of additive variance, additive × additive × additive interaction were higher in magnitude and also positive. This was followed by positive additive × additive × dominance interaction component. Dominance variance, additive × additive interaction and dominance × dominance interactions were negative in nature.

4.8.5. Double cross hybrid prediction

The actual and predicted yield of double crosses from 6 parents and differences in seed yield are presented in Table 56.

Among the 45 cross combinations the predicted values were positive for eight cross combinations ***viz.***, (1 × 4)(3 × 6), (1 × 5) (2 × 3), (1 × 6)(2 × 3), (1 × 6)(2 × 4), (1 × 6)(3 × 4), (1 × 6)(4 × 5), (2 × 5)(3 × 6) and (3 × 4(5 × 6). The remaining cross combinations showed negative values with varying quantity.

Table 55. Estimates of genetic components of variance

Components	Days to first flowering	Plant height	Height to first Productive node	Number of branches plant^{-1}	Number of Capsule plant^{-1}	Capsule length	1000 seed weight	Seed yield plant^{-1}	Oil content
Additive (S^2_{10})A	5035570.68	64897799.70	9008013.96	106274.14	62493659.90	43870.40	55857.17	1480337.00	17048830.50
Dominance (S^2_{01}) D	-525971.68	-6778034.60	-940683.73	-11096.95	-6525203.30	-4582.00	-5833.47	-154630.72	-1780707.90
Additive × Additive (S^2_{20})A×A	-12700943.00	-163688112.00	-22720241.00	-268048.96	-157626794.00	-110652.09	-140886.04	-3733755.60	-43001347.00
Additive × Dominance (S^2_{11}) A×D	2805146.40	36150161.30	5017242.90	59192.91	34805861.10	24437.85	31112.7095	824728.29	+9497088.02
Dominance × Dominance (S^2_{02}) D×D	-2805080.10	-36150212.00	-5017169.00	-59187.06	-34806675.00	-24438.07	-31113.736	-824657.65	-9497089.20
Additive × Additive × Additive (S^2_{30}) AAA	9350394.87	120507663.00	16727021.30	197345.73	116048326.00	81462.01	103721.57	2748750.25	31657527.7

Table 56. Predicted means of seed yield plant^{-1} for 45 possible double crosses from 6 parents of sesame based on the average single cross performance

Single cross	Yield/ plant	Double cross	Double cross		Difference
			Actual yield/ plant	Predicted yield/ plant	
1 × 2	32.79	(1 × 2) (3 × 4)	28.59	40.70	-12.11
		(1 × 2) (3 × 5)	23.69	39.04	-23.2
		(1 × 2) (3 × 6)	28.51	41.27	-12.76
		(1 × 2) (4 × 5)	28.03	43.54	-15.51
		(1 × 2) (4 × 6)	28.85	45.76	-16.91
		(1 × 2) (5 × 6)	25.24	44.10	-18.86
1 × 3	31.95	(1 × 3) (2 × 4)	26.38	41.67	-15.29
		(1 × 3) (2 × 5)	25.37	38.46	-13.09
		(1 × 3) (2 × 6)	25.95	40.81	-14.86
		(1 × 3) (4 × 5)	28.12	43.49	-15.37
		(1 × 3) (4 × 6)	24.68	45.85	-21.17
		(1 × 3) (5 × 6)	27.61	42.63	-15.02
1 × 4	52.01	(1 × 4) (2 × 3)	23.85	36.14	-12.29
		(1 × 4) (2 × 5)	24.12	38.03	-13.91
		(1 × 4) (2 × 6)	23.92	39.95	-16.03
		(1 × 4) (3 × 5)	24.86	38.58	-13.72
		(1 × 4) (3 × 6)	54.86	40.51	14.35
		(1 × 4) (5 × 6)	19.98	42.40	-22.42
1 × 5	42.0	(1 × 5) (2 × 3)	45.74	36.26	9.48
		(1 × 5) (2 × 4)	22.12	41.37	-19.25
		(1 × 5) (2 × 6)	24.00	41.16	-17.16
		(1 × 5) (3 × 4)	28.57	40.36	-11.79
		(1 × 5) (3 × 6)	24.94	40.15	-15.79
		(1 × 5) (4 × 6)	24.07	45.26	-21.19
1 × 6	50.69	(1 × 6) (2 × 3)	51.62	36.50	15.12
		(1 × 6) (2 × 4)	53.22	41.18	12.04
		(1 × 6) (2 × 5)	23.81	39.04	-15.23
		(1 × 6) (3 × 4)	51.44	40.3	11.14
		(1 × 6) (3 × 5)	24.98	38.16	-13.18
		(1 × 6) (4 × 5)	54.11	42.84	11.27
2 × 3	40.46	(2 × 3) (4 × 5)	27.93	40.03	-12.1
		(2 × 3) (4 × 6)	25.76	40.26	-14.5
		(2 × 3) (5 × 6)	26.05	40.39	-14.34
2 × 4	38.39	(2 × 4) (3 × 5)	24.72	40.64	-15.92
		(2 × 4) (3 × 6)	24.36	40.45	-16.09
		(2 × 4) (5 × 6)	24.71	40.16	-15.45
2 × 5	41.75	(2 × 5) (3 × 4)	28.61	39.09	-10.48
		(2 × 5) (3 × 6)	45.40	40.10	5.3
		(2 × 5) (4 × 6)	23.42	39.67	-16.25
2 × 6	41.97	(2 × 6) (3 × 4)	23.20	39.02	-15.82
		(2 × 6) (3 × 5)	22.03	40.22	-18.19
		(2 × 6) (4 × 5)	21.87	39.37	-17.50
3 × 4	41.42	(3 × 4) (5 × 6)	45.55	38.68	6.87
3 × 5	38.57	(3 × 5) (4 × 6)	24.64	39.76	-15.12
3 × 6	39.28	(3 × 6) (4 × 5)	20.46	39.34	-18.88
4 × 5	38.94	–	–	–	–
4 × 6	37.96	–	–	–	–
5 × 6	39.40	–	–	–	–
Mean			29.57	40.50	-11.12
SE			1.50	0.33	1.59

DISCUSSION

CHAPTER V

DISCUSSION

Since most plant breeding is dependent upon the release of variation as a consequence of recombination and segregation, a good deal of attention has been directed in plant breeding research to the management of this variation and to the control of its release.

Biometrical genetics that enables us to analyse the variation into its non heritable and various heritable components and also to set out their implications for the work of the plant breeder. The biometrical genetics has the power to trace the causation of basic phenomenon such as heterosis and in predicting the outcome of breeding programme. It can thus help the breeder to interpret the results that he obtains and also to plan the strategies for his breeding programmes.

Heritable variation is the plant breeders raw material and if it is inadequate or not readily available he may seek to induce the variation by other means such as recombination, mutation etc. From the resulted combination it is possible for the breeder to analyse the causation of heterosis, prediction of heterosis in different combinations and induction of variability through double cross programme. From the results of the above analyses, the discussion is presented below.

5.1. Pattern analysis

Genotype by environment interaction (G × E) for yield has been found to be of sufficient magnitude to complicate selection in many crop species (DeLacy ***et al.***, 1990). As a result genotypes being tested in plant breeding trials are often evaluated across a range of environments (Byth ***et al.***, 1976). Such multi-environment

testing is usually time consuming and costly. Therefore with limited resources for testing genotypes, procedures for determining the number of environments to be sampled is critical in any plant breeding programme.

One of the many analytical methods used to facilitate selecting the number of environments that are used in selection programmes, classification or cluster analysis has been found to be useful (Fox and Rosielle, 1982). Classificatory techniques has the advantage that relationships among genotypes based on their response pattern across environments can also be investigated (Mungomery ***et al***., 1974, Bull ***et al***., 1992 b).

The clustering and ordination procedure used in this study examined the actual environmental responses of the number of genotypes. The results indicated that individual genotypes had a relatively homogenous response. The information gained in this study had applications relating to the interpretation of adaptation responses for practical breeding situations.

The results of the present study helped to identify the genotypes of cluster 1 which revealed stable responses across environments and which may have the potential as parents. This information also helped to predict the average adaptation response of progeny derived from parents with known environmental responses.

The principal component analysis showed that the genotypes are responding differentially to the environments. The dendrogram identified genotypes (EC 357017, EC 357016), (EC 351905, EC 357019), (EC 357020, EC 357022), (EC 351880, EC 351907), (EC 351908, EC 357024), (EC 357023, EC 357018), (EC 351879, EC 357015), (EC 357025, EC 357026) and (TMV 3, TMV 4) that are similar in response to the changed environment.

Many of the sesame genotypes had similar net responses although this performance in certain individual environments may differ considerably for seed yield. It would be informative for a plant breeder to be able to differentiate among such genotypes when a large number of genotypes was being examined. The numerical classificatory and ordination procedure facilitated such a differentiation (Mungomery ***et al.***, 1974).

5.2. Additive Main effects and Multiplicative Interaction effects (AMMI)

For any genotype-environment combination, the main effects equals the genotype mean plus the environmental mean minus the grand mean and the interaction is the genotype PCA score times the environment PCA score. When a genotype and an environment have the same sign on the PCA axis the interaction is positive, if different, their interaction is negative. If a genotype or an environment has a PCA score of nearly zero, it has small interaction effect (Zobel ***et al.***, 1988).

In the present study, the Figure 3 displayed at a glance both main effects and interaction effects. Genotypes ***viz.***, 8 (EC 351908), 11 (EC 357017), 14 (EC 357020), 5 (EC 351905) and 16 (EC 357022) were stable across the environments. CO 1 (24) was an extremely interactive cultivar. Though 25 (SVPR 1) and 23 (TMV 6) were almost equal in yield, 25 (SVPR 1) was more interactive than 23 (TMV 6). TMV 3 (21) and 23 (TMV 6) were equal in yield and interaction. They were moderately stable. While comparing the three seasons, the third season was less interactive and stable for sesame genotypes (refer Table 1).

5.3. Diallel analysis

The analysis of diallel cross is considered as the most suitable method for the study of individual components of genetic variability. (Jinks, 1954 and Hayman, 1954). The method allows a good insight into the genetic nature of the parent genotype, F_1 hybrids and subsequent generations. (F_2, B_1, B_2). Furthermore, diallel crosses can be used to assess interaction between genes and environmental factors (Allard, 1956, Matzinger and Kempthorne, 1956). The performance of the parents and their hybrids may not always necessarily give an indication of the probable performance of the progeny. An analysis of diallel set crosses enables us to make prediction from the informations collected in the F_1 generations.

The analysis of diallel crosses may be used to assess the stability of genetic parameters which interact with environmental factors (Marinkovic, 1993). Analysis of diallel crosses may be helpful in the study of heterosis, which results from various gene actions and interactions as well as in the calculations of degree of heritability. Similar to the situations with other agricultural crops, the analysis of diallel cross has found wide application in the genetic analysis of sesame also.

In the present study, the estimation of genetic parameters were carried out both by genetic and graphic analysis and by means of combining ability effects. The implications of genetical and graphical analysis of Wr and Vr statistics have been discussed by Jinks and Hayman in a series of papers since 1953 and later by Mather and Jinks (1982). The essential points to be gained from the graphical analysis are (a) the average dominance from the distance from the origin and Wr intercept of the regression line; (b) the relative portion of the dominant and recessive genes in the parent from the distribution of their respective array points along the

regression line and (c) a measure of genetical diversity among parents from the distance between array points.

Likewise, the genetical analysis provides certain other informations (a) the mean degree of dominance, (b) the proportion of genes with positive and negative effects in the parents, (c) the proportion of dominant and recessive genes in the parents, (d) group of genes and (e) heritability estimates in the narrow sense.

The chosen sesame parents were diploids. The parents were maintained through selfing over years and the above features satisfy the requirements for subjecting these parents to diallel analysis which has been employed by different sesame workers for getting information on the nature of gene action and ultimately fix up the parents in breeding programme in sesame (Goyal and Sudhirkumar, 1991; Kadu ***et al.***, 1992; Reddy ***et al.***, 1993; Backiyarani, 1995; Navadhiya ***et al.***, 1995 and Vignesh, 1997).

5.3.1. Adequacy of diallel model

Before embarking on the diallel analysis proper, the material under study has to be tested for agreement with the assumptions laid out for diallel. The validity of the assumptions was tested by the t^2 test (Hayman, 1954 a). The t^2 values were significant for the height to the first productive node alone and significant deviation of 'b' from unity for days to first flowering, height to the first productive node, number of capsule plant^{-1}, seed yield plant^{-1} and oil content indicating thereby the non fulfilment of one or more assumptions.

Two other tests recommended by Mather and Jinks (1982) were also adopted to ascertain the goodness of fit of the data to the model. First consistency of the (Wr-Vr) differences over array was tested by a two way analysis of variance of array x blocks. Second, a joint regression analysis of Wr on Vr was performed in order to test

the significance of deviations of the joint linear regression coefficient from unity, as well as from zero over blocks. Both results showed a significant disagreement with the model for the characters studied. This indicated that one or more of the basic assumptions of the simple additive-dominance model were not satisfied.

5.3.2. Genetical and graphical analysis

5.3.2.1. Days to first flowering

Three analysis ***viz.,*** t^2, joint regression and variance of Wr+Vr and Wr-Vr indicated the presence of non-allelic interactions for days to first flowering. The assumptions of non-allelic interaction was difficult to satisfy in most of the studies wherever diallel analysis has been used (Jana, 1975).

Significance of D and H_1 and H_2 and h^2 components indicated the importance of both additive and dominance effects of the present set of material under study. This was also confirmed by the significant σ^2***gca*** and σ^2***sca*** estimates (Table 13). The value of $(H_1/D)^{\frac{1}{2}}$ suggested the partial dominance nature of this trait. It was also confirmed by the interception of unit regression line on Wr axis above the point of origin (Fig. 4a). The ratio of $H_2/4H_1$ showed the asymmetrical distribution of dominant and recessive alleles where as K_d/K_r ratio showed more dominant alleles in the diallel set. This was also supported by positive 'F' value. Usually the ratio underestimates the number of dominant genes and it provides no information about groups exhibiting little or no dominance (Halloran, 1975). High heritability estimate was observed in the present study for days to first flowering. Similar observations was reported by Biswas and Akbar (1995).

Besides additive gene action the presence of dominance was reported by earlier workers for this trait (Das and Sen, 1989; Goyal and Sudhirkumar, 1991 and Vignesh, 1997).

The values of Vr, Wr were positive over all the array points hence generating a curve (Fig. 4a). which is concave upward and thus indicated complementary type of non-allelic interaction. Mather (1967) has shown that with complementary interaction Δvr–Δwr is positive (***i.e.***, the change in Wr is less than the change in Vr) resulting in the Vr, Wr array paints to the right of the unit slope. Thus complementary interaction affects the distribution pattern of array points in a characteristic way, generating a curve which is concave upward. However, dispersed gene distribution where, the parents with balancing combinations of alleles with positive and negative effects are in excess over that expected from the independent distributions also produced a more or less similar distribution pattern of array points (Coughtrey and Mather, 1970). Therefore, it becomes difficult to distinguish between the effect of dispersed gene distribution and complementary interaction on a Wr, Vr graph.

The graphical analysis revealed that parents 4 and 6 have more number of dominant alleles for dominance gene action governing this character. The parent 3 contained more recessive alleles. However, parents 1, 5 and 2 had both dominant and recessive alleles for the inheritance of this character.

The standardised deviation graph revealed that the parental lines 4 and 6 may be utilised for developing early varieties through hybridisation programme since they contain dominant genes with negative influence for this character.

The positive and significant correlation between parental order of dominance (Wr+Vr) and the parental measurement

suggested that high mean expression associated with recessive and dominance is unidirectional.

5.3.2.2. Plant height

The fitness of data pertaining to plant height to the additive dominance model indicated the presence of non-allelic interaction by the three tests (Table 9). The high level significance of additive and dominance components H_1, H_2, h^2 and more than unity value of $(H_1/D)^{\frac{1}{2}}$ (Table 11) indicated that this trait was under the influence of dominance gene action. The point of intercept of regression line below the origin in Wr-Vr graph also suggested that dominant gene action was predominant in determining the plant height. This was in accordance with the earlier reports of Ramakrishnan and Soundarapandian (1990) and Balan (1994).

The positive F value and K_d/K_r ratio indicated the excess dominant alleles but the significance of H_2 value indicated the positive and negative effect of alleles which might have caused the inflation of dominance to overdominance. According to Hayman (1954 a) a particular combination of positive and negative genes have a complementary type of gene interaction or simply correlated gene distributions will seriously inflate the ratio and turn partial dominance into overdominance. According to Robinson (1966) no case of major significance has been brought to favour the importance of over dominance in the expression of quantitative gene action.

High heritability in narrow sense was noticed in the present material. The estimate derived was not considered reliable in all parents because they are solely a function of the number of parents in the diallel (Hayman, 1963) and represents only those in which some degree of dominance is involved as well as biased due to bidirectional dominance. This could be the reason for the estimates

of K=1 or just a few genes (Park and Davis, 1966). The number of block of genes controlling this trait could be possibly one.

The high magnitude of ΔVr generated a curve which is concave upward indicating the presence of complementary type of non-allelic interaction. Parents 2 and 1 had more number of dominant alleles for dominance gene action governing the character. Parents 4 and 5 contained more recessive alleles. However parents 3 and 6 had both dominant and recessive alleles for the inheritance of this character. Standardised deviation graph revealed that parents 1 and 2 may be employed for hybridisation whenever height of the plant has to be improved and parents 4, 5 and 6 possessed recessive genes with negative influence.

The positive correlation between mean values of the parents and the order of dominance suggested that high mean expression is associated with recessive genes. However the non-significance of correlation value indicated that the dominance is ambidirectional.

5.3.2.3. Height to the first productive node

Presence of non-allelic interaction was revealed by the three tests for this trait (Table 9). Both additive and dominance components (H_1 and H_2) were highly significant. This type of gene action was also reported by Deenamani (1989).

The graphical analysis and $(H_1/D)^{\frac{1}{2}}$ ratio indicated over dominance. The negative 'F' value and K_d/K_r ratio (Table 12) pointed out the existence of more recessive alleles. The non significant H_2 and $H_2/4H_1$ ratio indicated the asymmetrical distribution of genes with position and negative effects and over dominance nature as indicated by the mean degree of dominance. Dominance estimates however were not affected by non-allelic interaction.

Heritability estimate was high for this character. Chandrasekhara and Reddy (1993) also reported high heritability for height to first productive node. The estimates of h^2/H_2 indicated single block of genes controlling the inheritance of first productive node.

The high magnitude of ΔVr generated a curve which is concave upward indicating the presence of complementary type of non-allelic interaction. The Wr, Vr graph disclosed that parents 6, 5 and 4 had more number of dominant alleles and parents 2, and 1 had more number of recessive alleles for the inheritance of this character. The standardised deviation graph revealed that parents 4, 5 and 6 may be utilised for hybridisation programme to develop varieties with first productive node near to the ground since they contain dominant gene with negative influence for this character.

Significant positive correlation between mean values of the parents and the order of dominance suggested high mean expression associated with recessive and the order of dominance was unidirectional.

5.3.2.4. Number of branches plant^{-1}

The fitness of additive-dominance model for number of branches was revealed by all the three tests in this trait (Table 9). High level of significance of D, H_1, H_2 and h^2 indicated by the involvement of both additive and dominant gene effect in respect of number of branches. Similar results were reported by Kadu ***et al***. (1992) and Sajjanar ***et al***. (1995).

The regression line cut the Wr axis above the point of origin and the ratio of mean degree of dominance below unity indicating the presence of partial dominance amongst the crosses for this trait. The positive F value and K_d/K_r displayed the existence of more

dominant alleles where as the significant H_2 component and $H_2/4H_1$ ratio indicated the asymmetrical distributions of genes with positive and negative alleles which might be the cause for the inflation of partial to overdominance.

High heritability estimate was observed for number of branches. Chandrasekhara and Reddy (1993 a); Shadakshari ***et al***. (1995) and Singh ***et al***. (1997) also reported high heritability estimates for this character indicating the preponderance of additive gene action for this trait. The estimates of h^2/H_2 indicated that the genes controlling this trait was below one.

The Wr, Vr graph revealed that parents 4, 5 and 6 had more number of dominant genes and parent 3 had recessive genes. However parents 2 and 1 had both dominant and recessive allele for the inheritance of this character.

The parents 1 and 2 had recessive gene with positive influence for this trait. Parents 3, 4, 5 and 6 had both dominant and recessive genes with negative influence for this trait. Significant positive correlation between Yr and Wr+Vr estimates suggested that the order of dominance is unidirectional.

5.3.2.5. Number of capsules plant^{-1}

Presence of non-allelic interaction was evident by $1\text{-}b/SE_{(b)}$ value, Wr-Vr differences and joint regression for number of capsules plant^{-1}.

Significant D and non significant H_1, H_2 and h^2 values of diallel set indicating the predominance of additive gene action. The ratio of $(H_1/D)^{\frac{1}{2}}$ indicated that gene action was of overdominance. However, graphical analysis revealed that the gene action was partial dominance. The ratio of K_d/K_r and positive F value suggested that the frequency of dominant allele was in excess than the

recessive. The ratio of $H_2/4H_1$ and H_2 values suggested the inflation of dominance to overdominance. This was in accordance with the observation by Vignesh (1997).

Heritability estimates for this character was low. Similar result was observed by Kalimuthu (1996) for this trait. The block of genes controlling this character was probably one.

Graphical analysis revealed that parents 5, 6, 4 and 3 had more number of dominant genes for the inheritance of this trait, while parent 1 had recessive genes. Parent 2 had both dominant and recessive genes. Standardised deviation graph revealed that parent 3 may be utilised for hybridisation programme as it contain dominant genes with positive effect for the character while parents 4 and 5 possessed dominant genes with negative influence.

The negative but non-significant correlation between Yr value and Wr+Vr suggested that the order of dominance could not be predicted in a precise manner. Probably it may follow ambidirectional.

5.3.2.6. Capsule length

The non significant value of $b\text{-}0/SE_{(b)}$ indicated the presence of non-allelic interaction in the diallel set of cross. The high level significance of dominance components H_1 and H_2 and h^2 and non significance of additive components D, more than unity value of $(H_1/D)^{\frac{1}{2}}$ and point of intercept of regression line below the origin in Wr, Vr graph suggested the importance of dominance gene action determining the capsule length. Similar results were also obtained by Reddy ***et al***. 1984.

The positive F value and K_d/K_r ratio indicated the presence of excess dominant alleles. The significance of H_2 value indicated the

positive and negative effect of genes which might have caused the inflation of dominance to overdominance.

The location of parents 3, 4 and 5 near the origin in Wr-Vr graph suggested that dominance is associated with capsule length. Standardised deviation graph also supported the presence of dominant genes with positive influence for this character in case of parents 3, 4, 5 and 6.

The positive and non significant correlation between Wr+Vr and Yr estimates suggested that the order of dominance was not unidirectional. Low magnitude of heritability estimates was observed for this trait.

5.3.2.7. 1000 seed weight

Non-significance of b-0/$SE_{(b)}$ indicated the presence of non allelic interaction in this set of diallel crosses. The significant additive component D and dominance components H_1, H_2 and h^2 suggested that the trait was under the influence of both additive and dominance effects (Das and Sen, 1989; Geetha and Subramanian, 1992; Sajjanar ***et al.***, 1995 and Shanti, 1997). Mean degree of dominance, K_1/K_r ratio and positive F component indicated the control of dominant allele for this trait. The asymmetrical distribution of alleles were indicated by $H_2/4H_1$ ratio.

Parent 6 alone had more number of dominant genes controlling this character as revealed by Wr, Vr graph. Parent 1 alone had dominant gene with positive effect for this trait.

Heritability was moderate for this trait (Kalimuthu, 1996). The positive and non-significant correlation between (Wr+Vr) and Yr indicated that order of dominance was ambidirectional.

5.3.2.8. Seed yield plant^{-1}

Significance of b-1/$SE_{(b)}$, significant Wr-Vr difference and significant deviation from unity of joint regression analysis suggested the presence of complementary type of non-allelic interaction. This was revealed by the upward concave curve and magnitude of Wr-Vr.

The only significant H_1 components and non-significance of the remaining genetic parameters indicated the influence of dominance gene action. (Reddy and Haripriya, 1990; Shinde ***et al.***, 1991 and Quijada and Layrisse, 1995).

The ratio of $(H_1/D)^{\frac{1}{2}}$, K_d/K_r ratio, positive F value and intercept of Wr, Vr graph pointed out the importance of dominant gene action for this trait. The $H_2/4H_1$ ratio indicated the asymmetrical distribution of genes with positive and negative alleles.

The Wr, Vr graph showed that parents 5 and 6 had more number of dominant genes governing the dominance gene action and parent 1 had more recessive genes. Parents 2, 4 and 3 had both dominant and recessive gene action. Standardised deviation graph revealed that parent 2 could be utilised for hybridisation programme since it contained dominant genes with positive influence for this character.

Heritability estimate was low for the character. (Kalimuthu, 1996). The negative but non-significant correlation between Yr value and Wr+Vr suggested that the order of dominance could not be predicted in a precise manner. It may be ambidirectional.

5.3.2.9. Oil content

Non-significance of b-0/$SE_{(b)}$ indicated the presence of non-allelic interaction in this set of diallel crosses. The high level significance of dominance components and non-significance of D components indicated the importance of dominance effect in controlling this character. (Ramakrishnan and Soundarapandian, 1990 and Shanti, 1997).

The values of dominant components (H_1 and H_2) for this character indicated that the frequencies of dominant and recessive genes were not equal it $u \neq v$. This finding was corroborated by the ratio $H_2/4H_1$ which was lower for this character than the maximum value of 0.25 which is obtained when $u=v=0.5$ ***i.e.***, $H_2=H_1$. The prevalence of dominant gene for oil content was confirmed by the values of the ratio $[(4DH_1)^{\frac{1}{2}}+F]/[(4DH_1)^{\frac{1}{2}}-F]$ which was larger than one for this character.

Parents 3 and 2 had more number of dominant genes for this character. Standardised deviation graph revealed that parent 3 could be utilised for hybridisation programme.

Negatively significant correlation between parental order of dominance and mean parental value suggested that high mean expression was associated with dominance and order of dominance was unidirectional.

5.3.3. Combining ability analysis

The genetic worth of the parent is decided on the basis of its combining ability. General combining ability of the parents is reckoned as a factor in predicting the performance of a cross

combination. It has not been fully established that there exist a relationship between ***gca*** of parents and the performance of hybrids and segregants from the cross. It is still a debatable subject among the breeders. However, a majority of the published literature lend support to the view that ***gca*** can be related with the performance of progenies of the cross predicted on the basis of combining ability effects. The results of the present investigation about combining ability of single crosses are discussed below.

5.3.3.1. Gene action

The predominance of additive gene action was noticed in the inheritance of all traits. However, the significant σ^2***gca*** and σ^2***sca*** variance for all the nine characters in the present study indicated that both additive and non-additive gene action were equally important in the inheritance of characters. Predominance of additive gene action was reported by several authors for different characters. (Das and Sen, 1989; Dharmalingam and Ramanathan, 1993; Backiyarani, 1995; Fatteh ***et al.***, 1995; Sajjanar ***et al.***, 1995 and Vignesh, 1997).

5.3.3.2. General combining ability effects

The parents ***viz.,*** 1, 2 and 3 showed positive and significant ***gca*** effects for most of the characters except for days to first flowering and height to the first productive node. This result was corroborated with the findings of Backiyarani (1995) and Vignesh (1997).

The mean performance of these parents in their combinations could not produce a high expression for seed yield indicating lack of interaction between dominant genes in the parents. But these best

combiners when combined with poor combiners produced high seed yield.

5.3.3.3. Specific combining ability effects

The specific combining ability value of any cross is helpful in predicting the performance of the hybrid far better than the ***gca*** of the parent (Jain Yin Peng and Virmani, 1990).

The combinations 1 × 4, 1 × 6, 2 × 5, 4 × 5 and 5 × 6 showed positive and significant ***sca*** effects for seed yield and other closely related yield contributing attributes such as capsule number plant^{-1}, 1000 seed weight, plant height and also for oil content except for one combination ***viz.,*** 4 × 5 which recorded negative and significant ***sca*** for oil content.

Three hybrids ***viz.,*** 1 × 4, 1 × 6 and 2 × 5 involved one good and one poor combiners as their parents hence adoption of biparental mating in these cross combinations would help to realise transgressive segregants for high seed yield and oil content. The remaining two combinations ***viz.,*** 4 × 5 and 5 × 6 were resulted from the poor combiners. Hence they are under the influence of dominance gene action. In these combinations to obtain better productive segregants the selection may be postponed to later generation.

The exploitation of both σ^2***gca*** and σ^2***sca*** variances in any breeding programme involved the risk of selection on seed yield only. Without data of the components, the ***sca*** effects are unpredictable but a complete diallel crossing scheme would help to exploit both ***gca*** and ***sca*** effects. Significant σ^2***sca*** variance is usually attributed to dominance, epistasis or reciprocal effects. It is considered unpredictable and seldom exploited. Nevertheless it is

not unusual that the best families resulting from a diallel crossing programme are in fact attributable ***sca*** effects (Smeets and Garretsen, 1986).

5.4. Component analysis and recombinative heterosis

Sesame breeding methods during the last century have been developed to take advantage of the manifestation of heterosis in varietal crosses. The method of evaluation and the choice of varieties included for evaluation of heterosis were changed along with the course of new techniques available.

The manifestation of heterosis usually depends on genetic divergence of two parental varieties. Genetic divergence among varieties usually is unknown. Genetic divergence of parental varieties is inferred from the heterotic patterns manifested in the series of variety crosses. If the heterosis manifested from the cross of two parental varieties is relatively large , it is concluded that the two parental varieties are more genetically diverse than two varieties that manifest little or no heterosis in their variety crosses. The diallel cross analysis for a fixed set of varieties provides the basis for a preliminary analysis of the heterotic pattern among variety crosses.

A complex character such as yield is the result of the combined action of a number of component traits, most of which are also of a quantitative nature. These components may strongly influence each other. This not only causes ***sca*** effects, it also causes problems in the identification of phenotypic or molecular markers for complex character. It is impossible to improve complex character (yield) significantly, unless one knows which are the most influential components traits both in the receptor and in the donor genotype.

In plant breeding, recombinative heterosis plays a role in the non-additive inheritance of complex character and in the superior

performance of complex character in hybrids. But the genetic improvement of complex character is the objective. The application of component analysis is an essential and rewarding part of the breeding procedure because it allows exploitation of recombinative heterosis and improves efficiency in the breeding for complex character (seed yield) by providing the means to predict progeny performance.

The recombinative heterosis in a complex trait (yield) is due to its multiplicative nature. If the mode of inheritance of the components is additive, the F_1 value of the hybrid cross is expected to equal the mid parental value. The additivity employs absence of heterosis in the components. Nevertheless there may be heterosis in the complex trait because the complex trait is affected by component values in a multiplicative way.

In a population of potential parents, this is most likely to be the case if two component traits are very variable and little intercorrelated neither among themselves nor with their components. Such components will have a large influence on the variability of a complex trait (Piepho, 1995).

This suggested that the 'c_i' values could be used to identify component trait for exploiting recombinative heterosis. Accordingly in the present study, number of capsules plant^{-1} had the highest 'c_i' values would therefore be identified as the most promising component for exploiting recombinative heterosis. This was also same with the case of complementary determination. These two findings stressed that the need of attention to be bestowed for the component, number of capsules plant^{-1} for exploiting recombinative heterosis in sesame improvement programme because the 'c_i' value was a measure of the contribution of the ith component to the variability of yield among the genotypes. And also pairs of

components with high 'c_i' values which are only loosely correlated, may be a promising trait for exploiting recombinative heterosis. Independence among the component trait increases the chances that in addition to multiplicative effects heterosis will occur in more than one of the components thus increasing heterosis in the complex trait (Piepho, 1995).

In the present study, the correlation between individual component and its preceding primary characters illustrated that x_2 component is closely related with the preceding primary character ***viz.,*** number of capsule plant^{-1}, seeds per capsule and seed weight. The complementary determination indicated that the two most important components were x_2 and x_4 explaining 68% and 20% respectively of the variation of y (yield). The components x_1 and x_3 had less influence explaining 13% and 0% respectively.

The component analysis in the present study provided a better basis ***viz.,*** number of capsules plant^{-1} and seed weight for parent selection and parent combinations. These basis would help in the pursuit of recombinative heterosis.

The recombinative heterosis is the phenomenon that the progeny value of a complex character exceeds the mid parental value as a result of the multiplicative relationship between the complex character and its component traits. Recombinative heterosis was noticed in the combinations 1 × 3, 1 × 5, 1 × 6, 2 × 3, 2 × 4, 2 × 5, 2 × 6, 3 × 5, 3 × 6 and 5 × 6. This predicted progeny value of any component is assumed to inherit additively. Hence the progenies from the above mentioned crosses may inherit the high productivity since they are under the influence of fixable additive gene effects. The other combinations ***viz.,*** 1 × 4, 3 × 4, 4 × 5 and 4 × 6 had high seed yield. This heterotic effect was predominantly

due to the non-additive gene action. Earlier selection in these combinations may mislead.

5.4.1. The effect of multiplicative characters of heterosis

Many characters of agronomic interest (seed yield) are the product of sub-characters (components). Williams (1959) proposed that heterosis for a complex trait like yield is simply the consequence of multiplicative relationships at the phenotypic level between component characters. Williams (1959, 1960) discounted any genetic explanation for yield heterosis. Geiger and Wahle (1978) suggested an additive partitioning of the heterosis of a complex trait into (i) multiplicative combination of component heterosis and (ii) multiplicative interaction between complementary component differences in the parent. Schnell and Cockerham (1992) pointed out that multiplication effects between component traits, each having little heterosis, can produce an amount of heterosis in complex trait.

In the present study two cross combination ***viz.,*** 1 × 4 and 1 × 6 had showed significant differences for yield components existed between parents of each cross (Table 7). The estimates of the hybrid factor (HF) were greater for the complex character, seed yield (HF = 2.66 and 2.02). The estimates of HF for the subcharacters were considerably smaller.(Table 19).

Multiplication factors (MF) contributed most to the hybrid factor of the complex trait, seed yield and this was even more pronounced when partitioning the later into three sub-characters.

A factorisation of hybrid factor of a complex character was derived in terms of the hybrid factor of its sub-character and a multiplication factor (Fig. 13). This multiplicative breakdown allows an assessment of the contribution of the heterosis in each character and the multiplication effect to the heterosis of the complex trait. In

Fig. 13 a. Hybrid factor

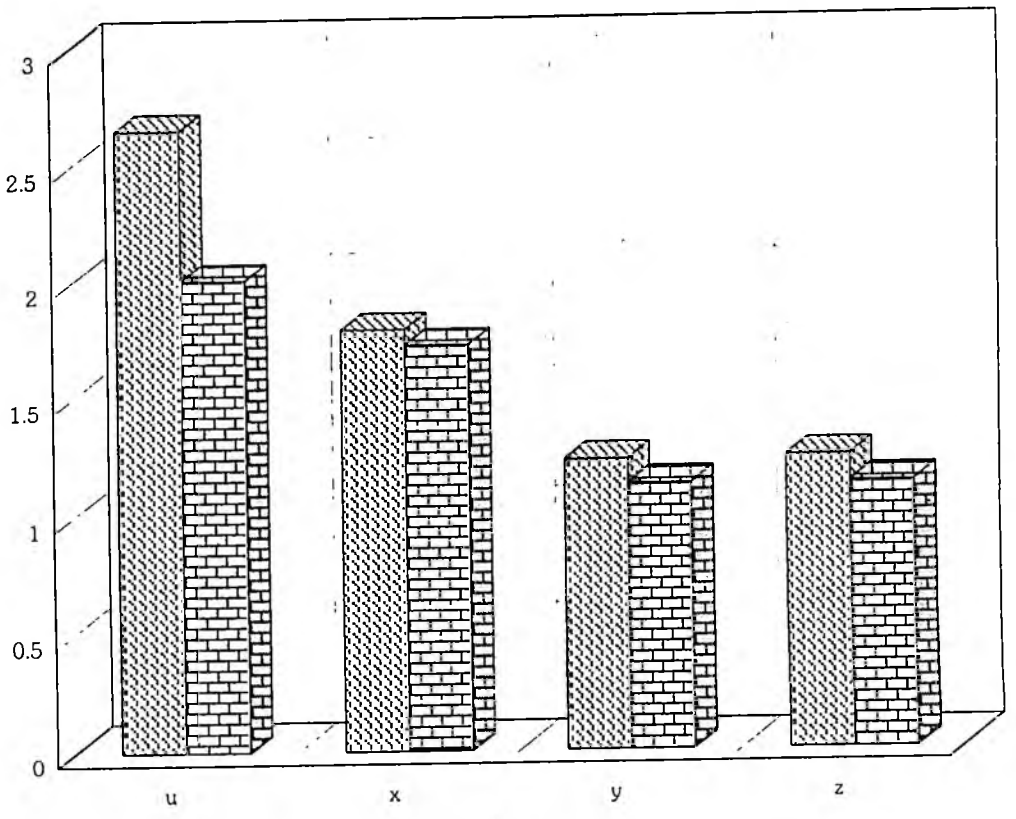
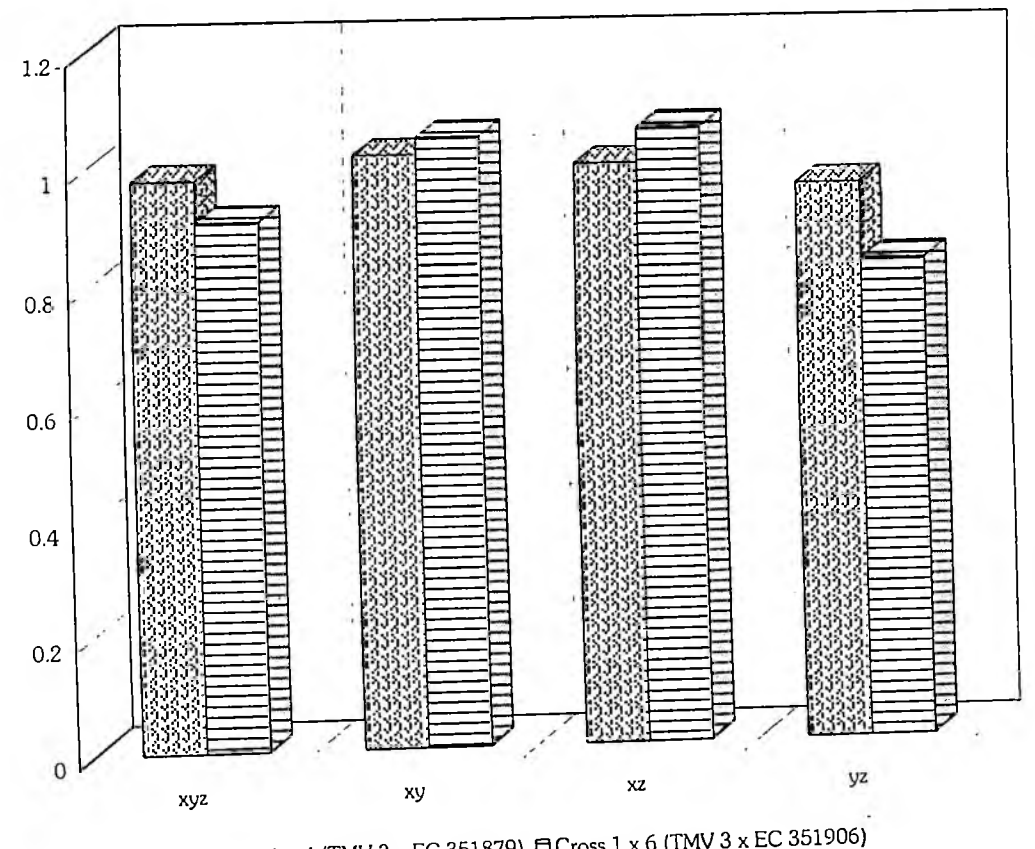


Fig. 13 b. Multiplication factor



the present study it was observed that the yield heterosis becomes simply an expression of inequality. The multiplication factors in the present study are completely determined by the parental differences for sub-characters. Thus parents of hybrids with superior heterosis could be pre-selected on the basis of their complementary for sub-characters if MF is of great importance relative to the product of HF of sub-characters and the parents show a similar performance for the complex trait. On the contrary if MF is small, it leads to the reduction in hybrid factor consequently the heterosis of complex character expressed in low magnitude.

In the present study, the number of seeds per capsule and seed weight retarded the expression of multiplicative characters. Hence for increasing the heterotic expression in sesame the parents should be divergent for seed weight and seed number.

5.5. Estimate of heterosis through Probability of Net Gain (PNG) of favourable alleles

In the present study an attempt has been made to assess the available sesame inbred cultivar as donors of alleles for enhancing the seed yields of parents of most outstanding single cross hybrids.

Four statistics were estimated for each hybrid and donor inbred combinations ***viz.,*** (i) a prediction was made for three way hybrid mean using the formula developed by Ali and Knapp (1996).

(ii) The relative number of favourable alleles present in a donor was estimated (Table 20) using the estimators described by Dudley (1984, 1987). Dudley (1987) proposed using one of the four μ_G estimators for each hybrid and donor inbred line combinations.

(iii) Net merit of a donor inbred line (N_1 or N_2) as the difference between the number of favourable alleles which could be gained and the number of favourable alleles which could be lost (μ_D or

μ_F) by using a donor to improve the parents of a single cross hybrid where μ_D is the number of class D alleles and μ_F is the number of class F alleles. Class D loci are fixed for favourable alleles in P_1 and unfavourable alleles in P_2 and P_D whereas class F loci are fixed for favourable alleles in P_2 and unfavourable alleles in P_1 and P_D. N_1 and N_2 were estimated as per Bernardo (1990).

(iv) The probability of net gain of favourable alleles (PNG_1 or PNG_2) from a donor inbred line as $[\mu_G/(\mu_G+\mu_D)]$ when a new inbred line is to be developed from $P_1 \times P_D$, and $[\mu_G/(\mu_G+\mu_F)]$ when a new inbred line is to be developed from $P_2 \times P_D$ (Metz, 1994).

The primary aim of the present study was to judge the donors for the single cross hybrids among the six parents. The predicted three way hybrid means were high for (4 × 6)1 combination. Even though the single cross hybrid 4 × 6 combination registered poor yield, its combinations with parent 1 has enhanced its performance to superior level. This might be due to the increase in number of favourable alleles which might have come from parent 1. The same was confirmed by N_1 and N_2 statistics. This was followed by the hybrids (1 × 2)4, (1 × 2)6, (1 × 3)4, (1 × 3)6, (1 × 5)4, (1 × 5)6 and (5 × 6)1. In all the above combinations either 1 or 4 or 6 was one of the parents. The general indication was that these parents had more favourable alleles for seed yield. Wherever the parents 1, 4 or 6 were involved as donor parents in any high yielding combinations (for example 1 × 4, 1 × 5, and 1 × 6) the enhancement for seed yield through predicted three way cross was apparent.

When developing a new female inbred line for $P_1 \times P_2$, the goal is to select donor inbred lines with a maximum number of favourable alleles which are absent in P_1 and P_2 and a minimum number of unfavourable alleles which are absent in P_1 and fixed in

P_2 (Dudley, 1984, 1987; Gerloff and Smith, 1988a, 1988b; Bernardo, 1990 and Metz, 1994.)

The estimates of PNG_1 and PNG_2 indicated that 1 × 4, 2 × 6, 3 × 6, 5 × 4, 5 × 6, 5 × 1, 4 × 6, 4 × 1, 6 × 1 and 5 × 1 were the best cross combinations for developing female inbred cultivar lines.

5.6. Best Linear Unbiased Prediction (BLUP)

Plant breeders historically have faced the problem of parental selection in order to obtain hybrid population with high expected mean performance and genetic variation. Identification of cross combinations which meet the above criteria results in higher probabilities of selecting progenies with sufficient genetic superiority to warrant potential cultivar release. Typically the mean of cross combinations is predicted by calculating mid parent values (MPV) or the mean of parental means, based on observed record of potential parents. In order to have the most confidence in these mid parent values as predictors of future progeny, it is important to obtain the most precise possible unbiased estimates of parental means.

Best linear unbiased prediction (BLUP) has been found useful for identifying superior single crosses prior to field evaluation. In the BLUP procedure the predictions are based on

(i) no genetic relationship among the parents (ii) the available performance data for crosses between parents.

One of the objectives of the present study was to identify the potential parents which are not involved in any hybrid combinations. The result of the MPV and BLUP predictions support the theoretical superiority of BLUP to MPV for identification of superior cross combinations under a wide range of circumstances. Variances of prediction errors were lower for BLUP than for MPV.

The present study indicated that using BLUP, one can increase the efficiency of identifying parental combinations with highest possibilities of producing superior lines. In the case of cross combinations 1 × 4, BLUP predicted at least 13.69 g/plant lower than MPV even though the predictive data were in the same trend in each case. These observation reflect one of the two important properties of BLUP in genetic application: (i) shrinkage of prediction towards the over all mean and (ii) the contributions of relatives to the predictions of breeding values of individuals (Panter and Allen, 1995).

Examinations of the genetic variance/covariance matrix among six parents which involved in 15 crosses revealed that parents of cross 1 × 4 share at least some of their genes with 3, 4, 5 and 6. The breeding value of 1 is affected most by 2. In the same way 1 was affected by 3, 6 and 4 (Table 23). The parent 2 tended to decrease the predicted breeding value of 1. The same principle holds for 2. These complex relationship coupled with shrinkage towards the over all mean have the net effect of decreasing the predicted value of cross 1 × 4. These principles were also demonstrated for cross 1 × 6.

The standard error (SE) of mean difference between actual and predicted means was less for BLUP than for MPV demonstrating that the variance in errors of prediction with BLUP were always less than those of MPV. These observations are in agreement with those of Hill and Rosenberger (1985) and Panter and Allen (1995).

From an applied plant breeding stand point, each of these points has very important implications. First when a breeder evaluates an individual for a quantitative trait predominantly controlled by additive genetic effects, it could be considered that common genetic portions (i.e. genes in common) of many related

individuals are being evaluated at the same time in different genetic settings. The theoretical magnitude of these genetic portions is expressed by the degree of genetic relationship existing between the individual being evaluated and its relatives. If the breeder utilizes BLUP, the estimated genetic covariances between pairs of individuals can be exploited to obtain better estimates of breeding values than are given by conventional MPV method.

Another important implication is that a breeder can expect that predictions from BLUP will be more precise than from MPV when equal amounts of information are available for potential parents. When future crosses are predicted, they are generally ranked in the order of descending priority based on the objectives of the breeding programme. The predicted yield levels are of limited importance due to the relatively large environmental effects, but the ranks are critical in order to choose the best cross combinations to make.

There is potential for the application of BLUP in several areas of plant breeding but particularly for parental selection. One possible scheme for using BLUP could be (i) predict the mean performance of progeny from all combinations of a group of potential parents, (ii) select the combinations with the highest predicted mean (iii) within the selected group make the cross combinations for which the parents are most genetically diverse (from the genetic relationship matrix).

5.7. Predication of seed yield for F_2 generation

The predicted yield of F_2 single plant displayed that the cross combinations TMV 3 × EC 351906, TMV 3 × EC 1879 and TMV 6 × SVPR 1 were superior in performance. They may throw high yielding segregants in the later generations. They are amenable

for pedigree type of breeding because the parents involved in these combinations were good general combiners.

5.8. Relation between crop yield potential and single plant yield potential

Crop yield per unit land area is the final aim of breeding programmes, but the individual plant is the basic unit of both natural and artificial selection. It is logical therefore for plant breeders to consider the interrelations between yield of single plants from genotypes. The best way to study this is to grow plants at different densities. The negative correlation between crop density and yield per plant can be used beneficially in breeding for higher yield and in the search for superior genotypes (Yan and Wallace , 1995).

One of the objectives of the present study was to identify suitable plant types for rainfed area and intercropping in sesame. Hence the plants resulted from the extreme phenotypes for number of branches plant^{-1}, number of capsules plant^{-1} and seed yield plant^{-1} were raised in different densities. The results indicated that the high yielding cross combinations ***viz.,*** TMV 3 × EC 351879 and TMV 3 × EC 351906 were highly suitable for thick density cropping as they had less number of branches plant^{-1} with more number of capsules plant^{-1} combined with high yield.

Narayanan and Narayanan (1987) and Dixit ***et al.*** 1997 reported that sesame at low density of planting produced more yield per unit area. They attributed the cause for increased yield mainly due to number of plants/unit area rather than number of branches. These results confirmed the findings of Chimanshette and Dhoble (1992) and Channabasavanna and Setty (1992).

5.9. Double cross hybrid analysis

Successful plant breeding emphasizes the need for incorporation of desirable effects of several genes into a single homogeneous not necessarily homozygous population. The genetic potential of populations for breeding purposes may be evaluated simply by observation of their performance or by analysis of their pedigree origin, and past genetic records. Intrinsic genetic properties of populations can only be evaluated through genetic designs.

The analysis of single cross hybrids or one of the forms of diallel analysis has been used to obtain information as to the relative importance of additive and dominance genetic variance. Estimates of additive and dominance variance are available from the single cross analysis, however, only with the assumption of no epistatic interactions.

A knowledge of relative importance of dominance and epistatic effects is desirable when a selected group of lines are to be tested for specific combining ability. The relative importance of dominance and epistatic effects determines how intensive the selection should be on the single cross performance. When epistatic effects contribute heavily to the non additive effects, prediction must be based on single crosses and the actual double cross performance.

For understanding the epistatic interaction involved among the parents, a double cross hybrid programme was designed with parents and 45 double cross hybrids were synthesised from 15 single cross hybrids. The information obtained from these double cross hybrids are discussed.

5.9.1. Days to first flowering

The economic importance of early sesame cultures in evaluation of sesame as a rainfed crop is doubtless and therefore the study regarding earliness in sesame is a priority and timely problem. Highly productive varieties that mature in about 60-70 days are not presently available for rainfed areas. For formulating breeding strategies to develop early maturing varieties, the knowledge about nature of gene action is of immense importance.

The 1-line general effect of parents 1, 4 and 5 were negative and significant, indicating that these lines involved only additive genetic effects and all the additive types of epistatic interactions. Hence they may be suitable as grand parents in any double cross programme for producing early hybrids.

In the evaluation of lines not only the general effects of the particular line but also the 2-line specific effect involving that line should be considered together to facilitate comparison and also to determine the relative importance of the general and specific effects in the computation of related statistics ***viz.,*** σ^2_{10}, σ^2_{01}, σ^2_{20}, σ^2_{11}, σ^2_{02} and σ^2_{30} (Ponnuswamy ***et al.***, 1974).

The negative and significant average 2-line specific interaction effects in the combinations ***viz.,*** 1 × 4 and 1 × 5 indicating that their interaction effect was due to all additive types of epistatic interaction. Therefore they would serve as grand parents in double cross hybrid programme. The significance of 2-line particular arrangements for these combinations suggested that the order effect has to be taken care while formulating breeding programmes (Ram ***et al.***, *1994* in rice and Backiyarani, 1995 in sesame).

The 3-line specific effect was found to be negative and significant for six triplets ***viz.,*** (1 × 2) 4, (1 × 3)4, (1 × 3)5, (1 × 4) 6,

(1 × 5) 6 and (2 × 5) 6 indicated that they are under the influence of additive × dominance interactions and all 3 factor or higher epistatic interaction except for all dominance types. But for combinations (1 × 3) 4 and (1 × 3) 5 the 3-line arrangement effect also was negative and significant indicating that the order effect has not shown any distinct differences in the case of these 2 triplets.

The estimate of 4-line specific effects was found to be negative and significant for 6 quadruplets ***viz.,*** (1 × 2) (3 × 4), (1 × 2) (3 × 5), (1 × 2) (4 × 6), (1 × 2) (5 × 6), (1 × 3) (5 × 6) and (3 × 4) (5 × 6) suggesting the involvement dominance × dominance interaction and all 3 factor interactions except the all additive types. The 4-line particular arrangement for the above combinations indicated that the order effect is important for producing double cross hybrids since the dominance and dominance epistasis is involved in these 6 double cross hybrids. To obtain early segregants, the selection may be postponed to later generation.

5.9.2. Plant height

Plant height is one of the most important yield contributing character since most of the area in the plants main stem is occupied by capsules. Parents 1 and 2 exhibited positive and significant general effects indicating that they may be utilised as appropriate grand parents to increase plant height in any hybrid combinations.

None of the combinations produced positive and significant 2-line 3-line specific interaction effect indicating the lack of interaction between parental genes. Only one combination (1 × 2) (4 × 6) recorded significant 4-line specific interactions effects. Non-significant estimates of 4-line arrangement effect for this cross combination indicated that a change in the parental order may effect a change in the expression of this trait.

5.9.3. Height to first productive node

The minimal distance at which the first capsule arise on the main stem may be an indication about the productivity of the sesame genotype.

The negative and significant 1-line general effect of parents 4, 5 and 6 indicated that they could be utilised as potential grand parents for developing double cross hybrid. The non significant 2-line specific interaction effect indicated the absence of interaction between dominant genes while the negative significance of 2-line arrangement effect .in cross combinations ***viz.,*** 1 × 4, 2 × 3, and 2 × 1 suggested the importance of parental order.

The 3-line specific effect was negative and significant for one cross combination ***viz.,*** (2 × 4) 5 alone showing the influence of additive × dominance interaction effect but the importance of order effect in this combinations was revealed by the non- significant of 3-line particular arrangement effect.

The predominance of dominance x dominance interaction and all 3 factor interaction of dominance was evident from the negatively significant 4-line specific interaction effect in cross combinations ***viz.,*** (1 × 2) (4 × 5), (1 × 2) (5 × 6), (1 × 3) (4 × 6), (1 × 3) (5 × 6), (2 × 3) (4 × 5), (2 × 3) (4 × 6) and (3 × 4) (5 × 6). However, particular arrangement of the above combinations indicated that only (1 × 2) (4 × 5) and (2 × 3) (4 × 6) combinations had order effects and others can produce the same effect in any form or order.

5.9.4. Number of branches plant^{-1}

Next to plant height number of branches plant^{-1} is another contributing character for seed yield in sesame. The 1-line general effects depicted that parents 1 could be an appropriate grand parent

for any double cross programme. The 2-line specific effect was not significant for any single cross combinations. The 3-line specific effect was positive and significant in cross combinations ***viz.,*** (1 × 2) 3, (1 × 2) 6 and (1 × 3) 5. But the 3-line arrangement effect was non significant suggesting that distinct differences for interaction effect exist in the parental order.

Positive and significant 4-line specific interaction effect was exhibited by three cross combinations ***viz.,*** (1 × 2) (3 × 6), (1 × 2) (4 × 6), and (1 × 3) (4 × 5). Lack of significant 4-line arrangement effect indicated that the order effect was highly important in the expression of number of branches in the above double was combinations.

5.9.5. Number of capsules plant^{-1}

Number of capsules plant^{-1} is one of the cardinal yield components in sesame.

The 1-line general effects emphasised the suitability of parents 2 and 3 as worthy grand parents in double cross hybrid combinations. The 2-line specific interaction effect was positive and significant for cross combinations 1 × 3, 2 × 3, 2 × 4, and 2 × 6 indicating the presence of additive type of epistatic interaction. Among these the 2-line arrangement effect was positive and significant for 2 × 3 and 2 × 6 combinations. Thus order effects has no significance in these particular combinations.

Positive and significant 3-line specific effect was registered by the cross combinations (1 × 2) 6, (1 × 3) 4, (1 × 3) 5, (1 × 3) 6, (1 × 4) 6, (2 × 3) 5, (2 × 4) 6 and (2 × 5) 6. Among these cross combinations (2 × 4) 6 alone showed positive and significant 3-line arrangement effect. This finding suggested that whatever may be the

parental order this combinations would produce the same effect for this character.

None of the combinations exhibited significant 4-line specific interaction effect indicating the lack of interaction between the dominant genes

5.9.6. Capsule length

The 1-line general effect assured the worthiness of parent 3 as grand parent in any hybrid combination. Like wise the positive and significant 2-line specific effect revealed the possibility of utilisation of cross combinations 1 × 3, 2 × 3, 2 × 4, and 5 × 6 as grand parents in double cross breeding programme. However the single cross parental order was important as showed by the non significant 2-line arrangement effect for the above combinations.

Lack of additive × dominance interaction and higher epistatic interaction except all dominance was revealed by the non significant 3-line specific interaction effect.

The presence of dominance × dominance and all dominance interactions were evident by the presence of positively significant 4-line specific interaction effects in 5 cross combinations (1 × 2) (3 × 4), (1 × 3) (5 × 6), (1 × 4) (5 × 6), (2 × 3) (4 × 6) and (2 × 4) (5 × 6). Except for one combination ***viz.,*** (1 × 2) (3 × 4), the parental order was important in rest of the 4 combinations.

5.9.7. 1000 seed weight

1-line general effect revealed the suitability of the parent 1 and 3 as grand parents in any hybrid combinations. 2-line specific effect was positive and significant for the cross combinations 1 × 2, 1 × 4, 1 × 6, 3 × 4 and 3 × 5. Except for combinations 1 × 2 the rest

showed non-significant 2-line arrangement effect confirming that parental order is important for the expression of this character.

The 3-line specific effect was positively significant for the cross combinations (1 × 2) 4, (1 × 2) 6 and (3 × 4) 5. The non-significance of 3-line arrangement for these cross combinations disclosed the importance of order effect in the expression of 1000 seed weight in any double cross hybrid programme. The 4-line specific effect was positive and significant in case of (1 × 2) (3 × 6) and (3 × 4) (5 × 6) cross combinations while the 4-line arrangement effect was non-significant. This suggested that changes in the parental order in these cross combinations would result in changes in the effect also.

5.9.8. Seed yield plant^{-1}

Seed yield plant^{-1} is the principle component which decide the seed yield in sesame. The 1-line general effect was positive and significant for parents ***viz.,*** 1, 2 and 3. These parents may be used as grand parents in any cross combinations for the manifestation of high seed yield in sesame.

The 2-line specific effect was positively significant in case of cross combinations 1 × 3 and 1 × 6. But the non significance of 2-line arrangement effect in these combinations indicated the importance of order effects with regard to this combination.

The 3-line specific effect was positive and significant in the cross combinations (1 × 2) 6, (1 × 3) 4, (1 × 3) 6 and (3 × 4) 5 showing the interactions of additive × dominance and all 3 factor epistatic interactions except dominance for seed yield plant^{-1} in these combinations. However the non-significance of 3-line arrangement effect revealed that the change in parental order would change the effect also.

The 4-line specific effect was significant and positive in the cross combinations (1 × 2) (3 × 6), (1 × 2) (4 × 6), (1 × 3) (4 × 5) and (2 × 3) (4 × 5). Since this effect is the result of all types of dominance interactions selections in later generations of these cross combinations would produce desirable segregants for high seed yield plant^{-1} in sesame through double cross hybrid programme. But the non-significance of 4-line arrangement effect throw the importance of parental order in these combinations.

5.9.9. Oil content

The ultimate aim of the production of high yielding sesame varieties is for the realisation of high oil concentration. In the present study only one parent (3) showed significant and positive 1-line general effect for this characters. Hence parent 3 may be utilized as a suitable grand parent in any hybrid combinations.

Lack of correspondence between dominant genes for this character was evident from the non-significant 2-line specific effect. The 3-line specific effect was positive and significant for the cross combinations ***viz.,*** (1 × 2) 5, (1 × 2) 6, (3 × 4) 5, (3 × 4) 6 and (3 × 5) 6. However, the non-significance of 3-line arrangement effect suggested the importance of parental order in these combinations.

The 4-line specific interaction effect was positive and significant in the cross combinations ***viz.,*** (1 × 2) (3 × 5), (1 × 2) (4 × 5), (1 × 2) (5 × 6), (1 × 3) (4 × 6), and (3 × 4) (5 × 6). But the 4-line arrangement effect in these combinations were non significant. Hence, it could be inferred that any form of parental order in these combinations would not result into the same effect.

5.10. Gene action

Estimates of component of genetic variance for all the nine traits revealed that dominance genetic variance and dominance epistasis were negative and hence considered equal to zero indicating the importance of additive and epistatic genetic variance (Table 55).

The magnitude of additive genetic variance was lower than the additive type of epistasis. It is attributed to the presence of linkage between loci showing additive genetic effects (Cockerham, 1956). The second important interaction was additive × dominance. In a situation where both additive and epistatic components influence the expression of earliness the pedigree type of selection has been found ineffective.

A population improvement programme which may allow the accumulation of fixable genetic effects (additive and additive × additive × additive epistasis) maintaining considerable variability and heterozygosity for exploiting non-fixable (Additive × dominance) gene- effects would prove to be the most efficient method (Ram ***et al.,*** 1994.)

5.11. Prediction of double cross hybrid

One of the contributions of genetics to agriculture experimentations has been predicting results following controlled crosses. Prediction methods have been used extensively in the study of qualitative traits. In quantitative traits parameters such as means rather than proportions of genotypes are of greater importance. Prediction of means as well as prediction of results from selection is one of the important contribution of quantitative genetics to plant breeding (Hallauer and Miranda, 1981).

Favourable epistatic combinations of genes in the cultivar genotype may be important in contributing to heterosis in the F_1 hybrids. If favourable epistatic combinations or genes become fixable in the parental lines during the selection process, the opportunity for recombination would not be present in the production of single cross hybrids. On the otherhand, because of the combination in the single crosses that would be used as parents in the production of double cross hybrids, the yields of double cross hybrids might be expected to be less than the single crosses.

One of the purposes of this study was to predict the yields of double crosses. Yield of double crosses would be difficult to estimate in any breeding programme. For if ten parents are used it would yield 630 double crosses and estimation becomes rather cumbersome and hence the need for prediction is evident. Prediction can be based on single crosses (in this case 45 single crosses) only need be estimated.

Results from the present study indicated an average yield superiority for single crosses over double crosses. On the simplest hypothesis, this relationship can be explained as a result of more complete utilization of both dominance and epistatic effects in single crosses than in double crosses (Weatherspoon, 1970).

The comparison of actual and predicted yield of double crosses indicated that prediction in the 45 double crosses exceeded the actual yield (Table 56). Epistatic effects were deducted for some of the predicted double crosses, hence the actual yields of these hybrids are expected to be less than the predicted means because of the nature of epistatic bias (Eberhart ***et al***., 1968).

The double cross hybrids ***viz.,*** (1 × 4) (3 × 6), (1 × 5) (2 × 3), (1 × 6) (2 × 3), (1 × 6) (3 × 4), (1 × 6) (4 × 5), (2 × 5) (3 × 6) and (3 × 4) (5 × 6) gave positive differences between actual and predicted yield. Most of these combinations involved the parents 1 or 2 or 3. These parents had significant 1-line general effect. Thus they proved their worthiness as grand parents for the expression of high yields in double cross combinations. Similarly the single cross combination 1 × 6 also proved its suitability as a single cross grand parent in double cross hybrid programme.

SUMMARY

CHAPTER VI

SUMMARY

The present investigation was carried out with 25 varied genotypes of sesame ***viz.,*** EC 351879, EC 351880, EC 351903, EC 351904, EC 351905, EC 351906, EC 351907, EC 351908, EC 357015, EC 357016, EC 357017, EC 357018, EC 357019, EC 357020, EC 357021, EC 357022, EC 357023, EC 357024, EC 357025, EC 357026, TMV 3, TMV 4, TMV 6, CO 1 and SVPR 1.

The study comprised of three distinct experiments ***viz.,*** (i) evaluation of genotypes for performance and their interaction effect with environment for three seasons; (ii) a 6 x 6 diallel programme with six selected parents without reciprocals to determine the combining ability, gene action, cause and effects for heterosis, prediction of single crosses through best linear unbiased prediction (BLUP), estimation of probability of net gain (PNG) of favourable alleles and prediction of performance of F_2 progenies from the performance of single cross hybrids and (iii) study of the effects of additive, dominance and epistasis effects in the possible 45 double cross combinations of six parents.

Nine yield and yield contributing characters ***viz.,*** days to first flowering, plant height, height to the first productive node, number of branches plant^{-1}, number of capsules plant^{-1}, capsule length, 1000 seed weight, seed yield plant^{-1}, and oil content were involved in the present study.

The salient findings of the present study are presented below.

6.1. Pattern analysis

1. The analysis of variance exhibited significant differences among the genotypes and the environment by interaction effect for all the nine characters studied.

2. Cluster analysis grouped 25 genotypes into three clusters. The first cluster consisted of the early maturing and mono/less branched 20 genotypes ***viz.,*** EC 351879, EC 351880, EC 351903, EC 351904, EC 351905, EC 351906, EC 351907, EC 351908, EC 357015, EC 357016, EC 357017, EC 357018, EC 357019, EC 357020, EC 357021, EC 357022, EC 357023, EC 357024, EC 357025 and EC 357026. The second cluster consisted of the medium maturing, medium branching SVPR 1 alone the third cluster consisted of the late maturing adapted cultivars ***viz.,*** TMV 3, TMV 4, TMV 6 and CO 1.

3. The genotypes of the first cluster generally had high adaptation for seasonal influence.

4. The dendrogram showed that genotypes (EC 357017, EC 357016), (EC 351905, EC 357019), (EC 357020, EC 357022), (EC 351880, EC 351907), (EC 351908, EC 357024), (EC 357023, EC 357018), (EC 351879, EC 357015), (EC 357025, EC357026) and (TMV 3, TMV 4) were similar in performance.

5. Genetical distance indicated that the early maturing mono/less branching type were genetically close. The remaining genotypes of the clusters were genetically divergent substantially.

6.2. AMMI analysis

1. The biplot of AMMI (Additive Main effects and Multiplicative Interaction effects) analysis revealed that genotypes ***viz.,*** EC 351908, EC 357016, EC 357020, EC 351905 and EC 357022 were stable across environments and less interactive.

2. The summer season (February – March) was identified as the best and least interacting environment for growing the present set of genotypes.

6.3. Diallel analysis

The genotypes differed among themselves for all the characters studied.

6.3.1. Genetical and Graphical analysis

1. Test of goodness of fit of data to the diallel analysis suggested the presence of non-allelic interaction for all the nine characters.

2. Significance D, H_1, H_2 and h^2 components indicated the importance of both additive and dominance effect for characters, days to first flowering, height to the first productive node, number of branches plant^{-1} and 1000 seed weight. The high level significance of dominance component H_1 and H_2 and h^2 non-significance of D, more than unity value of $(H_1/D)^{\frac{1}{2}}$ and point of intercept of regression line below the origin suggested the influence of dominance gene action for plant height, capsule length, yield plant^{-1} and oil content. However, for number of capsules plant^{-1}, significant D and non significant H_1, H_2 and h^2 values indicated the predominance of additive gene action.

3. The ratio H_2/H_1 was less than the theoretical expectation of 0.25 for all the characters indicating the asymmetrical distribution of positive and negative effects expressed by the parents.

4. The heritability estimate was high for days to first flowering, plant height, height to the first productive node and number of branches plant^{-1}; moderate for 1000 seed weight and less in number of capsules plant^{-1}, capsule length, yield plant^{-1} and oil content.

5. Graphical analysis revealed the presence of more number of dominant genes in parents, EC 351879 and EC 351905 for number of capsule plant^{-1} and EC 351905 and EC 351906 for yield per plant. Standardised deviation graph suggested the use of parents SVPR 1 and TMV 6 for hybridization programme for improving number of capsules plant^{-1} and seed yield plant^{-1}.

6.3.2. Combining ability analysis

1. Both σ^2 GCA and σ^2 SCA were significant for all the nine characters studied establishing the importance of both additive and non-additive gene action.

2. Parents namely TMV 3, TMV 6 and SVPR 1 were identified as the best general combiners for plant height and number of branches plant^{-1}. More number of heterotic crosses were resulted from good × poor general combiners combinations.

3. High ***sca*** effects were exhibited by the cross combinations TMV 3 × EC 351879, TMV 3 × EC 351906, TMV 6 × EC 351905, EC 351879 × EC 351905 and EC 351905 × EC 351966 for seed yield and yield contributing attributes.

6.4. Component analysis

1. Component analysis identified number of capsules plant^{-1} as the most promising component for productivity of recombinative heterosis.

2. The complementary determination also indicated that the number of capsule plant^{-1} to be the most important component character accounting for 68 per cent of the variations of the complex character seed yield.

6.5. Recombinative heterosis

1. Recombinative heterosis was noticed in the combinations TMV 3 × SVPR 1, TMV 3 × EC 351905, TMV 3 × EC 351906, TMV 6 × SVPR 1, TMV 6 × EC 351879, TMV 6 × EC 351905, SVPR 1 × EC 351905, SVPR 1 × EC 351906 and EC 351905 × EC 351906.

2. Recombinative heterosis of these hybrids were under the influence of fixable additive gene effects.

6.6. The effects of multiplicative characters of heterosis

The resulted heterosis in two crosses namely TMV 3 × EC 351879 and TMV 3 × EC 351906 had clearly indicated the multiplicative effect in determining heterosis.

6.7. Estimation of probability of net gain of favourable alleles

1. Wherever the parents TMV 3, EC 351879 or EC 351906 were involved as donor parents the enhancement for seed yield through predicted three way cross (PTC) was apparent.

2. The estimates of probability of net gain of favourable allele (PNG_1 and PNG_2) indicated that TMV 3 × EC 351879,

TMV 6 × 351906, SVPR 1 × EC 351906, EC 351905 × EC 351879, EC 351905 × EC 351906, EC 351905 × TMV 3, EC 351879 × EC 351906, EC 351879 × TMV 3, EC 351906 × TMV 3 and EC 351905 × TMV 3 were the best cross combinations for developing female inbred cultivar lines.

6.8. Best linear unbiased prediction (BLUP)

1. Best linear unbiased prediction identified genotypes TMV 3, TMV 6 and SVPR 1 with high prediction values as potential parents.

2. The cross combinations TMV 3 × TMV 6, TMV 3 × SVPR 1 and TMV 6 × SVPR 1 were identified as superior cross combinations under a wide range of circumstances.

6.9. Prediction of performance of F_2 progeny

The prediction of yield plant^{-1} of F_2 progenies displayed the superiority in performance for the cross combinations namely TMV 3 × EC 351906, TMV 3 × EC 351879 and TMV 6 × SVPR 1.

6.10. Relationship between crop yield potential and single plant yield potential

The relationship between crop yield potential and single plant yield potential revealed that the cross combinations namely TMV 3 × EC 351879 and TMV 3 × EC 351906 were highly suitable for thick density cropping.

6.11. Double cross hybrid analysis

1. The mean performance of double cross hybrids showed that hybrids ***viz.,*** (TMV 3 × EC 351879) (SVPR 1 × EC 351906), (TMV 3 × EC 351906) (EC 351879 × EC 351905), (TMV 3 × EC 351906) (TMV 6 × EC 351879), (TMV 3 × EC 351906) (TMV 6 × SVPR 1), (TMV 3 × EC 351906)

(SVPR 1 × EC 351879), (TMV 3 × EC 351905) (TMV 6 × SVPR 1), (TMV 6 × EC 351905) (SVPR 1 × EC 351906) and (SVPR 1 × EC 351879) (EC 351905 × EC 351906) exhibited their superior performance for seed yield.

2. The 1-line general effect depicted that genotypes TMV 6 and SVPR 1 were worthy grand parents for improving number of capsules plant^{-1} and seed yield and SVPR 1 for oil content. While parents EC 351879 and EC 351905 were worthy parents for days to first flowering and height to the first productive node.

3. The 2-line specific effect revealed that cross combinations namely TMV 3 × EC 351879 and TMV 3 × EC 351905 were worthy single cross grand parents for producing early maturing and four best cross combinations namely TMV 3 × SVPR 1, TMV 6 × SVPR 1, TMV 6 × EC 351879 and TMV 6 × EC 351906 were grand parents for more number of capsules plant^{-1} and TMV 3 × SVPR 1 and TMV 3 × EC 351906 for high seed yield in three way and double cross hybrids.

4. The 2-line arrangement effect revealed that parental order effect in single cross grand parents were significant for TMV 3 × SVPR 1, TMV 6 × EC 351879 for number of capsule plant^{-1} and TMV 3 × SVPR 1 and TMV 6 × EC 351906 cross combinations towards seed yield.

5. The 4-line arrangement effect revealed that parental order effect was important for the following double cross combinations (TMV 3 × TMV 6) (SVPR 1 × EC 351906), (TMV 3 × TMV 6) (EC 351879 × EC 351906), (TMV 3 × SVPR 1) (EC 351879 × EC 351905) and (TMV 6 × SVPR 1) (EC 351879 × EC 351905).

6. The estimate for components for genetic variance indicated that additive, additive × dominance and additive × additive × additive type of gene action were important in the inheritance for all the characters in the present study.

6.11.1. Double cross hybrid prediction

The prediction of performance of double cross hybrid from single cross indicated yield superiority for the following double cross hybrids ***viz.***, (TMV 3 × EC 351879) (SVPR 1 × EC 351906), (TMV 3 × EC 351905) (TMV 6 × SVPR 1), (TMV 3 × EC 351906) (TMV 6 × SVPR 1), (TMV 3 × EC 351906) (SVPR 1 × EC 351879), (TMV 3 × EC 351906) (EC 351879 × EC 351905), (TMV 6 × EC 351905) (SVPR 1 × EC 351906) and (SVPR 1 × EC 351879) (EC 351905 × EC 351906).

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* Originals not seen.

PLATES

Plate 1. Variability in capsule size and locule number through double cross

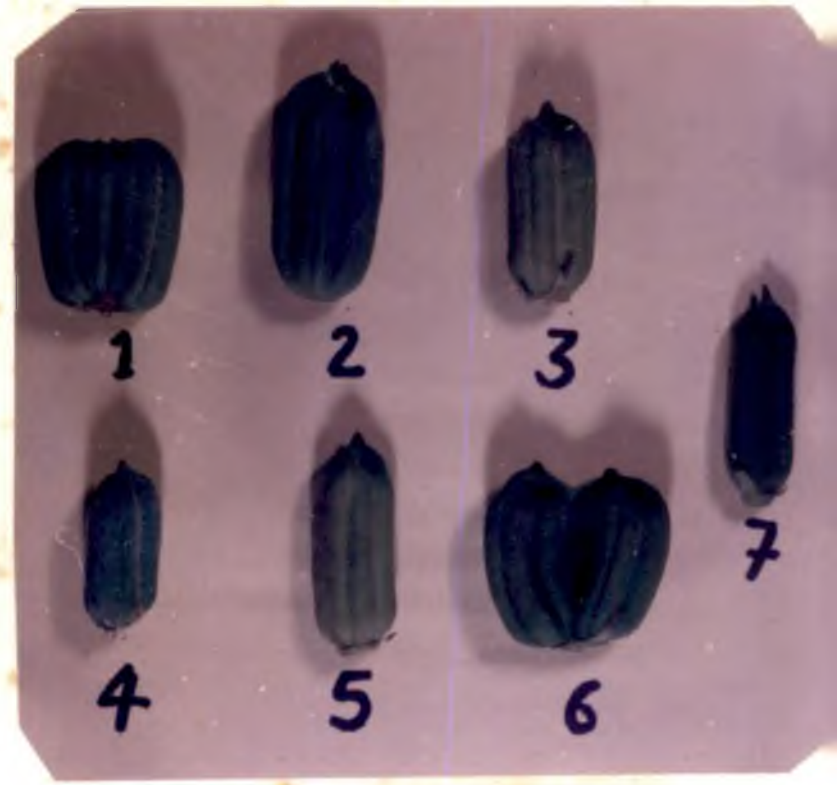

Plate 2. Best double cross hybrids based on over all performance

Plate 3. Best double cross hybrids based on more number of capsules and yield

(TMV 3 × EC 351879) (SVPR 1 × EC 351906)

(TMV 3 × EC 351906) (EC 351879 × EC 351

(TMV 3 × EC 351906) (TMV 6 × SVPR 1)