

SEED GENETICS IN RELATION TO YIELD IN SESAME
(*Sesamum indicum* L.)

VOLUME-III

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FOR DEGREE OF DOCTOR OF PHILOSOPHY (AGRICULTURE)
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DISCUSSION

5. DISCUSSION

Sesame "the Queen of oilseeds" ranks third in the edible oil production in India. Emphasis has been given since from last three decades for the improvement in sesame seed and oil production. Despite the concerted efforts the increases in sesame yield and oil production are not appreciable. This is mainly due to the lack of adapted and high yielding cultivars, poor stand establishment and susceptibility to biotic and abiotic stresses. Hence the ultimate aim of the sesame breeders is to improve agronomically superior varieties or hybrids that are more resistant or tolerant to biotic and abiotic stresses and above all for physiologically more efficient in producing increased biological yield with high harvest index to get maximum economic yield and consequently with enhanced reproductive fitness and improved local adaptation.

Search for genetic variability has been a goal in sesame breeding due to the cyclical nature of the breeding process, selection-hybridization-selection, itself requires the inflow of new genetic material. The wide adaptability complex characterized by this species has resulted in its being typified by a number of ecotypes. Thus considerable variability exist is for various plant characters. Efforts were made to evaluate the variability for yield and yield components but the variability for seed characters were so far not well studied. As the stand establishment is poor in sesame especially under stress condition, an exclusive study with ultimate emphasis to seed characters such as seed size and its components become inevitable along with yield and yield components.

Information on the nature of relative variability present for yield and seed characters, determination of heritable components of the actual variability, the kind and magnitude of correlation between different traits, causal basis of such association through path analysis, the extent of genetic divergence between the genotypes, the phenotypic stability of the genotypes and the nature of gene action on important genetic characters are the pre-requisites for planning sesame improvement through breeding.

In conventional sesame breeding programme selection of parents for hybridization is generally carried out in a single environment or season and mostly based on a single biometrical technique. Moreover the utility of the knowledge from different biometrical techniques often used in the evaluation of germplasm and selection of characters and parents have not been demonstrated in actual selection of parents for hybridization with a set of data studied over seasons.

To avoid such anomalies, the present well planned innovative investigation was carried out over seasons for sixteen characters with sixty genotypes of different eco-geographic origin and eighty one hybrids of sesame. Studies on gene action and effect through generation mean and variance analysis was carried out in single season. To have in depth knowledge on the characters' contribution towards seed size (weight of 1000 seeds), the seed size, yield and yield components were considered as independent variables considering weight of 1000 seeds as dependent variable besides seed yield.

In order to assess the relative role of crop duration and stature to the total dry matter production, yield and seed size, days to maturity, plant height and number of branches were taken into consideration. To estimate the reproductive efficiency number of flowers (reproductive potentiality) and number of capsules (reproductive capacity) were observed. Seed number per capsule and weight of 1000 seeds which play important roles in determining the seed yield were recorded. To use seed size and/or its component characters as a morphological marker for seed yield, the relative variability, reliability (heritability) and potentiality (combining ability and gene action) of the seed size and its component characters viz., volume of capsules, number of seeds per capsule, seed length, seed breadth, 1000 seed volume and seed density were studied. Oil content of the genotypes was also estimated as this is the end use product for consumption. Harvest index was worked out to find out the partitioning efficiency.

The results of the studies conducted on variability, correlation, path analysis, diversity, stability, combining ability, heterosis nature of gene action and cytoplasmic maternal effects are discussed below.

5.1. MEAN PERFORMANCE

In sesamum, there is an immediate need to identify better plant types with good yielding potential to serve for direct introduction as varieties and also as parents in hybridization programme as potential donors.

Among the sixty genotypes studied over three different seasons and pooled over three seasons, seven genotypes in SI viz., G3, G6, G11, G15, G31, G40 and G45; eighteen genotypes in SII viz., G7, G10, G11, G12, G13, G14, G16, G18, G26, G27, G28, G30, G32, G34, G39, G44, G50 and G58; twenty one genotypes in SIII viz., G7, G12, G16, G20, G22, G26, G27, G30, G31, G32, G34, G35, G36, G37, G38, G39, G44, G50, G57, G58 and G60 and fifteen genotypes in the pooled analysis viz., G7, G11, G12, G16, G20, G26, G27, G30, G31, G32, G34, G38, G39, G44 and G60 recorded a mean seed yield of above six grams.

None of the genotypes consistently showed higher mean seed yield (above 6g) in all the three seasons. Hence the genotypes which consistently performed with higher mean seed yield in any of the two out of the three seasons evaluated could be suggested for selection as parents for yield improvement. Accordingly, the following genotypes, viz., G7, G11, G12, G16, G26, G27, G30, G31, G32, G34, G39, G44, G50 and G58 were identified. The potentiality of these fourteen genotypes to be used as donors for the components of seed size, yield and yield component is furnished below.

Characters	Genotypes
Height of the plant maturity	G11, G12, G26, G27, G30, G31, G32, G34, G44, G58.
Number of branches	G30, G31, G58
Number of flowers	G26, G31, G32, G44.
Number of capsules	G7, G16, G26, G31, G32, G44.
Volume of capsules	G39, G44.
Length of seeds	G16.
Breadth of seeds	G44.
Density of seeds	G12, G30, G34, G44.
Oil content	G7.
Total dry matter production	G11, G16, G26, G27, G30, G31, G32.
Harvest index	G11, G12, G34, G44, G50, G58.

For eleven out of fifteen traits, the genotypes which were identified as donars for seed yield can also be used donors as they showed higher mean values than the grand mean consistently in all the three seasons.

5.2. VARIABILITY STUDIES

Effectiveness in breeding depends upon three main factors viz., (i) extent of genetic variation available, (ii) heritability of the variation and (iii) intensity of selection pressure that can be applied. As most of the characters of economic importance and related characters which influence the performance of the economic character in a given set of environment are highly influenced by the environmental conditions, the heritable (genotypic) variation is usually masked by non-heritable (environmental) variation and thereby creates difficulty in exercising selection. Hence it becomes necessary to partition the overall variability into heritable and non-heritable components to enable the breeders to plan for proper breeding programme.

The present investigation was, therefore, undertaken to assess the phenotypic variability for seed size, yield and their components and to determine their heritable components with the help of certain genetic parameters, such as genotypic variance, genotypic coefficient of variation, heritability estimates and genetic advance. As these genetic parameters can also be biased due to seasonal influence on the expression of characters under inquiry, they were studied over three seasons and the results are discussed along with the pooled analysis.

The analysis of variance for individual seasons and pooled over seasons indicated significant differences among the sixty genotypes for all the sixteen characters studied excepting for plant

plant height in the SI and pooled analysis. This explained that the genotypes selected for the present study are distinctly different.

The phenotypic variance were higher than the genotypic variance in almost all characters. However, the major part of the variances was contributed by the genotypic component and the environmental component was less. In general, all the characters studied had a higher PCV than GCV. But GCV followed closely with PCV.

Genotypic variance was higher for plant height, number of flowers, number of capsules, total dry matter and harvest index whereas GCV was higher for number of flowers, number of capsules, seed yield, total dry matter and harvest index. Due to the high GCV estimates for these characters observed in the genotypes studied, there is a scope for improvement by selection.

In sesame, El-Gizouli Osman and Osman Khidir (1974a), Govindadas (1975), Gupta (1975), Reddy and Reddy (1976), Shukla and Verma (1976), Murugesan et al., (1979a), Thngavelu (1980), Janardhanam et al. (1981), Chavan and Chopde (1982), Thangavelu and Rajasekaran (1982), Seenaiiah and Reddy (1984), Chandramony and Nayar (1985), Kandaswamy (1985) and Godawat and Gupta (1986) observed higher GCV for number of capsules per plant. The findings of these authors and that from Govinda Rasu (1982), Shrivasa and Kaushal (1982), Pathak and Dixit, (1986) and Reddy (1986) revealed the presence of higher

GCV for seed yield. On the contrary Desai et al., (1982), Pathak and Dixit (1986) observed low GCV for number of capsules per plant while Chavan and Chopde (1982), Desai et al. (1982) reported low GCV for seed yield.

Days to maturity followed by number of seeds per capsule, seed length, seed breadth, oil content and 1000 seed weight showed low GCV and PCV. Low variability estimates were also recorded by Gupta (1975), Thangavelu (1980), Desai et al. (1982) Govinda Rasu (1982), Thangavelu and Rajasekaran (1982), Godawat and Gupta (1986), Pathak and Dixit (1986) and Reddy (1986) for days to maturity; Janardhanam et al. (1981), Chavan and Chopde (1982) and Pathak and Dixit (1986) for number of seeds per capsule; Reddy and Reddy (1976), Janardhanam et al. (1981), Chavan and Chopde (1982), Desai et al. (1982) and Shrivastava and Kaushal (1982) for 1000 seed weight and El-Gizouli Osman and Osman Khidir (1974a), Desai et al. (1982), Thangavelu and Rajasekaran (1982), and Reddy (1986) for oil content.

The genetic coefficient of variation alone is not sufficient for determination of the amount of heritable variation (Swarup and Chaugale, 1962). Burton (1952) and Johnson et al. (1955a) reported that GCV simply measures the extent of genetic variability present in a character but does not assess the amount of genetic variation which is heritable and also emphasized that GCV should be considered in conjunction with heritability and genetic advance while assessing the effect of phenotypic selection.

5.3. HERITABILITY AND GENETIC ADVANCE

Heritability is the extent of transmission of the character from generation to generation. The magnitude of heritability is influenced by the variability existing between the populations and the extent to which a particular character is influenced by the prevailing environmental conditions. Thus the observed variability for different characters in a crop is partly heritable (due to genetic constitution) and partly non-heritable (due to environment). So broad sense heritability was calculated in order to estimate the proportion of total variance attributed to genotypic differences.

In the present investigation the estimates obtained were ranging from 5.86 per cent to 99.28 per cent. El-Gizouli Osman and Osman Khidir (1974a) stated that the estimates of heritability for different traits obtained in a particular study will be valid under the conditions of that experiment only. But the effectiveness of selection can be enhanced if the character is highly heritable.

High heritability values, 30 to 60 per cent and above (Robinson, 1966) were consistently observed for all the characters studied excepting plant height which exhibited low (5-10 per cent; Robinson, 1966) to high.

High heritability values recorded for days to maturity in the present study is in confirmity with the reports of El-Gizouli

Osman and Osman Khidir (1974a), Gupta (1975), Thangavelu (1980), Paramasivam and Prasad (1981), Govinda Rasu (1982), Shrivasa and Kaushal (1982), Thangavelu and Rajasekaran (1982), Godawat and Gupta (1986), Pathak and Dixit (1986) and Reddy (1986). However, Desai *et al.* (1982) recorded only low heritability for this trait.

The high heritability estimates observed for plant height in the present inquiry is in confirmity with El-Gizouli Osman and Osman Khidir (1974a), Gupta (1975), Reddy and Reddy (1976), Murugesan *et al.* (1979a), Thangavelu (1980), Rai *et al.* (1981), Desai *et al.* (1982), Thanagavelu and Rajasekaran (1982), Govinda Rasu (1982), Shrivasa and Kaushal (1982), Seenaiiah and Reddy (1984), Kandaswamy (1985), Godawat and Gupta (1986), PathaK and Dixit (1986) and Reddy (1986). The low heritability estimates registered for this trait is also in confirmity with Chandramony and Nayar (1985). As this trait showed high and low heritability in different seasons, it cannot be improved by direct selection.

High heritability estimates for number of branches found in the present investigation is in agreement with El-Gizouli Osman and Osman Khidir (1974a), for number of primary branches, Govindadas (1975) for both primary and secondary branches, Shukla and Verma (1976) for primary branches, Murugesan *et al.* (1979a) for primary and secondary branches, Paramasivam and Prasad (1981) Chavan and Chopde (1982) for primary branches, Govinda Rasu (1982) and Reddy

Reddy (1982) for primary and secondary branches on the contrary, Shukla and Verma, (1976) for secondary branches and Chandramony and Nayar (1985) for primary branches recorded low heritability estimates.

Naphade and Kolte (1973), El-Gizouli Osman and Osman Khidir (1974a), Govinda Das (1975), Gupta (1975), Reddy and Reddy (1976), Murugesan et al. (1979a), Thangavelu (1980), Janardhanam et al. (1981), Paramasivam and Prasad (1981), Chavan and Chopde (1982), Thangavelu and Rajasekaran (1982), Seenaiiah and Reddy (1984), Kandaswamy (1985), Godawat and Gupta (1986) and Pathak and Dixit (1986) recorded high heritability estimates for number of capsules per plant which is again in confirmity with the present study. However, medium heritability estimate was registered by Shukla and Verma (1976) and low heritability estimates were reported by Desai et al. (1982) and Chandramony and Nayar (1985).

High heritability estimates were observed in this study for capsule volume. High heritability estimates were recorded by E-El-Gizouli Osman and Osman Khidir (1974a) for capsule length, Govinda Das (1975) for capsule breadth, Gupta (1975), Reddy and Reddy (1976), Murugesan et al. (1979a), Janandhanam et al. (1981), Paramasivam and Prasad (1981), Govinda Rasu (1982), Gupta and Chopra (1984), Kandaswamy (1985) and Reddy (1986) for capsule length. However, medium heritability

estimates were also reported by Govindadas (1975), Chavan and Chopde (1982), Desai et al. (1982), Pathak and Dixit (1986) for capsule length and breadth.

Similar to the present study, high heritability estimates for number of seeds per capsule were reported by El-Gizouli Osman and Osman Khidir (1974a), Govinda das (1975), Reddy and Reddy (1976), Thangavelu and Rajasekaran (1982), Kandaswamy (1985), Pathak and Dixit (1986) and Reddy (1986). However Janardhanam et al. (1981), Chavan and Chopde (1982) obtained medium heritability and Chandramony and Nayar (1985) registered low heritability estimate for this character.

High heritability estimates reported for 1000 seed weight in this inquiry is in agreement with EL-Gizouli Osman and Osman Khidir (1974a), Govinda das (1975), Reddy and Reddy (1976), Murugesan et al. (1979a), Thnagavelu (1980), Janardhanam et al. (1981), Desai et al. (1982), Thangavelu and Rajasekaran (1982), Govinda Rasu (1982), Shrivasa and Kaushal (1982), Pathak and Dixit (1986) and Reddy (1986). However, Chavan and Chopde (1982) and Chandramony and Nayar (1985) reported low heritability estimates for this trait.

Desai et al. (1982), Thangavelu and Rajasekaran (1982), Reddy (1986) reported high heritability estimates for oil content which is in confirmity with the present study. However, El-Gizouli Osman and Osman Khidir (1974a), Seenaiiah and Reddy (1984) registered medium

heritability estimates and Chandrmony and Nayar (1985) observed low heritability estimate for this trait.

High heritability estimates estimated in this present investigation for seed yield per plant is in confirmity with El-Gizouli Osman and Osman Khidir (1974a), Govinda das (1975), Gupta (1975), Reddy and Reddy (1976), Shukla and Verma (1976), Murugesan et al. (1979a), Thangavelu (1980), Janardhanam et al. (1981), Paramasivam and Prasad (1981), Desai et al. (1982), Govinda Rasu (1982), Shrives and Kaushal (1982), Godawat and Gupta (1986), Pathak and Dixit (1986) and Reddy (1986). However, medium and low heritability estimates for this trait were reported by Chavan and Chopde (1982) and Chandramony and Nayar (1985) respectively.

The high heritability estimates recorded for days to maturity, number of branches, number of flowers, number of capsules, capsule volume, number of seeds per capsule, seed length, seed breadth, 1000 seed weight, 1000 seed volume, seed density, oil content, seed yield per plant, total dry matter production and harvest index suggest that quick improvement can be expected in a short time for these characters in the breeding programme as the genetic variance is mostly due to additive gene action. The low values of heritability indicate greater environmental influence on the expression of the character and therefore response for improvement of such trait i.e. plant height at maturity is very much restricted.

Genetic advance was calculated to predict the net effect of selection, as the heritability estimates alone do not provide sufficient information for the genetic improvement that would result from the selection

of best individuals. Ramanujam and Tirumalachari (1967) opined that broad sense heritability includes both additive and epistasis gene effects and hence such heritability estimates would be reliable, if they go hand on hand with high genetic advance.

The genetic advance as per cent of mean in the present study was found to be high (above 30 per cent) for seed yield, number of capsules, 1000 seed volume, harvest index, number of flowers, total dry matter, production, seed density and capsule volume.

High heritability coupled with high genetic advance as per cent of mean was observed for number of flowers, number of capsules, capsule volume, volume of 1000 seeds, seed density seed yield, total dry matter production and harvest index.

Earlier studies by Naphade and Kolte (1973), El-Gizouli Osman and Osman Khidir (1974a), Govinda das (1975), Reddy and Reddy (1976), Murugesan et al. (1979a), Thangavelu (1980), Janardhanam et al. (1981), Paramasivam and Prasad (1981), Chavan and Chopde (1982), Thangavelu and Rajasekaran (1982), Seenaiiah and Reddy (1984), Kandaswamy (1985) and Godawat and Gupta (1986) also indicated high heritability coupled with high genetic advance as per cent of mean for number of capsules per plant. Conversely Desai et al. (1982) reported low heritability with low genetic advance as per cent of mean for this trait. On the other hand, medium heritability with high genetic advance as per cent of mean was reported by Shukla and Verma (1976) and low heritability with high genetic advance as percent of mean was observed by Chandramony and

Nayar (1985). High heritability with medium genetic advance was also reported by Pathak and Dixit (1986) for this trait.

High heritability coupled with high genetic advance as percent of mean was observed in the present study for capsule volume. Reports of El-Gizouli Osman and Osman Khidir (1974a), Paramasivam and Prasad (1981) and Kandaswamy (1985) indicated high heritability coupled with high genetic advance as percent of mean for capsule length. On the other-hand, Gupta (1975), Reddy and Reddy (1976), Murugesan et al. (1979a) Govinda Rasu (1982), and Reddy (1986) reported high heritability coupled with medium genetic advance as percent of mean for capsule length. High heritability and low genetic advance as percent of mean was also reported by Janardhanam et al. (1981) for this trait. For capsule breadth, Govindadas (1975) observed high heritability with low genetic advance as percent of mean.

For seed yield, El-Gizouli Osman and Osman Khidir (1974a), Govindadas (1975), Gupta (1975), Reddy and Reddy (1976), Murugesan et al. (1979a), Thangavelu (1980), Janardhanam et al. (1981), Paramasivam and Prasad (1981), Govinda Rasu (1982), Shrivasa and Kaushal (1982), Godawat and Gupta (1986) and Pathak and Dixit (1986) reported high heritability and high genetic advance as per cent of mean. However, Desai et al. (1982) and Reddy (1986) obtained high heritability coupled with medium genetic advance as percent of mean for this trait.

High heritability coupled with medium genetic advance as percent of mean was observed for number of branches and 1000 seed weight.

High heritability coupled with medium genetic advance as percent of mean recorded in the present study for number of branches is in corroboration with Chavan and Chopde (1982) for number of primary branches. But El-Gizouli Osman and Osman Khidir (1974a), Govindadas (1975), Shukla and Verma (1976), Murugesan *et al.* (1979a), Paramasivam and Prasad (1981), Govinda Rasu (1982) and Reddy (1986) observed high heritability and high genetic advance as per cent of mean for number of primary branches. Similarly Govindadas (1975), Murugesan *et al.* (1979a), Govinda Rasu (1982) and Reddy (1986) reported high heritability coupled with high genetic advance as per cent of mean for number of secondary branches.

For thousand seed weight, reports from Govindadas (1975), Murugesan *et al.* (1979a), Thangavelu (1980), Janardhanam *et al.* (1981), Govinda Rasu (1982), Shrivastava and Kaushal (1982) and Thangavelu and Rajasekaran (1982) confirmed the present result of high heritability coupled with medium genetic advance as percent of mean for this trait. On the contrary high heritability coupled with high genetic advance as percent of mean for this character was also reported by El-Gizouli Osman and Osman Khidir (1974a), Pathak and Dixit (1986) and Reddy (1986). High heritability and low genetic advance as percent of mean was also reported by Desai *et al.* (1982).

High heritability coupled with low genetic advance as percent of mean was observed for days to maturity, number of seeds per capsule, seed length, seed breadth and oil content. This is in confirmity with Godawat and Gupta (1986) for days to maturity, Pathak and Dixit

(1986) for days to maturity and number of seeds per capsule. But El-Gizouli Osman and Osman Khidir (1974a) days and number of seed capsule. Thangavelu (1980), Paramasivam and Prasad (1981), Govinda Rasu (1982), Shrivasa and Kausal (1982), Thangavelu and Rajasekaran (1982) and Reddy (1986) reported high heritability coupled with high to medium genetic advance as percent of mean for days to maturity. Similarly high heritability with high to medium genetic advance as percent of mean was observed for number of seeds per capsule by El-Gizouli Osman and Osman Khidir (1974a), Govindadas (1975), Reddy and Reddy (1976), Thangavelu and Rajasekaran (1982), Kandaswamy (1985) and Reddy (1986).

On the contrary to the present study, Thangavelu and Rajasekaran (1982) reported high heritability with medium genetic advance as percent of mean for oil content. On the otherhand, high to medium heritability with negligible genetic advance as percent of mean was obtained by El-Gizouli Osman and Osman Khidir (1974a), Desai et al. (1982) and Reddy (1986). Seenaiah and Reddy (1984) found medium heritability and medium genetic advance as percent of mean for this trait.

Low heritability coupled with low genetic advance as percent of mean was observed for plant height. But most of the reports revealed high heritability with high genetic advance as percent of mean for this trait. El-Gizouli Osman and Osman Khidir (1974a), Govinddas (1975), Gupta (1975), Shukla and Verma (1976), Murugesan et al. (1979a), Thangavelu (1980), Shrivasa and Kaushal (1982), Thangavelu and Rajasekaran (1982) reported high heritability coupled with high genetic advance for plant height. On the otherhand, low heritability with low genetic advance as

per cent of mean was reported by Paramasivam and Prasad (1981). Reddy and Reddy (1976), Janardhanam et al. (1981), Rai et al. (1981), Chavan and Chopde (1982), Desai et al. (1982), Govinda Rasu (1982), Seenaiiah and Reddy (1984), Kandaswamy (1985), Godawat and Gupta (1986), Pathak and Dixit (1986) and Reddy (1986) observed high heritability with medium genetic advance as per cent of mean, medium heritability with low genetic advance as per cent of mean and medium heritability with high genetic advance as per cent of mean for this trait.

High heritability estimates coupled with high genetic advance as per cent of mean observed for number of flowers, number of capsules, capsule volume, volume of 1000 seeds, seed density, seed yield, total dry matter production and harvest index indicated that these traits are mostly governed by predominance of additive gene action (Johnson et al. 1955a).

High heritability with medium genetic advance as per cent of mean found out for number of branches and 1000 seed weight and high heritability coupled with low genetic advance as per cent of mean observed for days to maturity, number of seeds per capsule, seed length, seed breadth and oil content suggested that high heritability alone does not signify an increased genetic advance (Choudhary et al., 1977).

Low heritability coupled with low genetic advance as per cent of mean observed for plant height indicated that the scope for improving this trait through selection is very much limited. This limita-

tion may be due to the non-additive gene action for this trait (Johnson et al., 1955a; Panse, 1957).

On the otherhand, high heritability with medium and low genetic advance indicated that the traits are equally controlled by both additive and epistasis gene effects. So immediate selection is not possible for these traits.

From the foregoing discussions, it is inferred that in sesame, yield improvement could well be made through efficient selection for number of flowers, number of capsules, total dry matter production and harvest index as they showed high genotypic variance, GCV, heritability and Genetic advance as per cent of mean.

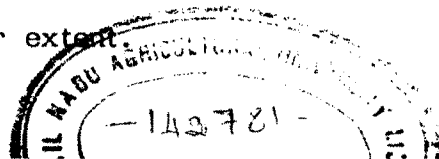
5.4. CORRELATION STUDIES

Seed yield is the foremost important attribute but a highly complex character influenced by a large number of component traits. Hence information on the strength and direction of association of these component characters with seed yield and also among themselves will be very useful in formulating an effective breeding programme for improvement in seed yield in a short time (Breese and Haywards, 1972). As seed size has defined effect on seed yield, it is also equally important study of the nature of association of the seed characters and seed yield. While studying correlations it is of prime importance to recognize the nature and size of the populatioin under study, in as much as the magnitude of the correlation coefficient can often be influenced by the choice of individuals upon which the observations are made (Dewey and Lu, 1959). Hence a large

number of diverse homozygous genotypes collected from different continents/ecogeographic regions were studied for sixteen characters. Clark (1987) has theoretically shown that genetic correlations do depend upon the environment, and that genotype-by-environment interactions affect genetic correlations. Hence, the correlations among these sixteen characters were studied over seasons.

In the present investigation, the genotypic correlation coefficients were mostly slightly higher than the phenotypic correlation coefficients, especially in almost all cases wherever the correlation coefficients were significant. A similar trend has been observed in sesame by Dixit (1975), Sanjeevaiah and Joshi (1975), Rathinaswamy (1980), Govinda Rasu (1982) and Reddy (1986). This may be due to the effect of environment in modifying the total expression of the genotypes, thus altering the phenotypic expression (Nandpuri et al., 1973).

The character association analysis in the present study revealed that the traits viz., number of flowers, number of capsules, weight of 1000 seeds and harvest index were positively and significantly associated with seed yield consistently in all the three seasons and pooled analysis. This indicated the high reliability of these traits in selection programme. The of these traits in selection programme. The traits viz., plant height at maturity, number of branches, seed density and total dry matter production were positively and significantly associated with seed yield mostly (three analyses) indicating the seasonal influence on character association. Days to maturity and length of seeds were positively and significantly associated with seed yield in only one season showing the vulnerability of association to seasonal changes to a greater extent.



Earlier studies by Sikka and Gupta (1949), Krishnamurthy (1960), Krishnamurthy et al. (1964), Muhammed and Dorairaj (1964), Dabral (1967), Osman Khidir and El-Gizouli Osman (1970). Phadnis et al. (1970), El-Gizouli Osman and Osman Khidir (1974b), Kaushal et al. (1974), Delgado and Yermanos (1975), Dixit (1975), Govindadas (1975), Solazer and Onora (1975), Gupta (1976), Shukla and Verma (1976), Sorafi (1976), Choudhary et al. (1977), Kaushal (1977), Murugesan et al. (1979b), Rao and Chary (1979), Paramasivam and Prasad (1980), Rathnaswamy (1980), Yadava et al. (1980), Chavan and Chopde (1981), Vinayak et al. (1981), Desai et al. (1982), Djigma (1983), Gupta and Labana (1983), Ibrahim et al. (1983), Thangavelu and Rajasekaran (1983), Reddy et al. (1984), Seenaiah and Reddy (1984), Sharma and Chavan (1984), Godawat and Gupta (1986), Krishnadoss and Kadambavanasundaram (1986), Bhele et al. (1987) and John Joel (1987) reported positive significant correlation between number of capsules per plant and seed yield. The observed positive relationship between 1000 seed weight and seed yield is in agreement with the reports of Muhammed and Dorairaj (1964), El Nadi et al. (1974), Delgado and Yermanos (1975), Salazar and Ohoro (1975), Kaushal et al. (1977), Rao and Chary (1979), Thangavelu (1980), Yadava et al. (1980), Desai et al. (1982), Govinda Rasu (1982), Djigma et al. (1983), Thangavelu and Rajasekaran (1983a), Sharma and Chavan (1984); Bhele et al. (1987), John Joel (1987) and Omar Sheik (1989). However, it was in disagreement with El-Gizouli Osman and Osman Khidir (1974b), Kaushal et al. (1974) and Ibrahim et al. (1983).

The positive correlation found in the present study between plant height and seed yield is in confirmity with earlier findings of Sikka and Gupta (1949), Dabral (1967), Muhammed et al. (1970), Osman KHidir and El-Gizouli Osman (1970), El-Gizouli Osman and Osman Khidir (1974b), El Nadi et al. (1974), Kaushal et al. (1974), Delgado and Yermanas (1975), Govindadas (1975), Gupta (1976), Sorafi (1976), Choudhary et al. (1977), Elahmar and Serry (1977), Kaushal et al. (1977), Murugesan et al. (1979b), Paramasivam and Prasad (1980), Rathanaswamy (1980); Desai et al. (1982), Govinda Rasu (1982), Gupta and Labana (1983), Thangavelu and Rajasekaran (1983a), Reddy et al. (1984), Seenaiiah and Reddy (1984), Godawat and Gupta (1986), Krishnadoss and Kadambavanasundaram (1986), Pathak and Dixit (1986), Umesh Kumar Reddy (1986), Bhale et al. (1987), John Joel (1987) and Omar Sheik (1989). But Dixit (1975), Naphade and Kolt (1975) and Shukla and Verma (1976) reported negative association among these two traits.

Sikka and Gupta (1949), Dabral (1967), Osman Khadir and El-Gizouli Osman (1970); Gupta (1976), Rao and Charry (1979), Choudhary et al. (1977), Rathnaswamy (1980), Chavan and Chopde (1981), Gupta and Labana (1983), Thangavelu and Rajasekaran (1983), Krishnadoss and Kadambavanasundaram (1986) John Joel (1987) and Omar Sheik (1989) obtained a positive association between number of branches and seed yield similar to the present investigation.

The association between crop duration (days to maturity) and seed yield was also positive (SII) which is in corroboration with El-Gizouli Osman and Osman Khidir (1974b), Paramasivam (1980), Rajasekaran

(1980), Thangavelu and Rajasekaran (1983), Umesh Kumar Reddy (1986) and Omar Sheik (1989). However, Kaushal *et al.* (1977), Desai *et al.* (1982), Godawat and Gupta (1986) and John Joel (1987) found negative association among these traits.

Number of seeds per capsule was the only character which showed negative association with seed yield (only in SI) in the present study which is in confrontation with Krishnamurthy (1960), Krishnamurthy *et al.* (1964), El Gizouli Osman and Osman Khidir, 1974, EL Gizouli Osman and Osman Khidir (1974b), Delgado and Yermanaos (1975), Chavan and Chopde (1981), Ibrahim *et al.* (1983) and Reddy (1986).

From the correlation studies between seed yield and its component characters it is inferred that the traits viz., plant height, number of branches per plant, number of flowers per plant, number of capsules per plant, weight of 1000 seeds, seed density, total dry matter production and harvest index showed mostly consistent positive significant association with seed yield. So these traits may be considered as the most important yield attributing traits dependable for selection for the yield improvement in sesame.

However, the information on the association of seed yield with other traits may not alone be sufficient as inter-relationships between the traits may also affect overall relationship of the characters. Under this study. Hence Doku (1970) suggested that the selection based on yield

components would be effective in improving the yield, provided the components are highly heritable and the genotypic correlations among them are not negative. Negative genotypic correlation between the components selected for in a breeding programme may hinder the rate of improvement of other desirable characters and nullify the progress.

The characters showing strong positive correlation (mostly) with seed yield such as plant height, number of branches, seed density, total dry matter production and consistently in all the seasons and pooled analysis viz., number of flowers, number of capsules, weight of 1000 seeds, and harvest index also showed strong positive association (mostly) among themselves excepting plant height with harvest index in SI and total dry matter production with harvest index in SII, where they exhibited strong negative association. These two character pairs evinced non significant association in the pooled analysis. So selection for plant height, total dry matter production and harvest index in these seasons is not advised.

Similar positive interrelationship between plant and number of branches was reported by Kaushal et al. (1977), Rathnaswamy (1980), Thangavelu and Rajasekaran (1983), Krishnadoss and Kadambavanasundaram (1986) and Omar Sheik (1989); between plant height and number of capsules per plant by El Gizouli Osman and Osman Khidir (1974b), Govindadas (1975), Gupta (1976), Rathnaswamy (1980), Rai et al. (1981), Thangavelu and Rajasekaran (1983), Seenaiiah and Reddy (1984), Krishnadoss and

and Kadambavana Sundaram (1986) and Omar Sheik (1989) between plant height and weight of 1000 seeds by Thangavelu and Rajasekaran (1983).

The positive significant association observed in this study between number of branches and capsules per plant is in confirmity with Krishnamurthy (1960), Krishnamurthy et al. (1964), Dixit (1975), Rathnaswamy (1980), Gupta and Labana (1983), Thanagavelu and Rajasekaran (1983), Reddy et al. (1984), Godawat and Gupta (1986), Krishnadoss and Kadambavana Sundaram (1986) and Omar Sheik (1989); between number of branches and 1000 seed weight by Thangavelu and Rajasekaran (1983). Kaushal et al. (1977) observed negative significant association between number of branches and 1000 seed weight.

Kaushal et al. (1977), Thangavelu and Rajasekaran (1983a) reported positive significant association between number of capsules per plant and 1000 seed weight, which are again in confirmity with the present result.

Days to maturity showed positive significant association with seed yield in SII only. It was positively correlated with plant height, number of branches, number of capsules, 1000 seed weight and oil content. Its positive association with plant height was reported by El Gizouli Osman and Osman Khidir (1974b), Kaushal et al. (1977), Thangavelu and Rajasekaran (1983). Umesh Kumar Reddy (1986) and Omar Sheik (1989); with number of branches by Kaushal et al. (1977), Thangavelu and Rajasekaran (1983) and Omar Sheik (1989); with number of capsules by El Gizouli Osman and Osman Khidir (1974b), Thangavelu and Rajasekaran (1983)

and Omar Sheik (1989) with 1000 seed weight by Thanagavelu and Rajasekaran (1983).

Number of seeds per capsule was the only character which exhibited negative association with seed yield. It also exhibited negative association with most of the traits which were positively associated with seed yield viz., number of branches, number of flowers, number of capsules, weight of 1000 seeds and total dry matter production (SI and SII). But with plant height it showed positive association. In other season (SIII) it evinced positive association with number of branches, flowers and capsules. However its association with all these traits in the pooled analysis was non significant. Thus this trait showed seasonal influence on its association with the components of seed yield and seed as well.

Chavan and Chopde (1981) reported such negative association between number of capsules and number of seeds per capsule, whereas Govindadas (1975) and Gupta (1976) observed positive association between these traits. The positive association found in the present study among number of seeds per capsule and plant height is in disagreement with Umesh Kumar Reddy (1986) who reported negative association among these traits.

Invariably in all the analyses, volume of capsules had a strong positive association with number of seeds per capsule which is in agreement with the report of Pathak and Dixit (1986) who observed a positive association among capsule girth and number of seeds per capsule.

Volume of capsule also exhibited a positive association with 1000 seed volume but only in one season (SI).

Seed length which evinced a rare positive association with seed yield also showed positive association with seed breadth and weight of 1000 seeds (mostly) and rarely with plant height, 1000 seed volume, oil content and harvest index. Trehan *et al.* (1975) observed such a positive association of seed length with oil content.

Seed breadth had a rare positive association with plant height, weight of 1000 seeds, volume of 1000 seeds and oil content. Trehan *et al.* (1975) reported such a positive association between seed thickness and oil content.

Volume of 1000 seeds exhibited a constant negative association with seed density and a rare negative association with number of capsules. It also evinced a rare positive association with plant height and weight of 1000 seeds.

Oil content consistently showed a positive association with number of flowers and number of capsules. Thangavelu and Rajasekaran (1983) and Seenaiiah and Reddy (1984) reported such a positive association between oil content and number of capsules. It also had positive association (mostly) with plant height and number of branches and rarely with days to maturity and 1000 seed weight. This is in confirmity with the earlier reports of Thangavelu and Rajasekaran (1983) for plant height and number of branches with oil content. Trehan *et al.* (1975), Ibrahim

et al. (1983), Thangavelu and Rajasekaran (1983.) for 1000 seed weight with oil content.

The present correlation studies among seed size, yield and their components indicated that seed yield and seed size can be improved in sesame by efficient selection for plant height, number of branches, number of flowers, number of capsules, weight of 1000 seeds, seed density, total dry matter production and harvest index, as they showed positive correlation with seed yield, seed size and among themselves. Eventhough total dry matter production evinced a negative and significant correlation with harvest index in one season (SII), it showed significant positive and non significant association with harvest index in SIII and pooled analysis respectively i.e., it behaved as neutral. Similarly plant height which showed positive significant association with seed yield, exhibited negative and significant association in SI, positive and significant association in SII and non-significant relationship in (neutral) in SIII and pooled analysis with harvest index. Hence these two traits are not reliable for selection for the improvement of harvest index.

Most of the characters which showed positive significant association with seed yield and seed size also exhibited positive significant association with oil content. So by selecting those characters, oil, seed size and seed yield can well be improved. As days to maturity showed positive significant association with seed size and seed yield in only one season and behaved as neutral character there is a scope for reducing the duration.

An offshoot but perspective learning from the present study is that genetic correlations do depend on the season and that genotype X season interactions affect genetic correlations, which follows the statement of Clark (1987).

5.5. PATH ANALYSIS

Yield is a complex entity and is associated with a number of other characters. Correlation is a simple measure of association of characters, and does not indicate the relative contribution of causal factors to yield. The component characters are themselves inter-related. Such inter-dependence of the contributory factor often affects their direct relationship with yield, thereby making correlation coefficients unreliable as selection indices.

Path coefficient analysis permits the separation of direct effects from indirect effects through other related characters by partitioning the correlation coefficients. According to Dewey and Lu (1959) correlation simply measures mutual association without regard to causation while the path coefficient analysis specifies the causes and measures their relative importance.

Path analysis like correlation studies has shown a strong seasonal influence in the contribution of the component characters towards seed size (1000 seed weight) and seed yield.

Days to maturity, plant height, number of branches, flowers, capsules, seed length, seed breadth, seed density, seed yield and total dry matter production in SI, number of capsules, 1000 seed volume, seed density, seed yield and harvest index in SII, plant height, number of branches, flowers, capsules, seed density, oil content, seed yield, total dry matter production and harvest index in SIII, and plant height, number of branches, flowers, capsules, seed length, seed yield, total dry matter and harvest index in pooled analysis exhibited positive significant association with 1000 seed weight. Number of seeds per capsule was the only character which showed negative significant association with 1000 seed weight that too only in pooled analysis.

Among these characters number of capsules and seed yield showed consistent positive significant association with weight of 1000 seeds over seasons and in pooled analysis. Plant height, number of branches, flowers, seed density, total dry matter production and harvest index mostly had positive significant association with 1000 seed weight. Seed length exhibited positive significant association with 1000 seed weight in two seasons only. The traits viz., days to maturity, seed breadth, 1000 seed volume and oil content evinced positive significant association in only one season.

When 1000 seed weight was considered as the dependent variable the path analysis revealed that number of capsules followed by oil content, total dry matter production, plant height, seed breadth, 1000 seed volume and days to maturity in SI, oil content followed by

days to maturity, number of seeds per capsule, number of capsules, plant height, capsule volume and number of flowers in SII, total dry matter production followed by harvest index, oil content, days to maturity, number of flowers, number of seeds per capsule, capsule volume, 1000 seed volume, number of branches, seed breadth, seed yield, seed length and plant height in SIII and total dry matter production followed by seed density, 1000 seed volume, harvest index, number of branches, seed length, days to maturity, number of seeds per capsule, oil content and number of capsules in pooled analysis showed positive direct effects towards 1000 seed weight. Negative direct effects were exhibited by seed density followed by capsule volume, harvest index, seed length, number of flowers, number of branches, number of seeds per capsule and seed yield in SI, seed density followed by harvest index, total dry matter production, seed breadth, seed length, seed yield, number of branches and 1000 seed volume in SII, seed density followed by number of capsules in SIII and seed yield followed by plant height, capsule volume, number of flowers and seed breadth in pooled analysis.

Oil content followed by days to maturity evinced consistent positive direct effect over seasons towards 1000 seed weight. The magnitude of the positive direct effect of these traits towards 1000 seed weight ranged from high to less. Seed density and seed yield showed negative direct effect. Number of capsules followed by oil content in SI, oil content followed by days to maturity in SII, total dry matter production followed by harvest index in SIII and total dry matter production followed by seed density in pooled analysis exhibited the maximum positive direct effect towards 1000 seeds weight. Seed density in SI, SII and SIII and

seed yield in pooled analysis evidenced the maximum negative direct effect towards 1000 seed weight.

Among the traits which showed consistent positive significant association with 1000 seed weight viz., number of capsules and seed yield, number of capsules showed positive direct effects in SI, SII and pooled analysis and negative direct effect in SIII, whereas seed yield exhibited positive direct effect in only one season (SIII) and negative direct effect in SI, SII and pooled analysis. Among the traits which mostly displayed positive significant association with 1000 seed weight (plant height, number of branches, flowers, seed density, total dry matter production and harvest index), plant height in SI, SII and SIII and pooled analysis evinced positive direct effects and negative direct effects rarely (pooled analysis and SII, respectively). Number of branches in SIII and pooled analysis, number of flowers in SI and pooled analysis, and harvest index in SIII and pooled analysis had positive direct effects. Number of branches in SI and SII, number of flowers in SII and SIII and harvest index in SI and SIII exhibited negative direct effects. Seed density, surprisingly exhibited negative direct effects mostly towards 1000 seed weight. It showed negative direct effect in SI, SII and SIII but in the pooled analysis it showed positive direct effect.

Comparison of the genetic correlation coefficients of the traits which showed positive significant association with 1000 seed weight with their direct effects revealed a general disagreement. The correlation coefficients were either higher or lower than the direct effects. This

warrants the analysis of the indirect effects of these traits towards 1000 seed weight.

The characters which were significantly and positively associated with 1000 seed weight over seasons and pooled analysis viz., number of capsules and seed yield showed indirect positive effects mainly through oil content. Apart through this character, number of capsules showed positive indirect effect via total dry matter production. Seed yield via total dry matter production and/or harvest index exhibited indirect positive effect towards 1000 seed weight.

Number of capsules exhibited maximum positive indirect effects through oil content followed by total dry matter production in SI, through oil content followed by days to maturity in SII, through oil content followed by total dry matter production, harvest index and capsule volume in SIII and through total dry matter production, harvest index, seed density, number of branches, oil content and days to maturity in pooled analysis. Negative indirect effects were maximum through capsule volume followed by seed density in SI, through harvest index followed by seed density, total matter production and capsule volume in SII, through days to maturity followed by seed density and capsule volume in SIII and through seed yield followed by plant height, 1000 seed volume, flower number and seeds per capsule in pooled analysis. However, the overall effect was positive.

Seed yield showed maximum positive indirect effect via capsule number followed by oil content, total dry matter production and seed length in SI, through oil content followed by days to maturity in SII, through total dry matter production followed by oil content, harvest index and capsule volume in SIII and through seed through seed density followed by harvest index, capsule number, branch number and oil content in pooled analysis negative indirect effect was maximum through capsule volume followed by seed density in SI, seed density followed by harvest index in SII, days to maturity followed by seed density and capsule number in SIII and through seed yield followed by plant height, flower number, capsule volume and number of seeds per capsule in pooled analysis. Considering the overall effect it was positive.

The characters which mostly showed positive significant association with 1000 seed weight such as plant height, number of branches, flowers, seed density, total dry matter production and harvest index also exhibited positive indirect effects mostly through oil content coupled with either capsule number and/or total dry matter production and to a lesser extent through harvest index too.

Plant height displayed its maximum positive indirect effect via capsule number, followed by total dry matter production, seed density and seed breadth in SI, through oil content followed days to maturity in SI via oil content followed by harvest index, total dry matter production, capsule volume and flower number in SIII and through total matter production, 1000 seed volume, number of branches, oil content, harvest index, seed breadth, days to maturity, capsule number and seed density in pooled

analysis. Negative indirect effect was maximum through capsule volume followed by oil content, number of branches, and seed length in SI, via seed density, total dry matter production and harvest index in SII, via days to maturity, seed density and capsule number in SIII and through seed yield followed by number of flowers in pooled analysis. However, the overall effect was positive.

Number of branches had its maximum positive indirect effect via capsule number followed by oil content, plant height, total dry matter production and seed length in SI, via oil content followed by days to maturity in SII, via total dry matter production followed by oil content, harvest index, number of flowers, seed density and capsule volume in SIII and through harvest index, total dry matter production, days to maturity, capsule number, oil content, 1000 seed volume, seed density and capsule volume in the pooled analysis. It had its negative indirect effect via capsule volume, followed by flower number, and seed density in SI, via seed density followed by harvest index in SII, via days to maturity followed by capsule number in SIII and through seed yield followed by days to maturity, flower number, number of seeds per capsule and seed breadth in pooled analysis. The overall effect was positive.

Number of flowers evinced positive indirect effect via capsule number followed by oil content and total dry matter production in SI, oil content followed by days to maturity in SII, oil content followed by total dry matter production, harvest index, capsule volume in SIII and through total dry matter production followed by seed density, harvest index, number of branches, number of capsules, oil content and days

to maturity in pooled analysis. It also evinced negative indirect effect via capsule volume followed by seed density in SI, seed density followed by total dry matter production in SII, days to maturity followed by capsule number in SIII and seed yield followed by plant height, 1000 seed volume and number of seeds per capsule in pooled analysis. Overall effect was positive.

Seed density exhibited its maximum positive indirect effect via oil content followed by capsule number in SI, oil content followed by days to maturity in SII, oil content followed by total dry matter production and harvest index in SIII and harvest index followed by total dry matter production. Capsule number, capsule volume and oil content in the pooled analysis. It also exhibited negative indirect effect via capsule volume in SI, total dry matter production in SII, seed density followed by days to maturity in SIII and 1000 seed volume followed by seed yield, flower number, days to maturity, plant height and seeds per capsule in pooled analysis. However the overall effect was positive.

Total dry matter production displayed its maximum positive indirect effect via capsule number followed by oil content and seed density in SI, oil content followed by harvest index and days to maturity in SII, oil content followed by harvest index and capsule volume in SIII and seed density followed by harvest index, capsule number, number of branches and oil content in the pooled analysis. Negative indirect effect was maximum through capsule volume followed by number of branches in SI, seed density in SII, days to maturity followed by seed density

and capsule number in SIII and seed yield followed by plant height, flower number, capsule volume and number of seeds per capsule in the pooled analysis.

Harvest index showed its maximum positive indirect effect via oil content in SI, oil content followed by days to maturity and total dry matter production in SII, oil content followed by total dry matter production and capsule volume in SIII and seed density followed by total dry matter production, number of branches, number of capsules and oil content in the pooled analysis. The negative indirect effect was maximum through seed density in SI, seed density followed by capsule volume in SII, days to maturity followed by seed density and capsule number in SIII and seed yield followed by 1000 seed volume, plant height, number of flowers and days to maturity in the pooled analysis. The overall effect was positive.

In this part of studies on correlation and causation among sixteen characters, it was found out that the characters showing positive significant or positive significant association (mostly) with 1000 seed weight such as plant height, number of branches, flowers, seed density, total dry matter production and harvest index and consistently in all the seasons and pooled analysis viz., number of capsules and seed yield, mostly showed strong positive significant or positive significant association among themselves excepting plant height with harvest index in SI and total dry matter production with harvest index in SII, where they exhibited strong negative association. Among these traits capsule number and total dry matter production showed mostly high positive direct effects

towards 1000 seed weight. Harvest index also showed high positive direct effects (SIII and pooled analysis). These characters also showed positive indirect effects among them mostly, next to oil content. The overall effects of these traits on 1000 seed weight were positive despite their negative indirect effects. That could be the cause for the consistent strong positive significant association of capsule number with 1000 seed weight and mostly positive significant association of total dry matter production and harvest index with 1000 seed weight.

The other traits which showed positive significant association with 1000 seed weight exhibited both positive and negative indirect effects excepting seed density, it evinced only negative indirect effects. These traits mostly exhibited positive indirect effects via capsule number, oil content and total dry matter production and negative indirect effects mostly through seed density followed by capsule volume, seed yield, plant height, flower number, 1000 seed volume and number of seeds per capsule. But the overall effects of these traits viz., plant height, number of branches, number of flowers, seed density and seed yield were found to be positive due to the high positive indirect effects made mainly through capsule number, oil content and total dry matter production. While the consistent high positive direct and indirect effects of total dry matter production can be attributed as cause to its positive significant association with 1000 seed weight, the high positive indirect effects made through capsule number, oil content and total dry matter production can well be the cause for the positive association of other traits viz., plant height, number of branches, number of flowers, number of capsules, seed density and seed yield with 1000 seed weight.

The positive significant association of seed length with 1000 seed weight in S1 was due to its high positive indirect effects via oil content, seed breadth and capsule number in SI, and due to harvest index, seed density, seed breadth, 1000 seed volume, number of seeds per capsule and oil content, in the pooled analysis. In the other seasons positive indirect effects were neutralized by the negative indirect effects. That may be the cause for the non significant association of this traits with 1000 seed weight in the other seasons. A similar reason can also be reasoned for the non significant association of plant height, seed breadth (SII, SIII and pooled analysis), 1000 seed volume (SI, SIII and pooled analysis) and oil content (SI, SII and pooled analysis) with 1000 seed weight in the other seasons.

The dominant negative indirect effects via capsule volume, total dry matter production, seed density, number of branches and plant height than the positive direct and indirect effects of number of seeds per capsule may be the cause for its significant negative association with 1000 seed weight in the pooled analysis. Neutralization of positive direct and indirect effects by the negative indirect effects could be the cause for its non significant association in the other seasons with 1000 seed weight.

The non significant association of capsule volume with 1000 seed weight in all the analysis can be due to the neutralization of their direct effects by their dominant indirect effects as well as compensation among the positive and negative indirect effects (Murugesan et al., 1979b; John Joel, 1987).

The trait which showed maximum or moderate or less or least positive or negative direct or indirect effects towards seeds yield in one season either exhibited maximum or moderate or less or least positive or negative direct or indirect effect in the other season or pooled analysis. Despite such a high seasonal influence on the causal factors of seed yield, by virtue of the overall effect the correlation was maintained overseasons.

From the present study of correlation and causation towards 4000 seed weight, it may be concluded that plant height, number of branches, flowers, capsules, seed density, seed yield, total dry matter production and harvest index are the major determinants of 1000 seed weight as their overall effect was positive and consistent over seasons. Among them primary importance may be given to capsule number and total dry matter production, as most of the traits showed positive indirect effects as well through these traits towards 1000 seed weight.

When seed yield was considered as the dependent variable, the path analysis revealed that harvest index followed by total dry matter production, 1000 seed volume, seed density, 1000 seed weight, number of branches, volume of capsules, number of flowers, and days to maturity in SI, days to maturity followed by harvest index, total dry matter production, oil content, seed breadth, seed length, number of branches and 1000 seed weight in SII, total dry matter production followed by harvest index, seed density, 1000 seed volume, number of capsules, number of seeds per capsule, days to maturity, seed length,

capsule volume, plant height, seed breadth, number of flowers and 1000 seed weight in SIII and harvest index followed by total dry matter production, seed density, plant height, 1000 seed volume, days to maturity, number of flowers, capsule volume and seed breadth in the pooled analysis showed positive direct effects. Negative direct effects were exhibited by number of capsules followed by oil content, seed breadth, plant height, seed length, and number of seeds per capsule in SI, seed density followed by 1000 seed volume, number of seeds per capsule, capsule number, plant height, capsule volume, and number of flowers in SII, oil content and number of branches in SIII and number of capsules followed by 1000 seed weight, number of seeds per capsule, seed length, oil content and number of branches in pooled analysis.

Harvest index followed by total dry matter production evinced the maximum positive direct effect consistently over seasons towards seed yield. Days to maturity also exhibited consistent positive direct effect eventhough the magnitude differed widely. Number of capsules, number of seeds per capsules, and oil content mostly showed negative direct effect. Number of capsules in SI and pooled analysis, seed density in SII and oil content in SIII showed the maximum negative direct effect towards seed yield.

Positive direct effect of plant height on seed yield observed in the present study is in confirmity with Gupta (1976) Govinda Rasu (1982), Pathak and Dixit (1986) and Reddy (1986). Similarly the negative

direct effect of plant height on seed yield observed in the present study is in confirmity with the findings of Dixit (1975), Naphade and Kolte (1975) and Gupta and Chopra (1984).

The negative direct effect of number of branches on seed yield observed in this study is in corroboration with the findings of Kaushal *et al.* (1977), Govinda Rasu (1982), Thangavelu and Rajasekaran (1983) and Reddy (1986). Similarly the positive direct effect of number of branches on seed yield is in confirmity with Dixit (1975), Naphade and Kolte (1975), Gupta (1976) and Thangavelu and Rajasekaran (1983).

The negative direct effect of capsule number per plant on seed yield is in disagreement with Ekbote and Tayyab (1974), Paramasivam (1980), Rathinaswamy (1980), Desai *et al.* (1982), Govinda Rasu (1982), Gupta and Labana (1983), Ibrahim *et al.* (1983), Thangavelu and Rajasekaran (1983), Gupta and Chopra (1984) and Reddy (1986). They observed direct positive effect of capsule number on seed yield.

The direct positive effect of 1000 seed weight on seed yield found in this inquiry is on line with Gupta and Gupta (1977), Kaushal *et al.* (1977), Yadava *et al.* (1980), Thangavelu and Rajasekaran (1983), Sharma and Chauhan (1984), Pathak and Dixit (1986) and Reddy (1986). The negative direct effect of 1000 seed weight on seed yield identified in this study is also in confirmity with Naphade and Kolte (1975).

Among the traits which showed consistent positive significant association with seed yield viz., number of flowers, capsules, 1000 seed weight and harvest index, the last character (harvest index) only showed consistent positive direct effect in all the analyses. Number of flowers, and 1000 seed weight exhibited positive direct effect in three analyses and negative direct effect in one analysis. Capsule number surprisingly evinced negative direct effect in three analyses and positive direct effect in only one analysis. Among the characters which mostly displayed positive association with seed yield viz., plant height, number of branches, seed density, and total dry matter production, the last trait (total dry matter production) only showed consistent positive direct effect over seasons. Seed density showed positive direct effect in three seasons and negative direct effect in only one season whereas plant height and number of branches exhibited positive direct effect in two analysis and negative direct effect in two analysis.

Comparison of the genetic correlation coefficients of the traits which had positive significant association with seed yield with their direct effects revealed only a fair agreement, that 1000 too for total dry matter production and harvest index in SI, harvest index, in SII, total dry matter production, harvest index and seed density in SIII and total dry matter production, and harvest index in pooled analysis. The direct effects of these characters were slightly less or high than their correlation coefficients. Other traits which showed positive genetic association with seed yield showed less and/or least direct effects. So an analysis of the indirect effects of these traits towards seed yield becomes inevitable.

The characters which were consistently and positively correlated with seed yield such as number of flowers, number of capsules and 1000 seed weight showed indirect positive effects mainly through total dry matter production and harvest index.

Number of flowers exhibited maximum positive indirect effect through total dry matter production in SI, through total dry matter production and harvest index in SII, through total dry matter production, harvest index, capsule number and seed density in SIII and through total dry matter production, harvest index, followed by plant height in pooled analysis. Invariably in all the analysis through total dry matter production, they showed maximum positive indirect effect. Negative indirect effect was maximum through capsule number, and harvest index in SI, through seed density and capsule number in SII, through number of branches in SIII and through capsule number and 1000 seed weight in pooled analysis. However the overall effect of number of flowers towards seed yield was positive.

Number of capsules showed maximum positive indirect effect via total dry matter production in SI, through harvest index and total dry matter production in SII, through total dry matter production, harvest index and seed density in SIII and through total dry matter production, harvest index, plant height, number of flowers and seed density in pooled analysis. It also evienced maximum negative indirect effect via harvest index in SI, via seed density in SII, via number of branches in SIII and via 1000 seed weight in pooled analysis. The overall effect was however positive towards seed yield.

Thousand seed weight had maximum positive indirect effect through total dry matter production, number of branches, harvest index and seed density in SI, through harvest index and total dry matter production in SII, through total dry matter production harvest index, seed density and capsule number in SIII and through total dry matter production, harvest index, plant height, seed density and flower number in the pooled analysis. It evidenced maximum negative indirect effect through capsule number in SI, through seed density, capsule number and plant height in SII, through plant height and number of branches in SIII and capsule number in pooled analysis. The overall effect was positive.

Harvest index in SI evinced only less positive indirect effects. In SII, through days to maturity, 1000 seed volume, and capsule volume, in SIII through total dry matter production, capsule number and seed density and in pooled analysis through total dry matter production, seed density, flower number and plant height it showed positive indirect effects. Negative indirect effects were maximum through total dry matter production, number of branches and 1000 seed weight in SI, through total dry matter production, seed density, capsule number and plant height in SII, through 1000 seed volume, number of branches, plant height and days to maturity in SIII and capsule number and 1000 seed weight in pooled analysis. The overall effect was however positive.

The characters which mostly showed positive association with seed yield such as plant height, number of branches and seed density

and total dry matter production also evinced indirect positive effects mainly through total dry matter production and harvest index.

Plant height exhibited maximum positive indirect effect via total dry matter production and number of branches in SI, through total dry matter production and harvest index in SII, through harvest index, total dry matter production, capsule number and seed density in SIII and through total dry matter production and harvest index in pooled analysis. Negative indirect effect was maximum through harvest index and 1000 seed weight in SI, through seed density and capsule number in SII, through number of branches in SIII and through 1000 seed weight and capsule number in pooled analysis. The overall effect was however positive.

Number of branches exhibited maximum positive indirect effect via total dry matter production followed by harvest index in SI, through harvest index followed by total dry matter production in SII, through total dry matter production followed by harvest index and number of capsules in SIII and through harvest index followed by total dry matter production in the pooled analysis. Negative indirect effect was less in SI and SIII and considerable through seed density and capsule number in SII and through capsule number followed by 1000 seed weight in the pooled analysis. The overall effect was positive, however.

Seed density evinced maximum positive indirect effect via harvest index followed by total dry matter production in SI, through days to maturity followed by 1000 seed volume, harvest index and total

dry matter production in SII, through total dry matter production followed by harvest index and capsule number in SIII and through harvest index followed by total dry matter production and flower number in pooled analysis. Negative indirect effect was maximum through 1000 seed volume in SI, through capsule number in SII, through 1000 seed volume followed by days to maturity in SIII and through 1000 seed volume, followed by capsule number in pooled analysis. However, the overall effect was positive.

Total dry matter production showed maximum positive indirect effect via capsule volume followed by number of branches in SI, through 1000 seed volume followed by days to maturity and capsule volume in SII, through harvest index followed by capsule number and seed density in SIII and through harvest index followed by plant height, number of flowers and seed density in pooled analysis. Negative indirect effect was maximum through harvest index followed by capsule number in SI, through harvest index followed by seed density and capsule number in SII, through 1000 seed volume followed by days to maturity, number of branches and plant height in SIII and through capsule number followed by 1000 seed weight in pooled analysis. The overall effect was however positive.

Analysis of the indirect effects of different traits towards seed yield clearly indicated that all the traits which were positively associated with seed yield had positive indirect effect via total dry matter production and harvest index in all the analysis.

In the present investigation on correlation and causation among sixteen characters, it was found out that the characters showing strong positive association (mostly) with seed yield viz., plant height, number of branches, seed density and total dry matter production and consistently in all the seasons and pooled analysis viz., number of flowers, number of capsules, weight of 1000 seeds and harvest index, mostly showed strong positive significant or positive significant association among themselves excepting plant height with harvest index in SI and total dry matter production with harvest index. In SII, where they exhibited strong negative association. Among these traits, total dry matter production and harvest index showed consistently high positive direct effect towards seed yield. These two characters showed positive (SIII and pooled analysis) as well as negative (SI and SII) indirect effects among them indicating seasonal influence in their contribution towards seed yield. However, the overall effects of these traits on seed yield were positive, even in SI and SII, mainly through their positive direct effect.

Other than total dry matter production and harvest index, the traits which showed positive significant association with seed yield viz., number of flowers, 1000 seed weight and seed density mostly showed positive direct effects whereas number of capsules exhibited mostly negative direct effects towards seed yield. Plant height and number of branches showed both positive (SIII and pooled analysis) and negative (SI and SII) direct effects. These traits mostly exhibited positive indirect effects via total dry matter production and harvest index in all the analysis and negative indirect effects mostly through number of branches,

number of capsules, 1000 seed weight, seed density and rarely through plant height. But the overall effects of these characters viz., plant height, number of branches, number of flowers, number of capsules, 1000 seed weight and seed density were found to be positive due to the high positive indirect effects made mainly through total dry matter production and harvest index mostly. While the consistent high positive direct effects of total dry matter production and harvest index can be attributed as cause to their positive association with seed yield, the high positive indirect effects made through the total dry matter production and harvest index can well be the cause for the positive association of other traits viz., plant height, number of branches, number of flowers, number of capsules, 1000 seed weight and seed density with seed yield.

The significant positive association of days to maturity with seed yield in SII was mainly due to its high positive direct effect. This is in corroboration with Reddy (1986) but at variance with Kaushal et al. (1977), Thangavelu (1980), Thangavelu and Rjasekaran (1983) and Pathak and Dixit (1986).

The significant positive association of seed length with seed yield in SII was due to its high positive indirect effect via days of maturity and harvest index. In the other seasons, the direct and indirect effects of these characters viz., days to maturity and seed length on seed yield were less and that may be the cause for the observed non significant association of these traits with seed yield in SI, SIII and pooled analysis.

The negative direct effect of number of seeds per capsule on seed yield can be attributed to its negative association with seed yield in SI. In SII, its negative direct effect was neutralized by its positive indirect effects made through days to maturity, seed length, 1000 seed volume and harvest index. In SIII, its positive direct effect was neutralized by its negative indirect effect via seed length and 1000 seed volume. In the pooled analysis also its negative direct effect was neutralized by its positive indirect effect via plant height, number of capsules, capsule volume and 1000 seed weight. Thus it can be the cause for the non significant association with seed yield in SII, SIII and pooled analysis. Negative direct effect of number of seeds per capsule towards seed yield was earlier reported by Chavan and Chopde (1981) and Reddy (1986). However, Pathak and Dixit (1986) indicated that seeds per capsule had the highest direct effect on seed yield.

The characters viz., plant height, number of branches, capsule volume, seed breadth, 1000 seed volume, seed density and oil content in SI, capsule volume, seed breadth, 1000 seed volume oil content and total dry matter production in SII, capsule volume, seed breadth, 1000 seed volume and oil content in SIII and pooled analysis showed non significant association with seed yield. This can be due to the neutralization of their direct effect by their dominant indirect effects, as well as compensation among the positive and negative indirect effects. Such a similar interpretation of neutralization of the causal effects as the cause for the non significant association was made by Murugesan et al. (1979b), and John Joel (1987).

The trait which showed maximum or moderate or less or least positive or negative direct or indirect effects towards seed yield in one season either exhibited maximum or moderate or less or least positive or negative direct or indirect effect in the other season or pooled analysis. Despite such a high seasonal influence on the causal factors of seed yield, by virtue of the overall effect the correlation was maintained over seasons.

Based on the correlation and causation studies, it may be concluded that the traits viz., plant height, number of branches, number of flowers, number of capsules, 1000 seed weight, seed density, total dry matter production and harvest index were the major yield components affecting the seed yield as their overall effects were positive and consistent over seasons. Among these primary importance may be given to total dry matter production and harvest index because they showed high positive, consistent direct effects towards seed yield which were close to the genetic correlation coefficient with seed yield and through these characters only the other major yield components exhibited their indirect positive effects towards seed yield. Thus they assumed primary importance. The observed overall positive effects of plant height and number of branches throw added scope in getting medium plant type. The positive significant association of days to maturity with seed yield in SII due to its positive direct effect and non significant association of this trait with seed yield in the other seasons throw some scope in getting short duration plant types.

Almost all the traits which showed positive significant genetic association with seed yield also displayed positive significant genetic correlation with 1000 seed weight. Seed yield and 1000 seed weight ^{wer} was also positively and significantly associated. So there is ample scope for evolving large seeds with high 1000 seed weight.

Considering the overall direct and indirect effects of various plant characters and its association on seed yield and 1000 seed weight, there is ample scope for improving the yield potential of sesame by evolving early maturity, medium plant types with high reproductive efficiency and harvest index coupled with good stand establishment through high seed and seedling vigour by evolving well filled large plumpy seeds.

It is assumed that the causal system visualized in path analysis takes into account the factors involved in determining the end product. Since the determination of such product is very complex, it is not obviously possible to have a complete path diagram. This warrants the inclusion of residual path in the analyses. In the present study, the residual effects of 0.1534 in SI, 0.1000 in SII, 0.1342 in SIII and 0.1436 in pooled analysis (seed yield as dependent variable), and 0.5422 in SI, 0.1000 in SII, 0.4537 in SIII and 0.9799 in the pooled analysis (1000 seed weight as dependent variable) also assumed importance. A high residual effects of 0.5473, 0.4838 and 0.2466 were observed by Kaushal et al. (1977), Govinda Rasu (1982) and John Joel (1987) in sesame. This indicated

that besides the characters already studied there are some more characters which also influence the seed yield and 1000 seed weight. Hence further study is suggested to identify the left out character(s) to minimise the residual effect.

The observed genetic correlations among the major seed size, yield and their components may be due to linkage or pleiotropism or genetically controlled physiological and developmental relationships or the combinations of all these items.

The causal factors determining the genetic correlations do depend on season and that genotype by season interactions affect the expression and contribution of the causal factors towards dependent variable, which in turn reflects on the direction and magnitude of genetic correlations. The differential contribution of different component traits in different seasons towards the same dependent variables were well evidenced from the differences in the magnitude and direction of genetic correlations among themselves as well as with the dependent variables.

5.6. STABILITY ANALYSIS

A successfully developed new cultivar should have stable performance and broad adaptation over a range of environments, seasons and locations, in addition to high yield potential. Evaluating performance stability and range of adaptation is becoming increasingly important in breeding programs. Since stability and adaptability are important selection criteria in breeding programs, in depth research on stability is needed

for a better estimate of crop performance and adaptability (Lin and Binns, 1988).

Genotype x season interaction is of major importance to the plant breeder in developing stable high yielding varieties of crop plants. When new varieties are tested over a series of seasons, the relative ranking of the varieties for any given attribute is rarely the same at each season. This increases the difficulty of identifying superior stable genotypes. Comstock and Moll (1963) have shown statistically the effect of large genotype x environment interaction in reducing the progress from selection.

In order to minimise the genotype x season interaction, stratification of the seasons can be practiced. The implication in stratification is that suitable selections could be made for the unfavourable and favourable seasons encountered within the sampling units proposed. Stratification of environments has been practised for a long time to identify suitable selection that could be made for the narrower range of environments encountered within the sampling units proposed. However, even with this refinement of technique, the interactions of genotypes with locations in a sub-region and with environments encountered at the same location in different years, frequently remain too large (Allard and Bradshaw, 1964). Little is known about the environmental factors contributing to such interactions. Sprague (1966) suggested that even if such information were available, the possibility of materially reducing genotype x environment interaction in field experiments would remain questionable.

On line with Allard and Bradshaw's (1964) statement, the interactions of genotypes with locations in a sub-region and with different seasons at the same location in different years, may remain too large. As far as sesame is concerned, practically nothing is known about the factors contributing to such genotype x season interactions. Hence, the progress in breeding a stable variety of sesame has been slow. Since sesame in India is grown essentially as rainfed crop, fluctuations in yield levels closely follow changes in the environment and seasons. Breeding for multiseasonal variety for many small regions within a state is being considered necessary. There is widespread awareness of achieving stability of production as well as improvement in yield of sesame under low and high input conditions as well as for different seasons.

Generally selection is done in one season and subsequent evaluation of the selected genotypes is done in the other season. This may result in the elimination of the genotypes which are at selection disadvantage in the immediate season but may have ample selection advantages in the other season. Finlay (1963, 1971), Perkins and Jinks, (1968b) and Bucio-Alanis et al. (1969) have demonstrated that stability index is a heritable trait in plants, which could be better exploited in sesame yield improvement programme.

A reliable method of estimating stability is one pre-requisite for effective selection for increased stability. Various procedures have been used to characterize individual varieties for behaviour in varying environmental conditions. Performance tests over a series of

environments, when analysed in the conventional manner, give information on genotype x environment interaction, but give no measurement of stability of individual entries.

Plaisted and Peterson (1959) presented a method to characterize the stability of yield performance when several varieties were tested in a number of locations within an year. But Eberhart and Russell (1966) pointed out that this method would call for a large number of analyses if large number of varieties were tested.

Finlay and Wilkinson (1963) proposed a simple model for measuring the varietal adaptation. They suggested that the average yield of all cultivars grown at a particular site provide a measure of that environment for use in a regression analysis of yield stability. The mean yield and the regression could provide for selection of cultivars adapted to environments with differing productivities. When only a small fraction of the variation for genotype x environment interaction is due to heterogeneity among regression coefficients, characterization of cultivars by the coefficient was not effective (Baker, 1969; Shukla, 1972; Freeman, 1973).

Later, Eberhart and Russell (1966) modified and elaborated this method based on the regression technique for measuring the stability of genotypes. This method of stability analysis was then used by many workers (Baker, 1969; Breese, 1969; Johnson et al., 1968; Perkins and Jinks, 1968a; Walton, 1976; Singh and Singh, 1980). Eberhart and Russell's

method was preferable because of its explicit nature (Jowett, 1972).

According to Eberhart and Russell (1966) the phenotypic stability could be measured by three parameters, namely mean performance over environments, the linear regression (b) and deviation from regression function ($\bar{Sd}^2$).

In the present analysis, sixty genotypes of diverse eco-geographic origin consisting 20 large, 20 medium and 20 small seeded lines were raised in three seasons viz., September 1988, January 1989 and June, 1989. The data were recorded on 16 quantitative traits comprising the seed size, yield and their components in all the three seasons and formed the testing ground for the effective evaluation of the breeding material in the present study.

5.6.1. Analysis of variance

Analysis of variance in individual seasons and in pooled analysis indicated that the genotypes differed among themselves for all the sixteen characters studied excepting the plant height at maturity in SI and in pooled analysis.

From the pooled analysis of variance, it was seen that the individual seasonal effects were highly significant for all the traits indicating differential effect of each season. The relative ranking of the three seasons in the present study revealed that SI was best for

plant height, number of branches, number of capsules, seed length, seed breadth and oil content. SIII was best for days to maturity, number of flowers, 1000 seed weight, 1000 seed volume, seed yield and harvest index. SII was best for capsule volume, number of seeds per capsule, seed density and total dry matter production. SII seemed to be the stress season as it showed better expression for only four yield contributing traits. SIII seemed to be best season as it showed maximum expression of seed yield, 1000 seed weight and harvest index. Thus the widely different seasons of the present investigation would thus make it possible for early selection of genotypes to create varieties well adapted to fluctuating seasons.

Different genotypes reacted differently to varying seasons which revealed the presence of highly significant genotype x season interaction mean squares for all the characters except plant height at maturity. Highly significant interaction of season on yield and yield components was also reported in many other crops such as soyabean by Schutz and Bernard (1967) and in tobacco by Gupton et al. (1974). In sesame, Kandasamy (1985) reported significant GxE interaction effects for yield, plant height, capsule length and number of seeds per capsule. This indicated that the genotypes of sesame like other crops showed differential responses when grown in different seasons, necessitating the need for conducting tests during several seasons.

The arithematic translation of the mean squares into the estimates of genotypic component (σ^2_g) and genotype x season interaction

component (σ^2_{gl}) indicated the relative importance of the corresponding source of variation computation of σ^2_g ; σ^2_{gl} ratio revealed the major share of the genotype x season component rather than the genotypic component in determining the character expression for 1000 seed weight (1:3.71), seed breadth (1:3.33), capsule volume (1:3.33), number of seeds per capsule (1:2.97), number of branches (1:2.77), harvest index (1:1.57), total dry matter production (1:1.55), oil content (1:1.54), seed yield (1:1.47), days to maturity (1:1.45), number of flowers (1:1.43) and number of capsules (1:1.43). For seed length and seed density the share of the genotypic component was equal to that of the genotype x season component (1:1.00). For plant height (1:0.93) and 1000 seed volume (1:0.72) the share of the genotypic component was more than of genotype x season component. The predominance of σ^2_{gl} compared to σ^2_g for most of the characters indicated the necessity for testing the breeding materials in a number of seasons. For the characters seed length and seed density, the equal share of the σ^2_g and σ^2_{gl} indicated the equal importance of GxS, in their expression, whereas for the traits, 1000 seed volume and plant height, the narrowest ratio of σ^2_g , σ^2_{gl} indicated the lesser influence of G x S component. A low G x S interaction component for characters has great significance for the plant breeder. In such a case, a variety breed and tested at one of the seasons will give a similar performance at other seasons.

5.6.2. Anova for stability

The G x S interaction effects were further partitioned into linear and non-linear components in the present study. The mean squares

due to regression (linear component of $G \times S$ interaction) were significant for days to maturity, plant height at maturity, number of branches, number of flowers, number of capsules, number of seeds per capsule, 1000 seed volume, oil content, seed yield, total dry matter production and harvest index. The non-linear component (pooled deviations) of the $G \times S$ interactions were also significant for the above mentioned characters except 1000 seed volume, when tested against their respective pooled error. The ratio of non-linear: linear component revealed preponderance of linear component for all the characters excepting capsule volume and total dry matter production. For capsule volume the linear and non-linear component was almost equal while for total dry matter production, linear component was less than the non-linear component. Predominant linear component suggested that the performance of the genotypes may be predicted across the seasons with great precision (Breese, 1969; Samuel et al., 1970; Singh and Singh, 1980). This response is not only predictable but perhaps is also simply inherited (Bains and Gupta, 1972; Kumar, 1975).

In the present study, the ratio of non-linear to linear component was the widest for 1000 seed volume (1:40.30) followed by plant height (1:21.99), days to maturity (1:12.93). For 1000 seed weight and number of seeds per capsule the linear component was six and two times greater than the non-linear component respectively. For seed yield also the linear component was two times higher than the non-linear component. The prediction with precision is possible for these characters. The

other characters excluding capsule volume and total dry matter production the linear component was marginally higher than the non-linear component. So the prediction of the characters with precision is less possible comparatively. The prediction with precision is hardly possible for capsule volume where linear and non-linear component was more or less equal and total dry matter production where the linear component was slightly less than the non-linear component. The performance of these characters depend on seasonal influence on their expression.

5.6.3. Stability of seed size, yield and component characters

Eberhart and Russell (1966) defined a stable genotype as one which showed a high mean yield, regression coefficient (b) around unity and deviation from regression nearer to zero. Later on Breese (1969), Samuel et al. (1970), Paroda and Hayes (1971), Cross (1977) and Chaudhary and Paroda (1980) advocated that linear regression (b) could simply be regarded as a measure of response of a particular genotype, whereas the deviation from regression ($\bar{Sd}^2$) as a measure of stability.

Grafius (1956) emphasized that the studies of individual yield component can lead to simplification in genetic explanation of yield stability. If traits associated with high yield stability could be found, the plant breeder might effectively select for yield stability by selecting for these correlated traits. For that the genetic association of the component trait with yield should also be known.

In the present study, out of 60 genotypes, only those which showed high mean (overall mean + 2SE) were considered for classification and characterisation. These genotypes were classified into four groups according to the methodology followed by Mehra and Ramanujam (1979) and Singh and Singh (1980).

Group	Mean	b	$\bar{S}d^2$
I	High mean	around unity*	around zero*
II	High mean	Significantly deviating from unity	around zero*
III	High mean	Significantly deviating from unity	significantly deviating from zero
IV	High mean	around unity*	significantly deviating from zero

* Deviation not significant.

Population falling in group I will have average responsiveness and highly stable over seasons. Populations in group II will have above or below average responsiveness, that is they will be suited for stress or favourable environments and will be stable in the respective environments. Behaviour of the population falling in group III and IV cannot be predicted.

Association analysis was also made among different characters based on the mean, 'b' and Sd^2 and discussed in detail. The genetic correlation reported in the chapter 4.1.3. for pooled analysis was considered here.

5.6.3.1. Days to maturity

When all the three parameters of stability viz., low mean performance, 'b' and $\bar{Sd}^2$ were considered together the genotypes could be classified as follows:

Group I	Group II	Group III	Group IV
G15,G19,G25	G4, G23,		G2, G8, G13,
G29, G40,G42	G37,G51,	--	G20, G38, G43,
G48	G52		G45, G46, G49, G50.

Seven genotypes (group I) showed non significant GxS interaction for days to maturity. Days to maturity showed non-significant association with seed yield in the pooled analysis. While the stability parameters 'b' of days to maturity had strong negative association with 'b' of seed yield, $\bar{Sd}^2$ of days to maturity showed non significant association with the $\bar{Sd}^2$ of seed yield. So the responsiveness of days to maturity had negative effect on the responsiveness of seed yield. But at the same time, the stability of days to maturity had no impact on the stability of seed yield. In the absence of any relationship between

the stability of days to maturity and seed yield, selection from among the range of genotypes, that showed low mean, may be effected for enhancing the yield potential only, provided other traits correlated with yield stability did not interfere.

5.6.3.2. Height of the plant at maturity

A simultaneous consideration of the three parameters of stability for individual genotype led to the grouping of the genotypes as follows:

Group I	Group II	Group III	Group IV
G3, G4, G5, G6 G21, G27, G32, G33 G34, G35, G38, G39, G44, G49, G58.	G8, G11,	--	G1, G12, G14, G16, G18, G20, G26, G30, G31, G36 G52.

In fifteen lines of group I, G x S interaction was absent. Genotypes G8 and G11 are suitable for stress or favourable seasons. Mean plant height was highly significantly and positively associated with mean seed yield. No association was observed between 'b' and $\bar{S}d^{-2}$ of plant height with 'b' and $\bar{S}d^2$ of seed yield. This suggested that the stability and responsiveness of plant height at maturity had no influence on the stability and responsiveness of seed yield.

5.6.3.3. Number of branches

Depending upon the type of interaction exhibited by individual genotypes and considering the stability parameters jointly, the genotypes were grouped as follows:

Group I	Group II	Group III	Group IV
G2, G3, G5, G6			G17, G18, G20,
G7, G11, G22, G25,	G1, G29	-	G42
G26, G27, G30, G31,			
G33, G39, G52, G53,			
G54, G57, G58, G60			

Twenty genotypes fell in group I and so they had average responsiveness over seasons and they were also stable. Genotypes G1 and G29 were responsive to favourable or unfavourable seasons and stable. Number of branches showed highly significant positive association with seed yield. But there were no association between 'b' and $\bar{Sd}^2$ of number of branches and 'b' and $\bar{Sd}^2$ of seed yield. So the stability and responsiveness of number of branches had no influence on the stability and responsiveness of seed yield.

5.6.3.4. Number of flowers

A simultaneous consideration of the three stability parameters led to the grouping of the genotypes as follows:

Group I	Group II	Group III	Group IV
G3, G4, G5, G7, G8 G11, G12, G18, G20, G26, G27, G30, G31, G32, G33, G36, G37, G40, G44, G49, G53, G58.	G14, G16, G35.	--	--

G x S interaction was absent for 22 genotypes which came under group I. Thus they exhibited average responsiveness and stability over seasons. Genotypes G14, G16 and G35 were suitable for stress or favourable seasons. This trait was highly significantly and positively associated with seed yield. There was no relationship between 'b' of number of flowers and 'b' of seed yield as also between $\bar{S}d^2$ of number of flowers and $\bar{S}d^2$ of seed yield. This implies that the stability of seed yield will in no way be affected by the stability or instability of number of flowers.

5.6.3.5. Number of capsules

On consideration of the stability parameters the population was grouped as follows:

Group I	Group II	Group III	Group IV
G4, G6, G7, G12, G14, G31, G35, G36, G40, G44, G58.	G3, G16,G30, G38.	--	G11, G18,G20, G24, G26,G27,G32,G33.

Eleven genotypes showed non-significant G x S interaction for number of capsules (Group I). Four genotypes fell in Group II were suitable for stress or favourable seasons. The other eight genotypes exhibited unpredictable behaviour of the G x S interaction (Group IV). Number of capsules showed highly significant positive association with seed yield. The 'b' and $\bar{S}d^2$ of this trait had non-significant association with 'b' and $\bar{S}d^2$ of seed yield. This implies that the stability and responsiveness of number of flowers had no influence on the stability and responsiveness of the seed yield.

5.6.3.6. Volume of capsules

An appraisal of the stability and mean volume of capsules of the individual genotypes on the basis of three stability parameters led to the grouping of the genotypes as follows:

Group I	Group II	Group III	Group IV
G1, G17, G32, G33, G44, G46, G47.	G14, G45.	--	G4, G6, G7, G12, G13, G18, G20, G28, G29, G30, G38, G39, G48, G49, G52, G58, G59.

Seven genotypes showed non-significant G x S interaction for volume of capsules (Group I). Seventeen genotypes exhibited unpredictable behaviour of the G x S interaction (Group IV). G14 and G45 showed linear G x S interaction and their performance was predictable across the seasons. Volume of capsules showed non-significant association with seed yield. There was a negative significant association between 'b' of capsule volume and 'b' of seed yield. So the responsiveness of capsule volume had a negative impact on the responsiveness of the seed yield. But there was non significant association between the $\bar{S}d^2$ of capsule volume and $\bar{S}d^2$ of seed yield. Hence the stability of capsule volume had no impact on the stability of the seed yield.

5.6.3.7. Number of seeds per capsule

A simultaneous consideration of the three stability parameters led to the grouping of the genotypes as follows:

Group I	Group II	Group III	Group IV
G6, G7, G17, G24, G39, G43, G46, G47, G51, G52.	G21, G48	--	G1, G4, G8, G12, G13, G14, G22, G29, G30, G33, G34, G38, G45, G50.

Ten genotypes were classified in Group I and thereby exhibited average responsiveness over seasons and they were also stable. Two genotypes viz., G21, and G48 came in Group II, and were responsive to favourable or stress season and stable. The behaviour of fourteen genotypes falling in Group IV were not predictable. The correlation between this trait and seed yield was non significant. The correlations of 'b' and $\bar{S}d^2$ of this trait with 'b' and $\bar{S}d^2$ of seed yield were also not significant. This implies that the responsiveness and stability of number of seeds per capsule had no influence with the responsiveness and stability of seed yield.

5.6.3.8. Length of seeds

Depending upon the type of interaction exhibited by individual genotypes and considering the stability parameters jointly, the genotypes were grouped as follows:

Group I	Group II	Group III	Group IV
G6, G9, G10, G13, G18, G31, G40, G60.	--	--	G3, G4, G5, G7, G8, G16, G22, G28, G36, G44, G45, G48, G50.

Eight genotypes (Group I) showed non significant G x S interaction for seed length and there by exhibited average responsiveness and stability. The behaviour of the thirteen genotypes falling in Group IV were not predictable. The correlation between seed length and seed yield was non-significant association among the 'b's of seed length and seed yield was also non significant. Similarly, there was non-significant association between $\bar{S}d^2$ of seed length and seed yield. So the stability and responsiveness of seed yield was not affected by the stability and responsiveness of the seed length.

5.6.3.9. Breadth of seeds

When all the three parameters of stability viz., high mean performance, 'b' and $\bar{S}d^2$ were considered together the genotypes could be classified as follows:

Group I	Group II	Group III	Group IV
G4, G9, G11, G12, G21, G24, G25, G26, G28, G29, G36 G41, G44, G45, G46, G58.	G40	--	G15, G19, G20, G32, G38, G39, G43.

Sixteen genotypes showed non significant G x S interaction for breadth of seeds and thus displayed average responsiveness and high stability. Genotype G40 falling in Group II was suited for favourable or stress seasons. The behaviour of the seven genotypes falling in Group IV were not predictable. Seed breadth evinced non significant association

with seed yield. The 'b' and $\bar{S}d^2$ of seed breadth also evidenced non significant association with the 'b' and $\bar{S}b^2$ of seed yield. Therefore, the responsiveness and stability of seed breadth had no way affected the responsiveness and stability of seed yield.

5.6.3.10. Weight of 1000 seeds

A simultaneous consideration of the three stability parameters led to the grouping of the genotypes as follows:

Group I	Group II	Group III	Group IV
G6,G9,G12,G20, G27,G32,G38	G34	--	G3,G8,G10,G11,G15,G18, G19,G21,G26,G31,G33, G40,G57,G60.

In seven genotypes G x S interaction was absent and evinced average responsiveness and high stability. Only one genotype namely G34 evidenced linear G x S interaction ('b' significantly deviating from unity) and so its performance was predictable over seasons. It was categorized to be suited to favourable or stress seasons.

Thousand seed weight was highly significantly and positively associated with seed yield. There were no relationship between 'b' of 1000 seed weight and 'b' of seed yield as also between $\bar{S}d^2$ of 1000 seed weight and $\bar{S}d^2$ of seed yield. This implies that the stability of

seed yield will no way be affected by the stability or instability of 1000 seed weight. Similarly the responsiveness of seed yield will no way be affected by the responsiveness or non-responsiveness of the 1000 seed weight. Therefore, it would be reasonable to state that the seed yield potential could be greatly enhanced without disturbing its stability, by selecting families with high 1000 seed weight. Seven genotypes included in Group I of the present study merit consideration for such a selection. Genotype G34 in Group II was specifically suited to either favourable or stress season. The fourteen genotypes of Group IV, which show high G x S interaction may also be considered for selection as they recorded high 1000 seed weight.

5.6.3.11. Volume of 1000 seeds

On consideration of the stability parameters the population was grouped as follows:

Group I	Group II	Group III	Group IV
G17, G20, G35, G46, G56.	G13, G14, G45	--	G5, G21, G22, G37, G39, G40, G41, G47, G48, G52, G55, G57, G58.

Five genotypes showed non significant G x S interaction for volume of 1000 seeds (Group 1). Thirteen genotypes exhibited unpredictable behaviour of the G x S interaction (Group IV). Genotypes G13,

G14, and G45 showed linear G x S interaction and their performance was predictable across the seasons.

Volume of 1000 seeds showed non significant association with seed yield. There were no relationship between 'b' of 1000 seed volume and 'b' of seed yield as also between $\bar{S}_d^2$ of 1000 seed volume and $\bar{S}_d^2$ of seed yield. This implies that the responsiveness and stability of seed yield will in no way be affected by the responsiveness and stability of 1000 seed volume.

The genotypes G17, G20, G35, G46 and G56 which exhibited high mean 1000 seed volume with average responsiveness coupled with high stability over seasons may be of much use for effective improvement of 1000 seed volume with high stability.

5.6.3.12. Density of seeds

Depending upon the type of interaction exhibited by individual genotypes and considering the stability parameters jointly, the genotypes were grouped as follows:

Group I	Group II	Group III	Group IV
G1, G4, G6, G9, G10,	G2, G8, G11, G19,		G7, G12, G15, G16.
G18, G25, G30, G32,	G31, G44, G49, G51, --		
G33, G34.	G54, G60		

Eleven genotypes exhibited average responsiveness over seasons and they were also stable i.e. G x S interaction was absent (Group I). Ten genotypes showed linear G x S interaction and their performance was predictable across the seasons (Group II). Four genotypes exhibited unpredictable behaviour of the G x S interaction (Group IV).

Seed density evidenced highly significant positive association with seed yield. However there were no relationship between the stability parameters ('b' and $\bar{S}^2d$) of seed density and seed yield. This suggested that the stability and responsiveness of seed density had no influence on the stability and responsiveness of seed yield.

The eleven genotypes (Group I) which exhibited high seed density across the seasons may be of much use for effective improvement of seed density with high stability.

5.6.3.13. Oil content

An appraisal of the stability and mean oil content of the individual genotypes on the basis of three stability parameters led to the grouping of the genotypes as follows:

Group I	Group II	Group III	Group IV
G1, G15, G19, G20, G35, G37, G48, G50, G52, G55.	G7, G26, G40	---	G5, G8, G13, G18, G21, G29, G31, G33, G34, G38, G42, G44, G45, G47, G53, G60.

Ten genotypes showed non significant G x S interaction for oil content (Group I). Genotypes G7, G26 and G40 showed linear G x S interaction and their performance was predictable across the seasons (Group II). Sixteen genotypes exhibited unpredictable behaviour of the G x S interaction (Group IV).

Oil content showed non-significant association with seed yield. There were non significant association between the stability parameters ('b' and $\bar{S}^2_d$) of oil content and seed yield. Hence the responsiveness and stability of seed yield will in no way be affected by the responsiveness and stability of oil content. Therefore it would be possible to increase the seed yield potential without disturbing its stability, by selecting families with high oil content. Ten genotypes included in Group I of the present study merit consideration for such a selection. Three genotypes in Group II were specifically suited to either favourable or stress season. Sixteen genotypes which showed high G x S interaction may also be considered for selection as they recorded high oil content.

5.6.3.14. Seed yield

A critical appraisal of the stability and productivity of the individual genotypes on the basis of three stability parameters led to the grouping of the genotypes as follows:

Group I	Group II	Group III	Group IV
G3, G12, G27, G30	--	---	G7, G11, G16, G20, G26, G31, G32, G34, G35, G38, G39, G40, G44, G45, G50, G58, G60.

The linear as well as non-linear components of G x S interactions for seed yield was non-significant for four genotypes viz., G3, G12, G27, G30 (Group I). The behaviour of seventeen genotypes were not predictable (Group IV). The four genotypes of Group I deserve utmost merit consideration for selection for further study to evolve superior stable varieties with high yield.

Seed yield exhibited highly significant positive association with plant height, number of branches, number of flowers, number of capsules, 1000 seed weight, seed density, total dry matter production and harvest index. The 'b' of seed yield was highly significantly and negatively associated with 'b' of days to maturity whereas with capsule volume it was negative and significant. However, the association among $\bar{S}^2_d$ of seed yield, days to maturity and capsule volume was non significant. Therefore, the responsiveness of the days to maturity and capsule volume had negative impact on the responsiveness of seed yield. However, the stability of seed yield was not affected by the stability of the days to maturity and capsule volume.

5.6.3.15. Total dry matter production

On consideration of the stability parameters the population was grouped as follows:

Group I	Group II	Group III	Group IV
G11, G12, G24, G27, G30 G52, G58, G59	--	--	G7, G14, G16, G20, G26, G31, G32, G34, G37, G39 G40, G48.

Eight genotypes showed non significant G x S interaction for total dry matter production (Group I). Twelve genotypes exhibited unpredictable behaviour of the G x S interaction (Group IV).

Total dry matter production evinced highly significant positive association with seed yield. There was no relationship between 'b' of total dry matter production and 'b' of seed yield as also between $\bar{S}^2_d$ of total dry matter production and $\bar{S}^2_d$ of seed yield. This implies that the responsiveness and stability of seed yield will in no way be affected by the responsiveness and stability of total dry matter production. Therefore, seed yield potential could be greatly enhanced without disturbing its stability, by selecting genotypes, with high total dry matter production. Eight lines included in group I of the present study merit consideration for such a selection.

5.6.3.16. Harvest index

A simultaneous consideration of the three stability parameters led to the grouping of genotypes as follows:

Group I	Group II	Group III	Group IV
G5, G11, G12, G22, G35, G44	G2	--	G3, G7, G10, G13, G16, G18, G27, G28, G29, G30, G31, G38, G39, G45, G50, G60.

Six genotypes showed non-significant G x S interaction (Group I). They had average responsiveness and high stability. Genotype G2, exhibited high or below average responsiveness and were suited for stress or favourable season. Sixteen genotypes evidenced unpredictable behaviour of G x S interaction (Group IV).

Harvest index displayed highly significant positive association with seed yield. The responsiveness and stability of harvest index ('b' and $\bar{S}^2_d$) had no relationship with responsiveness and stability of seed yield. In the absence of any relationship between stability parameters of harvest index and seed yield, selection from among the range of genotypes that showed a high mean, may be effected for enhancing the seed yield potential only, provided other traits correlated with seed yield stability did not interfere.

The intercorrelation among the traits which were positively associated with seed yield were mostly strong positive or positive significant. Some traits evidenced neutral association too. But no significant negative association among these traits was evinced.

The intercorrelation among the 'b's of the traits which were positively and significantly associated with seed yield were mostly neutral. The 'b' of plant height was positively and significantly associated with 'b' of total dry matter production and harvest index. The 'b's of number of flowers, number of capsules, and 1000 seed weight evinced

significant negative association with the 'b' of harvest index. So the responsiveness of number of flowers, capsules and 1000 seed weight had negative influence on the responsiveness of total dry matter production.

The intercorrelation among the traits which were positively associated with seed yield were mostly neutral. However, $\bar{S}^2_d$ of the plant height was positively and highly significantly associated with $\bar{S}^2_d$ of total dry matter production and harvest index. A similar positive highly significant association was found between $\bar{S}^2_d$ of total dry matter production and harvest index. $\bar{S}^2_d$ of number of capsules was positively and significantly associated with the $\bar{S}^2_d$ of 1000 seed weight. The notable association were the significant negative correlation of the $\bar{S}^2_d$ of number of branches with the $\bar{S}^2_d$ of 1000 seed weight and total dry matter production. So the stability of number of branches and 1000 seed weight had negative impact on the stability of the total dry matter production.

From the stability analysis it may be concluded that significant differences existed among the genotypes for all the characters studied excepting plant height at maturity. The seasons selected for the study varied significantly in respect of all the sixteen traits studied. Genotype x season interaction was significant for all the traits except plant height at maturity. Maximum phenotypic expression for plant height, number of branches, number of capsules, seed length, seed breadth and oil content was observed in SI. For days to maturity, number of flowers, 1000 seed weight, 1000 seed volume, seed yield and harvest index the

maximum expression was observed in SIII. In SII, capsule volume, number of seeds per capsule, seed density and total dry matter production displayed maximum expression.

Genotype x seasonal interaction was significant for all the traits except plant height at maturity indicating that different genotypes responded differently to changes in the season. The genotype x season interaction component was predominant for 1000 seed weight, seed breadth, capsule volume, number of seeds per capsule, number of branches, harvest index, total dry matter production, oil content, seed yield, days to maturity, number of flowers, and number of capsules. For seed length and seed density the share of the genotypic component was equal to that of genotype x season interaction component. For plant height and 1000 seed volume, genotypic component of variation (σ^2_g) was greater than the genotype x season component (σ^2_{gl}) indicating that these two characters were least sensitive to seasonal changes compared to other characters. A major portion of the variance attributed to genotype x season interaction was accounted for by the linear component (variance due to regression) for all the traits excepting capsule volume and total dry matter production. For capsule volume the linear and non-linear component was almost equal. For total dry matter production, linear component was less than the non-linear component. Preponderance of linear portion over non-linear portion was suggestive of possibilities of prediction of the performance of the genotypes across the seasons. 1000 seed volume followed by plant height, days to maturity and 1000 seed weight were the most predictable one.

Almost all the genotypes showed significant bivalues for all the 16 traits studied. This suggested that the degree of adaptation of different genotypes varied, leading to significant $G \times S$ (linear) mean square. Any generalization regarding the stability of a genotype for all the traits is too difficult since the genotypes studied did not exhibit uniform response and stability patterns. These two attributes namely, responsiveness and stability appeared to be specific for individual character within a given genotype and were not common for all the characters of that genotype. This may be explained on the basis of compromises and compensations among the developmental patterns of the different traits (Singh and Singh, 1980). Evidence are available (Grafius, 1956; Adams and Shank, 1959; Allard and Bradshaw, 1964; Bradshaw, 1965; Bains and Gupta, 1974; Singh and Singh, 1980), which suggested the importance of component compensation in imparting homeostasis for complex traits like yield.

The frequency of genotypes not interacting with seasons was maximum for number of flowers (22) followed by number of branches (20), seed breadth (16) and plant height (15) showing that a large majority of the genotypes had stability for this character. For seed yield a maximum number of genotypes exhibited unpredictable interaction with season indicating that a vast majority of genotypes were unstable for seed yield.

Correlation coefficients (pooled) indicated that among the sixteen traits studied only eight characters viz., plant height, number of branches, number of flowers, number of capsules, 1000 seed weight,

seed density, total dry matter production had strong positive association with seed yield. The intercorrelation among these characters were either highly significant positive or significant positive or neutral. None of them had negative association.

Stability and responsiveness of the traits which showed significant positive or strong significant positive association with seed yield viz., plant height, number of branches, number of flowers, number of capsules, 1000 seed weight, seed density, total dry matter production and harvest index were not associated with the stability and responsiveness of seed yield, i.e. the association between 'b's, $\bar{S}^2$ d s of these traits with seed yield was non-significant. In the absence of any relationship between the stability parameters of these positive traits with stability parameters of seed yield, selection from among the range of genotypes that showed high mean may be effected for enhancing the yield potential only, provided other traits correlated with yield stability did not interfere. In the present study yield stability and responsiveness were not associated with the stability and responsiveness of the traits which were positively and significantly associated with seed yield. So in sesame high yield and stability can be expected to be achieved simultaneously.

On the otherhand, the stability of weight of 1000 seeds was positively and significantly associated with the stability for number capsules and volume of 1000 seeds. It also exhibited negative significant

association with the stability of number of branches. So, among the traits which were positively and significantly associated with 1000 seed weight priority may be given to all the other traits excluding number of branches, as the stability of the later had showed negative impact on the stability of 1000 seed weight.

Finlay (1963, 1971), Perkins and Jinks (1968b) and Bucio-Alanis et al. (1969) have demonstrated that stability index is a heritable trait in plants. It is well known that the yielding ability and response to environmental changes are the two independent attributes of a genotype and are governed by separate sets of gene systems (Finlay and Wilkinson, 1963; Bucio-Alanis et al., 1969; Bains, 1976; Verma et al. 1978 and Singh and Gupta, 1984). In the present study while the mean of the characters viz., plant height, number of branches, number of flowers, number of capsules, 1000 seed weight, seed density, total dry matter production and harvest index showed highly significant positive association with seed yield, their stability parameters viz., 'b' and $\bar{S}^2d$ were not associated with the 'b' and $\bar{S}^2d$ of seed yield. This clearly indicated that in sesame, separate set of gene systems govern the yielding ability, and response to the season. In fact it was well evidenced from the association pattern of number of branches with 1000 seed weight. When the per se performance of number of branches showed positive significant association with 1000 seed weight, their stability parameters did not exhibit such an association. So, by selecting and manipulating these positively associated traits we can achieve higher yield without disturbing yield stability.

The absence of relationship of linear component of yield (b) with the linear component of the component traits excepting days to maturity and capsule volume, and the lack of relationship of non-linear component of seed yield ($\bar{S}^2d$) with the non-linear components of other traits are an indicative of independent genetic mechanisms controlling their response to seasonal variations (Bains and Gupta, 1974). In other words, as inferred by Jatsara and Paroda (1979), the stability parameters for such characters appeared to be governed by different genes or gene combinations.

So, the stability and average responsiveness of the genotypes viz., G3, G12, G27 and G30 could not be attributed to the stability of any other trait which were positively and highly significantly associated with seed yield. Because the associations among the stability parameters of these traits with those of seed yield were non significant. Moreover many of the genotypes which exhibited high stability for these traits were highly unstable for seed yield. Similarly it could not be attributed solely to the responsiveness of the days to maturity and capsule volume, because inspite of a highly significant negative and significant negative (respectively) association of 'b's of these two component traits with those of seed yield, many of the families which exhibited high stability for these traits were highly unstable for seed yield.

A critical perusal of the present results provided interesting information regarding the relative importance of the component traits

in imparting high seed yield may not impart stability of seed yield. Crop varieties may have the same yield but have it as a result of interaction of different component characters. Similarly, these may have the same yield stability but may be or may not be due to the stability of different component traits. Thus, for maximal fitness of an organism, all the traits may not have the same degree of stability. Bradshaw (1965) observed that fitness of an organism was the outcome of interaction of all the component characters. These component characters may each have their own plasticity and response to environmental and seasonal variation. Maximal fitness can, therefore, be obtained by adjustment in the plastic component traits. Grafius (1956) and Singh and Singh (1980) presented an analysis of such relationship of yield and yield components in oats and wheat respectively. The changes in the components compensate each other in such a way that their product is relatively invariable. The components of yield are therefore, homeostatic devices (Bains and Gupta, 1974; Singh and Singh, 1980).

It may be inferred that days to maturity and capsule volume may be the homeostatic devices which by adjusting themselves impart homeostasis for the final complex trait namely seed yield. Therefore, the variability in the stability of these component traits could be successfully utilized in imparting homeostasis for yield.

The genotypes were identified as stable or unstable for the sixteen traits studied by following the methodology of Mehra and Ramanujam (1979) and Singh and Singh (1980) and are presented below.

The genotypes listed in Table 189, can be utilized for improving the seed yield without disturbing the stability, as they showed high mean and stability for the characters viz., plant height, number of branches, number of flowers, number of capsules, 1000 seed weight, seed density, total dry matter production and harvest index as these traits showed highly significant positive association with seed yield.

Table 189. Stability of the sixty genotypes for sixteen characters.

Genotypes	Characters	
	Group I	Group II
G1	X1,X6,X12,X13	X3
G2	X3	X12,X16
G3	X1,X2,X3,X4,X14	X5
G4	X2,X4,X5,X9,X12	
G5	X2,X3,X4,X16	
G6	X2,X3,X5,X7,X8,X10,X12	
G7	X3,X4,X5,X7	X13
G8	X4	X2,X12
G9	X8,X9,X10,X12	
G10	X1,X8,X12	
G11	X3,X4,X9,X15,X16	X11,X12
G12	X1,X4,X5,X9,X10,X14,X15,X16	
G13	X8	X11
G14	X5	X1,X4,X6,X11
G15	X13	

Genotypes	Characters	
	Group I	Group II
G16	X1	X4,X5
G17	X6,X7,X11	X1
G18	X4,X8,X12	
G19	X13	X12
G20	X4,X10,X11,X13	
G21	X2,X9	X7
G22	X2,X16	
G23	-	-
G24	X7,X9,X15	X13
G25	X3,X9,X12	
G26	X1,X3,X4,X9	
G27	X1,X2,X3,X4,X10,X14,X15	
G28	X9	
G29	X9	X3
G30	X3,X4,X12,X14,X15	X5
G31	X3,X4,X5,X8	X12
G32	X2,X4,X6,X10,X12	X1
G33	X2,X3,X4,X6,X12	
G34	X2,X12	X10
G35	X2,X5,X11,X13,X16	X4
G36	X4,X5,X9	
G37	X4,X13	
G38	X2,X10	X5

Genotypes	Characters	
	Group I	Group II
G39	X1,X2,X3,X7	
G40	X4,X5,X8	X9,X13
G41	X9	-
G42	-	-
G43	X7	-
G44	X2,X4,X5,X6,X9,X16	X12
G45	X9	X6,X11
G46	X6,X7,X9,X11	-
G47	X1,X6,X7	
G48	X13	X7
G49	X2,X4	X12
G50	X13	
G51	X7	X12
G52	X3,X7,X13,X15	
G53	X3,X4	
G54	X3,	X12
G55	X13	
G56	X11	
G57	X3	
G58	X2,X3,X4,X5,X9,X15	
G59	X15	
G60	X3,X8	X12

Sesame which has long been a crop of low input management may be difficult to respond to high in-put practices. Genotypes which are classified in Group I are widely adaptable and can be incorporated in sesame improvement programme. Genotypes G3, G12, G27 and G30 which were highly stable for seed yield also stable for most of the component traits which were significantly and positively associated with seed yield.

Genotype G3 showed high stability and average responsiveness for plant height, number of branches and number of flowers. G12 exhibited high stability and average responsiveness for number of flowers, capsules, weight of 1000 seeds, total dry matter production and harvest index. G27 expressed high stability and average responsiveness for plant height at maturity, number of branches, flowers, 1000 seed weight, and total dry matter production. G30 evinced high stability and average responsiveness for number of branches, flowers, seed density and total dry matter production.

Thus, the present study has focussed attention on the necessity for testing sesame genotypes in varied seasonal conditions. Intensified efforts could well be directed towards determining what morphological and developmental features of component characters complement each other when grown in different seasons. By directing their selection towards stable genotypes at the time of selection of parents for hybridization itself, sesame breeders may be able to develop

varieties with high yield potential and high stability to perform advantageously in both optimal and sub-optimal seasons.

5.7. STUDIES ON GENETIC DIVERGENCE

Genetic divergence among parents is important in self pollinated crops because a cross involving genetically diverse parents is likely to produce high heterozygous as well as heterotic effect. In such a cross, more variability could be expected in the segregating generations due to the accumulation of the genes of both the parents. It is known that estimates of genetic divergence are also influenced by environments and seasons. Therefore, if the divergence analysis is conducted in a number of seasons and parents are selected on the basis of consistent divergence over the seasons, the problem of influence of seasons on divergence analysis can be largely overcome.

Genetic divergence, as one of the criteria of selection of parents, is considered in plant breeding as early as 1962 (Murty et al., 1962; Timothy, 1963). Later Joshi and Dhawan, (1966), Murthy and Arunachalam (1966), Arunachalam et al. (1984) and Lefort - Buson (1987) also stated that for exploiting heterosis as a means of increasing production it is necessary to have parents of maximum genetic divergence. The more diverse the parents, more is the chance for pronounced heterotic effects and increased spectrum of variability in the segregating generations.

Limited information on genetic diversity in sesame is available so far. The present study was undertaken to collect information on genetic diversity in 60 genotypes of different eco-geographic origin studied in three different seasons, analysed individually as well as over seasons. The relative contributions of the sixteen characters to the total diversity were also brought out. Mahalanobis D^2 statistic has been utilized as a powerful tool in quantifying the degree of divergence at genotypic level (Trehan et al., 1974; Govinda Rasu, 1982; Rathinaswamy and Jagathesan, 1984; Thangavelu and Rajasekaran, 1983 ; Dhamu et al. 1983 and Reddy, 1986; John Joel, 1987).

5.7.1. D^2 analysis

D^2 analysis of the sixty genotypes confirmed the presence of high diversity among the types by their resolution into twelve clusters in SI, six clusters in SII and pooled analysis, and eight clusters in SIII. Genotypes of different eco-geographic origin were grouped in a single cluster as well as in different clusters.

Cluster in SI consisted sixteen genotypes originating from Tamil Nadu (eight genotypes), Gujarat (two genotypes), Israel (one genotype), Greece (one genotype) and four other genotypes for which the origin is not traceable. In SII, a total of fifty one genotypes representing Tamil Nadu (26 genotypes), Andhra Pradesh (Five genotypes) Gujarat (two genotypes), Maharashtra (three genotypes), and one genotype from each of Rajasthan, Ceylon, Japan, Tanzania, Venezuela, Israel, Greece and eight genotypes of non traceable origin were clustered in

cluster I. Cluster I in S III also showed fifty one genotypes inclusive of twenty three genotypes of Tamil Nadu, five genotypes of Andhra Pradesh, four genotypes of Gujarat, two genotypes of Maharashtra, and one genotype from each of Punjab, Haryana, Pakistan, Tanzania, Venezuela, Israel, Greece and ten genotypes of non-traceable origin. But in pooled analysis only forty seven genotypes were grouped in cluster I. It consisted twenty four genotypes of Tamil Nadu, five genotypes of Andhra Pradesh, three genotypes of Gujarat, two genotypes of Maharashtra, one genotype from each of Pakistan, Tanzania, Venezuela, Israel and Greece. It also had eight genotypes of non-traceable origin. The other clusters also consisted different genotypes of varying origins (Table 190).

On the otherhand, the twenty eight genotypes of originated from Tamil Nadu were found scattered in different clusters in the different seasons and pooled analysis. Those from Tamil Nadu might also be from different sources. In SI, out of that 28 genotypes, eight genotypes were found in cluster I, fourteen in cluster II, one genotype in each of clusters IV, VI, VII, VIII, IX, X and XII. In S II, 26 were in cluster I and one in each of clusters II and IV were observed. In SIII, 23 in cluster I, two in cluster II and one in each of the clusters V, VI and VIII were recorded. Similarly in the pooled analysis, 24 in cluster I, two in cluster II, and one in each of the clusters III and V were found. Such a similar pattern of distribution was also found with the genotypes of Gujarat and Maharashtra. This indicated the presence of wide range of genetic diversity among the types of Tamil Nadu, Gujarat and Maharashtra.

Table 190. Overall clustering pattern

Genotypes	Seasons			
	S I	S II	S III	Pooled analysis
Tamil Nadu				
G 2	VII	I	I	I
G 3	II	I	I	I
G 4	IV	I	I	I
G 5	II	I	I	I
G 6	II	I	I	I
G 11	VIII	I	I	I
G 12	II	I	I	I
G 13	IX	I	I	II
G 15	II	I	I	I
G 20	I	I	V	II
G 27	I	I	I	I
G 28	II	I	I	I
G 29	I	I	I	I
G 30	II	I	I	I
G 31	II	I	VI	I
G 32	I	I	I	I
G 33	II	I	I	I
G 34	II	I	I	I
G 40	I	I	I	I
G 44	II	IV	I	I
G 52	I	I	I	I
G 53	II	I	I	I

Table 190. Contd..

Genotypes	Seasons			
	S I	S II	S III	Pooled analysis
G 54	II	I	VIII	I
G 55	I	I	I	I
G 56	XII	I	II	V
G 57	VI	II	II	III
G 58	I	I	I	I
G 59	II	I	I	I
Andhra Pradesh				
G 7	II	I	I	I
G 8	II	I	I	I
G 18	II	I	I	I
G 36	II	I	I	I
G 42	II	I	I	I
Gujarat				
G 1	IV	I	I	I
G 26	I	III	I	I
G 41	I	II	I	II
G 49	II	I	I	I
Maharashtra				
G 16	II	I	I	I
G 17	V	I	IV	VI
G 24	II	I	I	I
Rajasthan				
G 48	XI	I	II	IV
Panjab				
G 23	X	II	I	III
Hariyana				
G 46	VI	V	I	II
Ceylon				
G 14	V	I	III	II

Table 190. Contd..

Genotypes	Seasons			
	S I	S II	S III	Pooled analysis
Pakistan				
G 10	II	II	I	I
Japan				
G 45	XI	I	VII	IV
Tanzania				
G 50	II	I	I	I
Venezuela				
G 25	II	I	I	I
Israel				
G 37	I	I	I	I
Greece				
G 35	I	I	I	I
Non-traceable				
G 9	II	I	I	I
G 19	II	I	I	I
G 21	I	I	I	I
G 22	I	I	I	V
G 38	II	I	I	I
G 39	I	I	I	I
G 43	III	II	I	I
G 47	I	I	I	I
G 51	III	VI	I	III
G 60	III	I	I	I

Trehan et al. (1974) and Joel (1987) also contemplated with a similar conclusion, that a wide genetic diversity exists among the genotypes of Tamil Nadu. In fact the observation of clusters carrying only one genotype that too of Tamil Nadu origin, confirmed this. These genotypes can be well exploited in heterosis breeding.

The tendency of genotypes from diverse geographic regions to group together in one cluster or scattered distribution of genotypes of same origin in different clusters has been observed in the present study. The studies of several workers confirmed this tendency, that the geographical distribution and genetic diversity could not be directly related in any of the crops, tobacco (Murty, 1965), linseed, wheat, sorghum (Murty and Arunachalam, 1966), cotton (Singh and Gupta, 1968), greengram (Singh et al., 1976), safflower (Ranga Rao et al., 1980), and sesame (Govinda Rasu, 1982; Thangavelu and Rajasekaran, 1983, Reddy, 1986 and John Joel, 1987). This is not surprising, since we know that there is free exchange of genetic material for breeding purposes throughout the world.

Genetic drift and selection in different environments could cause greater diversity than geographical distance (Murty et al., 1965). However, geographical isolation could be important in the alteration of the breeding structure as pointed out by Wallace (1963).

In certain cases, the effect of geographic origin appeared to have influenced the clustering pattern. Five types collected from

Andhra Pradesh were clustered in a single cluster only, in all the analysis. The only one genotype of Rajasthan (G 48) and only one genotype of Japan (G 45) were mostly grouped in a single cluster. Probably, G 45 may be introduced from Japan to Rajasthan, where some natural infiltration of genes might have happened among these genotypes. Such an effect of geographic origin on clustering pattern has been recorded by Jeswani et al., (1970) in linseed, Ziauddin Ahamad et al., (1980) in triticale, Govinda Rasu (1982) and Joel (1987) in sesame. It suggests that although geographical distribution could not be taken as a sole criterion of genetic diversity in sesame, the influence of the former could still be traced.

Cluster III including three genotypes in S I, cluster I consisting fifty one genotypes in S II, cluster II representing three genotypes in S III and Cluster V having two genotypes in pooled analysis showed the least intracluster divergence in the concerned seasons and analysis. This indicated the closeness of types. This may be explained on the basis that yield being a complex character of polygenic inheritance similar phenotypes could be produced by many different combinations of genes and such combinations may have similar selective advantage (Singh and Gupta, 1968). Further, under constant selection on the segregating population such similar types are expected to be established. The highest intra-cluster divergence was recorded, for the cluster XI in SI, II in SII, I in S III and III in the pooled analysis. While the limited gene exchange between the types or selection for diverse characters could be responsible for such high intra-cluster divergence, the

penetrance and expressivity of the genotypes have also to be considered in a given set of season, as the cluster and the composition, differed widely season after season.

Highest inter-cluster distance was observed between clusters VII and XI in S I. Cluster VII exhibited higher mean values for number of branches and seed density. Cluster XI expressed maximum mean value for 1000 seed volume. So by crossing the genotypes which were grouped in VII and XI clusters will be useful to improve the seed yield as well as 1000 seed weight. Number of branches and seed density were positively and significantly associated with seed yield and 1000 seed weight. Thousand seed volume was positively and significantly associated with 1000 seed weight, it is possible to improve both seed yield and seed size.

In S II, clusters III and VI exhibited highest inter-cluster distance. Cluster III showed maximum mean value for plant height at maturity number of branches, number of flowers, number of capsules, oil content and total dry matter production. Excepting oil content all the other traits were positively and significantly associated with seed yield and seed size. Oil content mostly showed positive significant association with all these component traits. Cluster VI expressed minimum value for days to maturity and plant height. So there is a possibility to obtain genotypes with high seed yield, seed size and oil content coupled with early maturing, medium statured plant types.

Similarly, for most of the traits which were positively and significantly associated with seed yield and seed size cluster VI evidenced maximum mean value in S III. In this season cluster VII had maximum mean value for seed breadth and 1000 seed volume. These two clusters expressed maximum intercluster distance. Hence, there is a possibility to get higher seed yield, seed size coupled with higher oil content by inter-crossing among the genotypes of these clusters.

In the pooled analysis, cluster III evinced minimum number of days to maturity and cluster IV had maximum mean value for capsule volume, seed length, seed breadth, 1000 seed volume and oil content. These two clusters showed maximum inter-cluster distance. By inter-mating among the genotypes of these clusters there is a possibility to obtain higher seed size with higher oil content. As cluster III also showed lesser plant height there is a possibility to get medium statured genotypes.

As pointed out by Sokal (1965), the choice of the characters is important in multivariate analysis and the choice made in the present study appears to be appropriate. Cyclic inbreeding and crossing may be helpful in bringing new genes into a population of sesame and thus, expanding the range of adaptation. As brought out by Mather (1943) polygenic variability which is necessary for prospective, adaptive and evolutionary change need not exist as true phenotypic variation which effect fitness. Therefore, phenotypic uniformity with genetic diversity within the population appears to be very useful in sesame.

In fact, this is possible with a proper use of the suggested parents in the formation of gene complexes to replace the existing varieties.

It can be concluded that there is no relationship between genetic and geographical diversity in the material under investigation. Inter and intra-cluster distances were also not related. The grouping pattern was not consistent across seasons, indicating that genetic diversity do depend on the season and that genotype x season interaction affect genetic diversity. This is not unexpected because genetic diversity itself depend on the penetrance and expression of genes and there by the expression of traits in a given set of environment or season.

It is highly desirable that the extent of genetic divergence between populations reflected through any analysis, should be comparatively stable over seasons and environments to be of utility to plant breeders. The differential grouping of different genotypes of varying origin in different seasons, does not mean that a breeder should study divergence in only one season. In fact, it really suggests the need of studying the divergence in varying seasons.

The approaches suggested by Singh and Gupta (1984) and Singh et al. (1988) were followed in the present study to suggest the parents based on the divergence pattern in varying seasons.

- a. One may select the parents on the basis of divergence exhibited in the richest and most productive season, because it provides

opportunity for the fullest expression of genetic potential of a genotype. The relative ranking of the three seasons in the present study revealed that S III was best for days to maturity, number of flowers, 1000 seed weight, 1000 seed volume, seed yield and harvest index. Since this season exhibited higher mean performance for 1000 seed weight, seed yield and harvest index, seemed to be the best season. Using this criterion, divergent genotypes in season III may be selected from different clusters having high inter-cluster distances. Clusters VI and VII showed maximum inter-cluster distance in S III. Only one genotype in each of these two clusters viz., G 31 and G 45 were found respectively. Eventhough these genotypes were high yielding they were not stable. So, they are not suitable for breeding programme. Among the other combinations of clusters viz., IV and V, IV and VII, VII and VIII, II and VI, II and IV and I and VII, cluster I and VII having the inter-cluster distances slightly lower than the highest were selected which consisted both high yielding stable genotypes and high yielding responsive (not stable) genotypes. These cross combinations will involve G 45 (Japanese origin) with fifty one genotypes of Cluster I.

- b. Selection of parents can also be made on the basis of divergence which is consistent over the seasons. This can be taken as reliable indication of genetic divergence. Utilizing this criterion among the genotypes studied, following genotypes showed consistent divergence in all the three seasons:

- i. G 56 was consistently divergent with the following genotypes:
G 10, G 23, G 26, G 41, G 44 and G 46.
- ii. G 45 and G 48 were consistently divergence from G 10, G 23, G 26, G 41, G 44 and G 46. Added to this G 45 was also consistently different from G 57.
- iii. G 14 and G 17 were consistently divergent from G 10, G 23, G 26, G 41, G 44, G 46 and G 57.
- iv. G 23 was consistently divergent from G 14, G 17, G 31, G 45 and G 54.
- v. G 46 was consistently divergent from G 14, G 17, G 20, G 31, G 45, G 48, G 54 and G 56.

It is interesting to conceive that the divergent genotypes viz., G 14, G 17, G 45, G 48 and G 56 were also consistently divergent from the divergent genotypes G 23 and G 46. But the divergence among these two groups were not consistent. Thus they exhibited highly dissimilar response to the season due to genotype and genotype x season inter-action. On the contrary, the following genotypes viz., G 21, G 27, G 29, G 32, G 35, G 37, G 39, G 40, G 47, G 52, G 55 and G 58 were highly iso-responsive, and they were grouped in cluster I in all the analysis.

- c. One may also argue that the divergence expressed in pooled analysis may be reliable estimate and therefore should be used for selecting parents. If this criterion is followed genotypes viz., G 13, G 14, G 20, G 41 and G 46 were divergent from the rest of the sixty genotypes investigated. G 23 and G 51 were divergence from all other fifty eight genotypes. G 45 and G 48 were divergent from the remaining 58 genotypes. Similarly G 22 and G 56 were divergent from the genotypes G 1 to G 21, G 23 to G 55 and G 55 to G 60. G 17 was also divergent from the other fifty nine genotypes of the study.

It is highly interesting to note that the genotypes which were described as consistently divergent in the second (b) approach based on consistency in divergence in all the three seasons, also divergent in the pooled analysis excepting a small difference. In the second approach it was described that G 14 was consistently divergent from G 41 and G 46, but in pooled analysis they were grouped together (Cluster II). Similarly the genotype G 46 which was classified as consistently divergent from G 14, and G 20 were grouped together in cluster II in the pooled analysis. Excepting this small discrepancy both the classifications brought out the same result. Such a small discrepancy was also evidenced in the divergence pattern among the two divergent groups described at the end of approach 'b'. In the approach 'b', it was found that the divergent genotypes G 14, G 17, G 45, G 48 and G 56 consistently divergent from the divergent genotypes G 23, and G 46

But in the pooled analysis, G 14 and G 46 were grouped together (Cluster II).

On an over all consideration, both the approaches viz., based on consistency over seasons and pooled analysis hold good in the identification of the divergent genotypes. This overruled the dispute that pooled analysis may under estimate divergence because measures of divergence estimated in different seasons may cancel each other in the pooled analysis. In fact, this was supported by the realized more or less similar maximum intra-cluster distances in the pooled analysis as well as in the three different seasons. This again indicated a more or less similar cluster constitution. However, the cancellation effect was evidenced from the reduction of inter-cluster distance in the pooled analysis than that of individual sesason wise analysis.

In the present study, all the three method of approaches yielded a similar result confirming all the three approaches are suitable for selecting the divergent genotypes. A sesame breeder can select any of the three approaches based on his requirement urgency and policy changes. The following genotypes and crossings are suggested for cross breeding programme (Table 191).

i) Using the first criteria, (approach 'a') it may be concluded from the above discussion that the following cross combinations involving high yielding stable and high yielding responsive (unpredictable) genotypes are suitable to be used in future breeding programmes.

Table 191. Genotypes and crossings suggested based on genetic diversity

Approach 'a'	Approach 'b'	Approach 'c'
G45 x G 1, G 2, G 3, G 4, G 5, G 6	G14, G17, G45, G48, G56	G17, G45, G48, G56
G 7, G 8, G 9, G10, G11, G12,	G10, G23, G26, x	G10, G23, G26, G46, x
G13, G14, G15, G16, G18, G19,	G41, G44, G46	G41, G44
G21, G22, G23, G24, G25, G26,		
G27, G28, G29, G30, G32, G33,	G14 G17	G14 G17
G34, G35, G36, G37, G38, G39,	x G57	x G57
G40, G41, G42, G43, G44, G46,		
G47, G49, G50, G51, G52, G53,	G23 G46	G23 G46
G55, G58, G59, G60	G45 G 46	G45 G46
	x G57 x G20	x G57 x G56
Common genotypes and crosses : G45 x G10, G23, G26, G41, G44, G46		

EC 137935 (G 45)	x	S. 00028	(G 3)
	x	Si. 1150	(G 12)
	x	PDK.8	(G 27)
	x	S.0516	(G 30)

Genotype, G 45 is Japanese origin and G 3, G 12, G 27 and G 30 are Tamil Nadu origin. As both geographical and genetic diversity exists among these genotypes, these cross combinations involving these genotypes are expected to give high heterotic hybrids in F_1 generation and useful segregants in the later generations. Added to this, one can expect heterosis for yield as well as response to the seasons or environments, because the genotypes G 3, G 12, G 27 and G 30 were high yielding stable with average responsiveness and G 45 was high yielding responsive (unpredictable).

ii) Using first and second criterion, the following genotypes which are common in both the approaches ('a' and 'b'), also suggested for future breeding programme.

Ec 137935 (G 45)	x	Si. 1088	(G 10)
	x	IS.212	(G 23)
	x	N.36950	(G 26)
	x	A.T.9	(G 41)
	x	Co.1	(G 44)
	x	HT.6	(G 46)

iii) The divergence of above crosses was also confirmed by the third criterion, i.e., on the basis of pooled analysis and hence the above six crosses can also be utilized in breeding programme. However, when we consider high seed yield coupled with high mean performance of the traits which were positively associated with seed yield and seed size, priority must be given to the following crosses:

EC 137935 (G 45)	x	N.36950	(G 26)
	x	Co.1	(G 44)

These three genotypes showed high mean seed yield. Added to this, G 26 exhibited high *per se* performance for number of branches and flowers, and G 44 expressed high *per se* performance for number of flowers, capsules, seed density and harvest index. Eventhough the behaviour of these three genotypes can not be predicted with reference to seed yield, they were highly divergent. So heterosis can well be expected for these traits.

The foregoing discussions and suggestions are purely based on high genetic divergence coupled with stability and average responsiveness to get heterosis for both yield and responsiveness. This is possible because yielding ability and response to environmental changes are two independent attributes of a genotypes and are governed by separate sets of gene systems, (Finlay and Wilkinson, 1963; Bucio-Alanis et al., 1969; Bains, 1976; Verma et al., 1978; Singh, 1982; Singh and Gupta, 1985 and Singh, 1988).

For obtaining the high yielding hybrids, that show heterosis effects due to sets of genes responsible for yield and not for response, crossing among the divergent varieties within the cluster is recommended (Singh, 1988).

The following twelve genotypes were grouped in cluster I consistently in all the analyses. They are G, 21, G 27, G 29, G 32, G 35, G 37, G 39, G 40, G 47, G 52, G 55 and G 58. Out of these twelve genotypes only five genotypes viz., G 27, G 32, G 35, G 39 and G 40 showed high mean seed yield. Added to this they also exhibited high mean performance for most of the characters that were positively and significantly associated with seed yield and seed size. By crossing among these genotypes high yielding genotypes with a response similar to the parents can be obtained.

5.7.2. Character contribution towards genetic diversity

Relative ranking of the contribution of sixteen characters towards genetic diversity based on D^2 -statistic, revealed high Genotype X Season interaction in their percentage contribution towards genetic diversity. Volume of 1000 seeds followed by oil content exhibited highest contribution towards genetic diversity in SI, SIII and pooled analysis. In SII, oil content followed by number of capsules exhibited the highest contribution. The highest contributor-volume of 1000 seeds scored eleventh rank in this season (SII) (Table 192). Eventhough oil content scored second rank in three seasons, its contribution was constant across seasons and pooled over seasons.

**Table 192. Relative ranking of characters contributing towards diversity
(Based on D^2 statistic)**

Rank	SI	SII	SIII	Pooled
1.	Volume of 1000 seeds	Oil content	Volume of 1000 seeds	Volume of 1000 seeds
2.	Oil content	Number of capsules	Oil content	Oil content
3.	Length of seeds	Length of seeds	Number of capsules	Days to maturity
4.	Density of seeds	Volume of capsules	Days to maturity	Number of flowers
5.	Days to maturity	Number of flowers	Seed yield	Volume of capsules
6.	Weight of 1000 seeds	Days to maturity	Number of flowers	Length of seeds
7.	Number of flowers	Breadth of seeds	Total dry matter production	Density of seeds
8.	Volume of capsules	Total dry matter production	Harvest index	Number of capsules
9.	Number of branches	Weight of 1000 seeds	Volume of capsules	Seed yield
10.	Number of capsules	Number of seeds per capsule	Length of seeds	Weight of 1000 seeds
11.	Breadth of seeds	Volume of 1000 seeds	Density of seeds	Total dry matter production
12.	Total dry matter production	Height of the plant at maturity harvest index	Number of seeds per capsule	Number of branches
13.	Harvest index	Number of branches	Height of the plant at maturity;	Number of seeds per capsule; harvest index;
14.	Number of seeds per capsule; seed yield	Density of seeds; seed yield	Weight of 1000 seeds	Height of the plant at maturity; Breadth of seeds.
15.	Height of the plant at maturity		Breadth of seeds; Number of branches	

It is highly interesting to know that the characters which showed high genotypic variance and genotypic coefficient of variation showed less contribution towards genetic diversity. The only character which showed high genotypic coefficient of variation and contributed maximum towards genetic diversity was volume of 1000 seeds. It may indicate that the genotypes showing high variability for volume of 1000 seeds may be genetically divergent. Thus, the possibility of using genetic variability as a marker for genetic diversity was identified. On the other hand, oil content which contributed maximum towards genetic diversity next to volume of 1000 seeds showed only a fair amount of genotypic coefficient of variation.

5.8. Combining Ability and Heterosis

A successful approach of crop breeding programme depends on the proper choice of best parents for hybridization and the ideal selection adopted in the early generation. But the selection of parents for hybridization programme is relatively tough in the case of complex traits like yield and their components as they are governed by large number of quantitative genes which are influenced by environments and seasons. Thus breeders often meet with difficulty to fix in advance the desirable parents which will give superior progenies. In such a situation, knowledge the nature of gene action on such complex quantitative traits of economic importance is necessary to plan and adopt appropriate selection techniques (Simmonds, 1979) and breeding methodology.

Combining ability analysis gives useful information regarding the selection of parents in terms of the performance of their hybrids. This analysis elucidates the nature and magnitude of various types of gene action involved in the expression of quantitative traits (Dhillon, 1975). Thus, the knowledge of combining ability serves as useful tool for selection of parents for hybridization and further exploitation. Combining ability consists of general and specific combining ability. The general combining ability provides an indication of the importance of genes of largely additive nature, while specific combining ability indicates the importance of non-additive gene effects.

Several biometrical techniques are available to estimate the general combining ability of parents and specific combining ability of hybrids. Among them, line x tester analysis is extensively used both in self and cross pollinated crops. The advantage of line x tester analysis is that a large number of inbred lines can be evaluated than diallel analysis. Besides, it provides additional information on performance of specific hybrids and gene action in contrast to top cross or polycross. The line x tester analysis is an efficient biometrical approach for assessing the combining ability of parents and hybrids (Kempthorne, 1957).

Many workers published results relating combining ability and heterosis in different crops. Studies on combining ability and heterosis over seasons is practically scanty. As combining ability and heterosis

is also influenced by seasonal variations, an exclusive study is inevitable to find out the extent of seasonal influence on these two parameters. The present study was conducted in two seasons to find out the seasonal influence also on the combining ability and heterosis.

5.8.1. Analysis of variance

The analysis of variance within each season (individual season) revealed the presence of significant variation among the hybrids, lines and line x tester interaction for eleven out of sixteen characters analysed. Capsule volume, seed length, seed breadth, 1000 seed weight and seed density exhibited non-significant variances. Additionally, the variance due to line x tester interaction was non-significant for number of branches in S_2 . The variance due to testers was also significant for eleven out of sixteen traits studied. Capsule volume, seed length, seed breadth and seed density displayed non-significant variances both in S_1 and S_2 . Apart from these traits, 1000 seed volume in S_1 and oil content in S_2 showed non-significant variation. The pooled analysis of variance over seasons revealed the presence of significant variation among hybrids, lines, line x tester interaction, line x season interaction and (line x tester) x season interaction for eleven out of sixteen characters studied. Capsule volume, seed length, seed breadth, 1000 seed weight and seed density exhibited non-significant variances. The variance due to testers, season and testers x season interaction was significant for twelve out of sixteen characters studied. Capsule volume, seed length, seed breadth and seed density displayed non-significant variances. This indicated that lines, testers and hybrids were influenced by the

seasons. The non-significant variances may atleast partially due to the narrow genetic bases.

5.8.2. Combining ability variance

The estimates of combining ability variances showed higher values of **sca** variances than **gca** variances for all the traits examined in individual analyses. This indicated the predominance of non-additive gene action for all the traits studied. However, the variance due to **gca** was higher than the **sca** variance for seed density in the pooled analysis. This may indicate the existence of both additive and non-additive gene action in the expression of seed density. For all the other traits in the pooled analysis the variances were not comparable due to the negative sign. Variances of general combining ability and specific combining ability and their interaction with different environments is useful for formulating an efficient breeding programme (Matzinger et al., 1959). The **sca** x season interaction variances were higher than **gca** x season interaction variances. This indicated that hybrids interacted more than parents with the seasons.

5.8.3. Proportional contribution of lines, testers and line x testers interactions to the total variance

Considering the proportional contribution by lines, testers and line x testers interaction to the total variance, the lines x testers interaction per cent contributions were higher than either lines or testers for almost all the characters studied. This clearly indicated the importance of hybrid vigour non-additive gene action

5.8.4. Per se Performance, combining ability variance and effects of parents and hybrids and heterosis of hybrids

5.8.4.1. Days to maturity

The variance due to specific combining ability was higher than that of general combining ability in both the seasons as well as in the pooled analysis. Hence non-additive gene action is assumed to be controlling this character. This is in confirmity with the findings of Chavan *et al.*, (1982) and Omar Sheikh (1989). But Fatteh *et al.*, (1982). Sharma and Chauhan (1985) Padmavathi (1987) and Khorgade *et al.*, (1989) reported additive gene action for this trait, where as Khorgade *et al.* (1988) found both additive and non-additive gene action for this trait.

The highest negative and significant gca effect was observed for L_{24} followed by L_{16} , L_{21} , L_{22} and L_{23} in S_1 , L_{21} followed by L_{11} , L_{16} , and L_{22} in S_2 and L_{21} followed by L_{22} , L_{27} , L_{16} and L_{11} in pooled analysis. The lines L_{16} , L_{21} and L_{22} seemed to be good general combiner for this trait as they showed significant negative estimate in all the analyses. Hence these lines will be useful used as donors of good general combining ability. Among the testers T_1 in S_1 and pooled analysis and T_3 in S_2 exhibited highest negative significant gca effect. A high magnitude of significant sca effect was seen in $L_3 \times T_1$ followed by $L_{18} \times T_2$ and $L_3 \times T_3$ in S_1 , $L_{22} \times T_1$ followed by $L_{27} \times T_2$ and $L_{25} \times T_3$ in S_2 and $L_3 \times T_1$ followed by $L_2 \times T_1$, $L_{18} \times T_2$ and $L_{25} \times T_3$ in pooled analysis. Among these cross combinations, $L_3 \times T_1$, $L_{18} \times T_2$ and $L_{25} \times T_3$ seemed to be good specific combiner

for this trait. Eventhough, the tester T_2 was a poor general combiner, it was a good specific combiner for this trait. However, among these three testers T_1 ranked first as it displayed earliness in the hybrids irrespective of the seasons and analysis. The high magnitude of significant negative sca effect of $L_{22} \times T_1$ in S_2 was also reflected by the *per se* performance of this combination and highly significant negative heterobeltiosis and standard heterosis. The line L_{22} and tester T_1 exhibited good general combining abilities and their cross combination displayed good specific combining ability (Plate 10).

Fifteen hybrids in S_1 , sixty four in S_2 and seventeen in the pooled analysis recorded negative significant heterosis. Heterobeltiosis was negative significant for thirty four hybrids in S_1 , sixty three hybrids in S_2 and twenty two hybrids in pooled analysis. Whereas twenty five in S_1 , forty five in S_2 and thirty in the pooled analysis expressed negative and significant standard heterosis. The magnitude of negative heterosis was not so high in the present study. The number of crosses which showed negative heterobeltiosis and standard heterosis was more than the positive ones. This is in accordance with the findings of Murty (1975), Padmavathi (1987) and Omar Sheikh (1989). However, Pal (1945), Shrivastava and Singh (1981) reported higher heterotic vigour for this trait. Heterosis in the positive direction was noted by Yermanos and Kotecha (1978) and Chavan et al. (1982).

5.8.4.2. Height of the plant and maturity (Fig.30)

Estimates of combining ability variances showed that general combining ability variance was lesser than the specific combining ability variance for this trait in individual season as well as in pooled analysis. This lead to the inference that this trait is under the influence of non-additive gene action irrespective of the seasons and analyses. This is in corroboration with the reports on gene action by Chavan et al., (1982), Chaudhari et al., (1984), Krishnadoss et al., (1987) and Omar Sheikh (1989). But, additive geneaction was reported for this trait by Murthy (1975), Yermanos and Kotecha (1978), Reddy et al., (1982), Padmavathi (1987) and Khorgade et al., (1989). Both additive and non-additive gene action were reported by Dixit (1976a), Fatteh et al., (1982) and Dora and Kamala (1987).

Among the lines, L_3 followed by L_{26} and L_6 in S_1 , L_{10} followed by L_{24} and L_{13} in S_2 and L_3 followed by L_{23} and L_{24} in pooled analysis exhibited high positive significant gca effects. Among the testers T_3 expressed high positive significant gca effect in S_1 and pooled analysis and T_1 showed high positive significant gca effect in S_2 . Among the hybrids $L_3 \times T_3$ followed by $L_6 \times T_3$ in S_1 , $L_{10} \times T_1$ followed by $L_3 \times T_3$ in S_2 and $L_3 \times T_3$ followed by $L_6 \times T_3$ and $L_{24} \times T_3$ in the pooled analysis expressed highest positive significant sca effect. Among these hybrids $L_3 \times T_3$ was found to be a good specific combiner as it displayed highest positive significant sca effect in individual seasons as well as pooled analysis. Next to this, $L_6 \times T_3$ seemed to be a good specific combiner. The high magnitude of significant positive sca effects of $L_3 \times T_3$, $L_6 \times T_3$ of S_1 , $L_3 \times T_3$

of S_2 and $L_3 \times T_3$ and $L_{24} \times T_3$ of pooled analysis were also reflected by the *per se* performance of these combinations. Similarly, the high positive significant *sca* effects of the hybrids $L_3 \times T_3$, $L_6 \times T_3$ of S_1 , $L_{10} \times T_1$ of S_2 were reflected by the highly significant positive heterosis, heterobeltiosis and standard heterosis, where as the high positive significant *sca* effects of $L_3 \times T_3$, $L_6 \times T_3$ and $L_{24} \times T_3$ of pooled analysis were reflected in the standard heterosis only. In general, L_3 , L_6 , L_{24} and T_3 were good general and specific combiners. These lines and testers can be utilized for the exploitation of the hybrid vigour for plant height.

Among the lines L_{20} followed by L_{11} and L_1 in S_1 , L_{21} followed by L_{27} and L_{22} in S_2 and L_{20} followed by L_{21} and L_{11} in pooled analysis exhibited high negative significant *gca* effects. Among the testers, T_1 followed by T_2 in S_1 , T_3 in S_2 and T_1 and T_2 recorded maximum negative and significant *gca* effects. Among the hybrids, $L_3 \times T_2$ followed by $L_{18} \times T_3$ and $L_3 \times T_1$ in S_1 , $L_3 \times T_2$ followed by $L_{20} \times T_3$ and $L_{13} \times T_1$ in S_2 and $L_3 \times T_2$ followed by $L_{18} \times T_3$ and $L_3 \times T_1$ exhibited high negative significant *sca* effects. Mostly, L_{11} and L_{20} among the Lines, and T_1 and T_2 among the testers and $L_3 \times T_2$ among the hybrids showed consistent negative *gca* and *sca* effects respectively.

Forty four hybrids in S_1 , thirteen hybrids in S_2 and nineteen hybrids in the pooled analysis exhibited significant positive relative

heterosis for this trait. Twenty eight hybrids in S_1 , three hybrids in S_2 and fourteen hybrids in the pooled analysis displayed significant positive heterobeltiosis for this trait. Eleven hybrids in S_1 , only one in S_2 and three in the pooled analysis revealed significant positive standard heterosis for plant height at maturity. Eight hybrids in S_1 , thirtythree in S_2 and sixteen in pooled analysis showed negative significant relative heterosis. Nine hybrids in S_1 , forty in S_2 and twenty eight in pooled analysis exhibited significant negative heterobeltiosis. Fiftysix hybrids in S_1 , fiftynine in S_2 and fifty eight in pooled analysis expressed negative significant standard heterosis for this trait. The magnitude of positive heterosis was higher than the negative heterosis, however. This revealed the usefulness of heterosis breeding for this trait. The results of the present study is in agreement with the findings of Srivastava and Singh (1968), Dixit (1976a), Shivaprakash (1986), Jadon and Mehrotra (1988), and Omar Sheikh (1989).

5.8.4.3. Number of branches (Fig.30)

The higher estimates of sca variance than the gca variance indicated the predominance of non-additive gene action for this trait in both the seasons as well as pooled analysis. Earlier studies of Dixit (1976a), Reddy et al., (1982), Krishnadoss et al., (1987) and Omar Sheikh (1989) also explained the same fact. While Rathinaswamy and Jagathesan (1984) and Khorgade et al., (1989), reported additive gene action for this trait. Shrivastava and Singh (1981), Chaudhari et al., (1984) and Khorgade et al., (1988) recorded both additive and non-additive gene action for this trait.

In S_1 , L_1 , L_{16} and L_{23} , in S_2 , L_{10} , L_{23} and L_{25} and in pooled analysis L_1 , L_{23} and L_{25} recorded the high positive *gca* effects for this trait. L_{23} in all the analysis showed high positive *gca* effect. Among the testers, T_2 in S_1 and pooled analysis and T_3 in S_2 displayed high positive *gca* effects. Among these lines and testers, the *per se* performance was higher with L_{21} , L_{23} and T_3 . Among the hybrids, $L_{16} \times T_2$ followed by $L_{11} \times T_2$ and $L_{25} \times T_2$ in S_1 , $L_1 \times T_2$ followed by $L_{27} \times T_1$ and $L_2 \times T_1$ in S_2 and $L_{16} \times T_2$ followed by $L_{11} \times T_2$ and $L_{25} \times T_2$ showed high positive significant *sca* effects in the pooled analysis. The high magnitude of positive significant *sca* effects of $L_{16} \times T_2$, $L_{11} \times T_2$ and $L_{25} \times T_2$ of S_1 and $L_{16} \times T_2$ and $L_{25} \times T_2$ of pooled analysis were also reflected in their high *per se* performance, resulting in high positive significant relative heterosis, heterobeltiosis and standard heterosis in general. In toto, L_{23} and T_2 were good general combiners and $L_{16} \times T_2$ followed by $L_{25} \times T_2$ and $L_{11} \times T_2$ were good specific combiners.

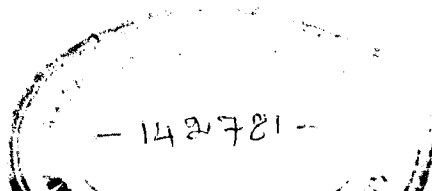
Fifty six hybrids in S_1 , ten hybrids in S_2 and twenty seven hybrids in the pooled analysis expressed significant positive relative heterosis. Thirteen hybrids in S_1 , only one in S_2 and twelve in the pooled analysis displayed significant positive heterobeltiosis for this trait. Forty four hybrids in S_1 , four hybrids in S_2 and twenty five hybrids in the pooled analysis exhibited significant positive standard heterosis. On the basis of the high number of crosses showing positive significant standard heterosis and the observed magnitude of standard

heterosis in the positive direction, this trait can well be exploited by heterosis breeding. This is in corroboration with the results of Dixit (1976a), Rathinaswamy (1980), Dora and Kamala (1986), Jadon and Mehrotra (1988), Omar Sheikh (1989). On the contrary, Shirvas and Singh (1981) observed negative magnitude of heterosis for this trait.

5.8.4.4 Number of flowers (Fig.30)

In the present study, the *sca* variance was higher than *gca* variance in individual seasons as well as pooled analysis. Thus indicated the importance of non-additive gene action for this trait.

Among the lines, L_{23} followed by L_6 and L_{16} in S_1 , L_{23} followed by L_{16} and L_{17} in S_2 and pooled analysis recorded the highest significant and positive *gca* effects. In the case of testers, T_3 in S_1 and pooled analysis and T_2 in S_2 showed the highest significant and positive *gca* effects. The lines L_{23} followed by L_{16} was found as good and stable general combiners. Similarly, T_3 was a good general combiner. Among the hybrids significant positive and highest *sca* effects were observed in $L_{23} \times T_3$ followed by $L_{21} \times T_3$ and $L_{14} \times T_2$ in S_1 , $L_2 \times T_2$ followed by $L_{24} \times T_3$ and $L_{23} \times T_2$ in S_2 and $L_{23} \times T_3$ followed by $L_{21} \times T_3$ and $L_{14} \times T_2$ in the pooled analysis. Thus these cross combinations were good specific combiners. The high magnitude of significant positive *sca* effects of $L_{23} \times T_3$ and $L_{21} \times T_3$ of S_1 , $L_{23} \times T_2$ and $L_2 \times T_2$ of S_2 were accompanied by high *per se* performance and highly



significant positive heterosis. The parents L_{23} and T_3 were good and stable general and specific combiners, whereas L_{21} , L_{14} and T_2 were good specific combiners only. L_{16} was found as a good stable general combiner.

Twenty four hybrids in S_1 , forty one in S_2 and eighteen in the pooled analysis displayed significant positive relative heterosis. The heterobeltiosis was significant and positive in eleven hybrids in S_1 , twenty eight in S_2 and nine in the pooled analysis. Twenty seven hybrids in S_1 , seventy two in S_2 and fifty seven in the pooled analysis recorded significant positive standard heterosis for this trait. The observed high number of crosses in the positive direction as well as the high magnitude of relative heterosis, heterobeltiosis and standard heterosis than that of negative direction in individual seasons and pooled analysis explained the usefulness of this trait in heterosis breeding.

5.8.4.5. Number of capsules (Fig.30)

The importance of non-additive gene action in influencing this trait was evidenced from the higher sca variance than the gca variance in all the analyses. Such predominance of non-additive gene action in the expression of this trait was earlier reported by Dixit (1976a), Reddy et al. (1982). However, Gupta (1981), Sharma and Chauhan (1984) and Khorgade et al. (1989), Gupta (1981), Sharma and Chauhan (1984) and Khorgade et al. (1989) reported additive gene action for this trait. But Shrivastava and Singh (1981), Krishnaswamy and Appadurai (1984), Khorgade et al. (1988) and Omar Sheikh (1989) indicated the importance of both additive and non-additive gene action for this trait.

Among the lines, highest positive and significant **gca** effects were recorded by L_{23} followed by L_6 and L_{21} in S_1 , L_{16} , followed by L_{23} and L_{25} in S_2 and L_{23} followed by L_{16} and L_{25} in the pooled analysis. L_{23} was found as stable and good general combiner. With regard to testers, T_3 in S_1 and pooled analysis and T_2 in S_2 exhibited highest significant positive **gca** effects.

Highest positive significant **sca** effects were registered by $L_{23} \times T_3$ followed by $L_{21} \times T_3$ and $L_{14} \times T_2$ in S_1 , $L_{24} \times T_1$ followed by $L_{23} \times T_2$ and $L_{10} \times T_2$ in S_2 and $L_{23} \times T_3$ followed by $L_{21} \times T_3$ and $L_{10} \times T_2$ in the pooled analysis. The high magnitude of positive significant **sca** effect in $L_{23} \times T_3$ of S_1 was reflected in the high **per se** performance, heterobeltiosis and standard heterosis for this trait. The parents $L_{23} \times T_2$ and T_3 were found as stable good general and specific combiners where as T_1 was observed as good specific combiner only. The high magnitude of significant positive **sca** effects observed for number of flowers with $L_{23} \times T_3$ and $L_{21} \times T_3$ in S_1 , $L_{23} \times T_2$ in S_2 and $L_{23} \times T_3$ and $L_{21} \times T_3$ were also reflected for number of capsules also.

Eighteen hybrids in S_1 , thirty nine in S_2 and nineteen in pooled analysis expressed significant positive relative heterosis for this trait. Heterobeltiosis was significant positive in nine hybrids in S_1 , twenty six in S_2 and twelve in the pooled analysis. Twenty five hybrids in S_1 , fifty four in S_2 and forty in the pooled analysis registered significant positive standard heterosis for this trait. The magnitude

of positive heterosis, heterobeltiosis as well as standard heterosis was higher than that of the negative direction in both the seasons and pooled analysis. This clearly revealed the possibilities of using this trait in heterosis breeding. Similar findings were reported by Srivastava and Singh (1968), Kinnison (1978), Krishnaswami and Appadurai (1984), Singh *et al.* (1986), Jadon and Mehrotra (1988) and Omar Sheikh (1989). On the contrary, higher magnitude of negative heterosis was reported by Shrivastava and Singh (1981) and Krishnaswami *et al.* (1985).

5.8.4.6. Volume of capsules

The dominance estimate of *sca* variance was higher than the additive estimate of *gca* variance in both the seasons. The *gca* variance and *sca* variance in the pooled analysis was zero. This indicated the importance of non-additive gene action in the expression of this trait. Predominance of dominance gene action for this trait was also reported by Deenamani (1989). Similarly, Anitha (1988) found the predominance of epistasis for this trait. Additive gene action for capsule width and non-additive gene action for capsule length was reported by Khorgade *et al.* (1989).

The estimates of *gca* effects were highest and positive significant with L_{27} , followed by L_{20} and L_{21} in S_1 , L_{20} followed by L_{24} and L_{11} in S_2 and L_{20} followed by L_{24} and L_{27} in the pooled analysis. Among these L_{20} was found as stable and good general combiner. Among the testers T_3 in S_1 and T_2 in S_2 and pooled analysis displayed highest positive significant *gca* effects. Among the hybrids, $L_{27} \times T_3$ followed

by $L_{20} \times T_3$ followed by $L_{12} \times T_3$ in S_1 , $L_{15} \times T_2$ followed by $L_{11} \times T_2$ and $L_6 \times T_2$ in S_2 and $L_{27} \times T_3$ followed by $L_{12} \times T_2$ and $L_6 \times T_1$ in the pooled analysis expressed maximum positive significant *sca* effects. The high magnitude of *sca* effects of the hybrids $L_{27} \times T_3$ of S_1 was accompanied by high *per se* performance of the hybrids, relative heterosis, heterobeltiosis and standard heterosis, whereas the high positive and significant *sca* effects of $L_{11} \times T_2$ and $L_{15} \times T_2$ of S_2 and $L_{27} \times T_3$ of pooled analysis were accompanied with high *per se* performance of the hybrids and standard heterosis. Among the parents L_{20} , T_2 followed by T_3 were good general combiners. L_{20} and T_2 were found as both good general and specific combiner $L_{27} \times T_3$ was found as good specific combiner.

Thirty three hybrids in S_1 , forty four in S_2 and fifteen in the pooled analysis revealed significant positive relative heterosis. Twenty three hybrids in S_1 , thirty two in S_2 and eight hybrids in pooled analysis registered significant positive heterobeltiosis. Standard heterosis was significant positive in seventy nine hybrids in S_1 , twenty three in S_2 and forty four in the pooled analysis. The higher magnitude of positive heterosis revealed the usefulness of this trait in heterosis breeding.

5.8.4.7. Number of seeds per capsule

The estimates of *gca* variance was less than the *sca* variance in both the seasons. In the pooled analysis both the estimates were negative and so zero. This indicated the importance of non-additive

action in the expression of this trait. This is in conformity with the report of Omar Sheikh (1989). However, Padmavathi (1987) and Khorgade et al. (1989) reported the importance of additive gene action for this trait. On the other hand, Chaudhari et al. (1984) and Dora and Kamala (1987) reported the importance of both additive and non-additive gene action for this trait.

Among the lines L_{20} followed by L_{16} and L_{19} in S_1 , L_{20} followed by L_{24} in S_2 and L_{20} followed by L_{24} and L_{27} in the pooled analysis showed high and positive significant gca effects. L_{20} was found as stable and good general combiner with regard to testers, T_3 in S_1 and T_2 in S_2 and pooled analysis showed high positive and significant gca effects.

Among the hybrids, $L_{20} \times T_3$ followed by $L_6 \times T_1$ and $L_{12} \times T_2$ in S_1 , $L_6 \times T_1$ followed by $L_{15} \times T_2$ and $L_{12} \times T_2$ in S_2 and $L_6 \times T_1$ followed by $L_{12} \times T_2$ and $L_{17} \times T_1$ showed maximum positive significant sca effects. Among these hybrids, $L_6 \times T_1$ was found as stable and good specific combiners. It is note worthy to observe that the cross combination, $L_{20} \times T_3$ exhibited consistent positive significant relative heterosis and heterobeltiosis in both the seasons and pooled analysis indicating the stability of these hybrids for this trait. This combination ($L_{20} \times T_3$) exhibited high sca effect high per se performance, significant positive relative heterosis and heterobeltiosis and there by exhibited good correspondence between sca effect and heterotic phenomenon.

Thirty one hybrids in S_1 , twenty three in S_2 and three in pooled analysis showed significant positive relative heterosis. Ten hybrids in S_1 , twelve in S_2 and only one in the pooled analysis exhibited significant positive heterobeltiosis for this trait. The standard heterosis was significant and positive in forty nine hybrids in S_1 , twenty one in S_2 and fifteen in the pooled analysis. In general the magnitude of positive heterosis was lesser than the negative heterosis in the present study. Lesser magnitude of heterosis was reported by Srivastava and Singh (1968), Sarathe and Dabral (1969), Jadon and Mehrotra (1988) and Omar Sheikh (1989). However, higher heterosis was also reported for this trait by Paramasivam et al. (1982) and Dora and Kamala (1986)

5.8.4.8. Length of seeds

In the present investigation, the magnitude of *sca* variance was higher than the *gca* variance in both the seasons. In the pooled analysis *gca* variance was negative and *sca* variance was zero. This indicated the existence of non-additive gene action for this trait. Dora and Kamala (1987) also found the predominance of non-additive gene action for this trait.

Among the lines highest positive and significant *gca* effects were recorded by L_7 followed by L_{15} and L_{23} in S_1 , L_6 followed by L_{10} and L_{12} in S_2 and L_6 followed by L_7 and L_{13} in the pooled analysis. T_3 in S_1 and pooled analysis and T_1 in S_2 showed highest positive and significant *gca* effects. Among the hybrids, $L_7 \times T_1$ followed by

$L_{10} \times T_2$ and $L_2 \times T_2$ in S_1 , $L_{10} \times T_2$ followed by $L_{12} \times T_3$ and $L_{25} \times T_3$ in S_2 and $L_{10} \times T_2$ followed by $L_9 \times T_1$ and $L_{14} \times T_2$ recorded the highest positive and significant sca effects. $L_{10} \times T_2$ showed consistently maximum sca effects in both the seasons and pooled analysis there by exhibiting stability in sca effects. The high magnitude of positive significant sca effects observed in $L_7 \times T_1$ in S_1 , $L_{10} \times T_2$ and $L_{12} \times T_3$ in S_2 and $L_{10} \times T_2$ in pooled analysis were reflected in high positive and significant heterosis, heterobeltiosis and standard heterosis as well as in *per se* performance of the hybrids. Thus a good correspondence between sca effects, *per se*, performance and heterosis vigour was observed. The parents L_7 , L_{10} , L_{12} , T_1 and T_3 were found as good general and specific combiners. T_2 was identified as a good specific combiner.

Ten hybrids in S_1 , thirty seven in S_2 and twenty one in the pooled analysis exhibited significant positive relative heterosis. Heterobeltiosis was significant positive in only one hybrid in S_1 , nineteen in S_2 and thirteen in the pooled analysis. Four hybrids in S_1 , thirteen in S_2 and three in pooled analysis expressed significant positive standard heterosis for this trait. In general, the magnitude of positive heterosis was lesser than the negative heterosis in the present study for this trait. Dora and Kamala (1986) reported significant positive relative heterosis and heterobeltiosis for this trait.

5.8.4.9. Breadth of seeds

The estimates of sca variance was higher than the gca variance in both the seasons as well as in pooled analysis thereby indicating the importance of non-additive gene action in the expression of this trait. Dora and Kamala (1987) found predominance of non-additive gene action for this trait.

Among the lines, L_4 followed by L_{23} and L_9 in S_1 , L_6 followed by L_7 and L_{14} in S_2 and L_6 followed by L_7 and L_9 exhibited maximum positive significant gca effects. T_3 in S_1 and pooled analysis and T_1 in S_2 expressed maximum positive significant gca effects.

Among the hybrids highest positive and significant sca effect was observed in $L_{17} \times T_1$ followed by $L_4 \times T_1$ and $L_{10} \times T_2$ in S_1 , $L_{25} \times T_3$ followed by $L_{10} \times T_2$ and $L_{22} \times T_2$ in S_2 and $L_{10} \times T_2$ followed by $L_{17} \times T_1$ and $L_4 \times T_1$. Among these hybrids, $L_{10} \times T_2$ was observed as a stable specific combiner. The high magnitude of positive significant sca effect of $L_{10} \times T_2$ (S_2) was accompanied by high *per se* performance of hybrids and heterotic vigour. Thus there was a good correspondence between sca effect, *per se* performance of hybrids and heterotic vigour.

Twenty three hybrids in S_1 , forty one in S_2 and sixteen in the pooled analysis expressed significant positive x relative heterosis. Eight hybrids in S_1 , fifteen in S_2 and five in the pooled analysis showed

significant positive heterobeltiosis for this trait. Sixty nine hybrids in S_1 , thirty hybrids in S_2 and fifty one hybrids in the pooled analysis displayed positive significant standard heterosis. The magnitude of positive heterosis was lesser than that of other traits and slightly higher than the negative direction in general. Dora and Kamala (1986) reported significant positive relative heterosis for this trait.

5.8.4.10. Weight of 1000 seeds (Fig.30)

The magnitude of sca variance was higher than gca variance in both the seasons and pooled analysis, indicating the existence or non-additive gene action for this trait. This is in corroboration with the result of Padmavathi (1987) and Khorgade et al. (1989). But Dixit (1978) and Djigma (1984) reported the control by additive gene action, whereas Dora and Kamala (1987), Khorgade et al. (1988) and Omar Sheikh (1988) found the existence of both additive and non-additive gene action for this trait.

Among the lines, L_8 followed by L_{19} and L_{22} in S_1 , L_{25} followed by L_2 and L_{14} in S_2 and L_{19} followed by L_{26} and L_5 in the pooled analysis expressed highest positive gca effects. T_1 in S_1 , T_3 in S_2 and T_3 followed by T_1 in the pooled analysis displayed significant positive gca effects.

Among the hybrids, $L_{22} \times T_1$ followed by $L_8 \times T_1$ and $L_{26} \times T_1$ in S_1 , $L_{25} \times T_3$ followed by $L_{26} \times T_3$ and $L_{12} \times T_2$ in S_2 and $L_8 \times T_1$ followed by $L_{10} \times T_2$ and $L_7 \times T_3$ expressed maximum

positive significant **sca** effects. The high magnitude of positive significant **sca** effects of $L_8 \times T_1$, $L_{22} \times T_1$ (S_1) and $L_{25} \times T_3$ (S_2) were reflected in the high **per se** performance of the hybrids and heterotic vigour. Among the parents L_8 , L_{22} , L_{25} , T_1 and T_3 were found as good general and specific combiners.

Thirty two hybrids in S_1 , thirty five in S_2 and twenty five in the pooled analysis displayed significant positive relative heterosis. Twenty two hybrids in S_1 , twelve in S_2 and fourteen in the pooled analysis expressed significant positive heterobeltiosis. Thirty two hybrids in S_1 , eleven in S_2 and twenty one in the pooled analysis exhibited significant positive standard heterosis. The observed more number of crosses with positive significant heterosis and higher positive heterosis indicated the possibility of using this trait in heterosis breeding. Srivastava and Singh (1968), Tyagi and Singh (1981), Sharma and Chauhan (1983), Dora and Kamala (1986), Jadon and Mehrotra (1988) and Omar Sheikh (1989) reported similar findings. However, Kinnison (1978) observed non-significant heterosis for this trait.

5.8.4.11. Volume of 1000 seeds

The estimates of **sca** variance was higher than **gca** variance in both the seasons. In the pooled analysis both the estimates showed negative sign and considered as zero. This indicated the importance of non-additive gene action in the expression of this trait.

Among the lines highest positive and significant **gca** effects were recorded by L_{13} followed by L_{22} and L_8 in S_1 , L_5 followed by L_{25} and L_{13} in S_2 and L_{13} followed by L_{22} and L_8 in the pooled analysis. Among these, L_{13} was found as stable and good general combiner. T_1 in S_1 , T_3 in S_2 and pooled analysis exhibited significant positive **gca** effects.

Among the hybrids, $L_{22} \times T_1$ followed by $L_{13} \times T_2$ and $L_{20} \times T_3$ in S_1 , $L_5 \times T_3$ followed by $L_2 \times T_3$ and $L_1 \times T_3$ in S_2 and $L_{22} \times T_1$ followed by $L_5 \times T_3$ and $L_{13} \times T_2$ expressed highest positive and significant **sca** effects. The highest positive significant **sca** effects of $L_{22} \times T_1$ (S_1) and $L_5 \times T_3$ (S_2) were accompanied by high **per se** performance of the hybrids and heterotic vigour. Thus a good correspondence between high **sca** effect, high **per se** performance and heterotic vigour was evidenced. The parents, L_5 , L_{13} , L_{22} , T_1 and T_3 were good general and specific combiners. T_2 was a good specific combiner. Line L_8 was a good general combiner.

Twenty nine hybrids in S_1 , thirty two in S_2 and twenty in pooled analysis showed significant positive relative heterosis. Nineteen hybrids in S_1 , twenty three in S_2 and sixteen in pooled analysis expressed significant positive heterobeltiosis. The standard heterosis was significant positive in seventy nine hybrids in S_1 , twenty in S_2 and sixty five in pooled analysis. The higher number of crosses showing heterotic vigour and the higher magnitude of positive heterosis than negative direction outlined the usefulness of this trait in heterosis breeding.

5.8.4.12. Density of seeds (Fig.30)

In this study, the **sca** variance was higher than the **gca** variance in both the seasons, where as in the pooled analysis **gca** variance was higher than the **sca** variance. This explained the existence of both additive and non-additive gene action. Dora and Kamala (1987) observed predominance of non-additive gene action for seed thickness.

Among the lines, L_{19} followed by L_5 and L_2 in S_1 , L_3 followed by L_7 and L_{14} in S_2 and L_{19} followed by L_3 and L_2 expressed highest positive significant **gca** effects. T_1 in all the analysis exhibited significant positive **gca** effects and deserved as a good and stable general combiner.

Among the hybrids, $L_4 \times T_3$ followed by $L_1 \times T_1$ and $L_{21} \times T_1$ in S_1 , $L_2 \times T_1$ followed by $L_1 \times T_2$ and $L_{27} \times T_3$ in S_2 and $L_4 \times T_3$ followed by $L_3 \times T_3$ and $L_2 \times T_1$ displayed maximum positive significant **sca** effects. The high magnitude of positive significant **sca** effects of $L_3 \times T_3$ and $L_2 \times T_1$ (S_2) and $L_2 \times T_1$ (pooled) were accompanied with high **per se** performance of the hybrids and heterobeltiosis. Thus a good correspondence between high **sca** effect, **per se** performance of hybrids and heterotic vigour was evidenced. The parents L_2 , L_3 and T_1 were found as good general and specific combiners.

Thirty nine hybrids in S_1 , eighteen in S_2 and thirty eight in pooled analysis exhibited positive significant relative heterosis. Twenty four hybrids in S_1 , eight in S_2 and eighteen in pooled analysis showed significant positive heterobeltiosis. Twelve hybrids in S_1 , four hybrids in S_2 and six hybrids in pooled analysis expressed significant positive standard heterosis. The higher number of crosses showing positive significant heterotic vigour and higher magnitude of positive heterosis added a scope in using this trait in heterosis breeding.

5.8.4.13. Oil content:

The sca variance component was found to be larger than the gca variance in both the seasons as well as in the pooled analysis. This indicated that this character is under the control of non-additive gene action. Similar results were noted by Murthy (1975), Fatteh et al. (1982), Padmavathi (1987) and Omar Sheikh (1989). In contrast, additive gene action was reported for this trait by Reddy et al., (1982), Sharma and Chouhan (1985) and Khorgade et al. (1989). On the otherhand both additive and non-additive gene action were pointed out by Reddy et al. (1984d) and Dora and Kamala (1987).

Among the lines, L_{17} followed by L_{11} and L_{14} in S_1 , L_{20} followed by L_{16} and L_{23} in S_2 and L_{17} followed by L_7 and L_{23} in the pooled analysis displayed highest positive and significant gca effects, while T_3 was only positive and significant for gca effects among testers (S_1 and pooled analysis).

Among the hybrids, $L_{10} \times T_2$ followed by $L_{20} \times T_2$ and $L_{12} \times T_1$ in S_1 , $L_{10} \times T_2$ followed by $L_{27} \times T_3$ and $L_{26} \times T_1$ in S_2 and $L_{10} \times T_2$ followed by $L_{12} \times T_2$ and $L_{25} \times T_3$ exhibited higher positive and significant *sca* effect. Among these hybrids, $L_{10} \times T_2$ consistently showed higher significant *sca* effect in both the seasons as well as in the pooled analysis. Thus it was found as a stable and good specific combiner. The high *per se* performance and standard heterosis of this combination in the pooled analysis might be due to the high *sca* effect. This combination could be probably used for exploiting heterosis for this trait.

Twenty seven hybrids in S_1 , forty seven in S_2 and thirty five in the pooled analysis displayed significant positive heterosis over their mid parents. Fourteen hybrids in S_1 , twenty five in S_2 and twenty in the pooled analysis expressed positive and significant heterobeltiosis. Standard heterosis was recorded only in S_2 and pooled analysis. It was significant positive in forty hybrids in S_2 and five in the pooled analysis. Although the magnitude of heterosis was not very high, considerable number of hybrids showed positive and significant heterotic values, indicating the possibility of using these parents as donors in sesame. Similar results were obtained by Sharma and Chauhan (1983), Dora and Kamala (1986) and Omar Sheikh (1989). However, Murty (1975) and Kinnison (1978) reported non-significant heterosis for oil content.

5.8.4.14. Seed yield (Fig.30)

The specific combining ability variance was greater in magnitude than the general combining ability variance in both the seasons and pooled analysis. This lead to the inference that this trait is governed by non-additive gene action. This is in corroboration with the reports of Krishnadoss *et al.*, (1987), Anandakumar and Sree Rangaswamy (1987) and Omar Sheikh (1989). On the contrary, additive gene action for this trait was reported by Dixit (1976a), Rathinaswamy and Jagathesan (1984) Padmavathi (1987) and Khorgade *et al.* (1989). But, Shrivastava and Singh (1981) and Chaudhari *et al.* (1984) reported that both additive and non-additive gene action is important for the expression of this trait.

Among the lines, L_{23} followed by L_6 and L_{21} in S_1 , L_{12} followed by L_{10} and L_{16} in S_2 and L_{23} followed by L_{10} and L_{12} in the pooled analysis expressed high positive and significant *gca* effects. In the case of testers, T_3 in S_1 and pooled analysis and T_1 in S_2 exhibited significant and high positive *gca* effects.

Among the hybrids, $L_{21} \times T_3$ followed by $L_{23} \times T_3$, $L_{16} \times T_2$ and $L_6 \times T_3$ in S_1 , $L_{13} \times T_2$ followed by $L_{16} \times T_1$, and $L_{12} \times T_1$ in S_2 and $L_{21} \times T_3$ followed by $L_{13} \times T_2$ and $L_6 \times T_3$ exhibited highest positive and significant *sca* effects. The high *per se* performance and heterotic vigour of the hybrids viz., $L_{21} \times T_3$ (S_1), $L_{16} \times T_1$ and $L_{12} \times T_1$ (S_2) and $L_6 \times T_3$ and $L_{13} \times T_2$ (pooled) may be due to the

high sca effect. The parents L_6 , L_{21} and L_{23} (S_1) and L_{12} and L_{16} (S_2), T_1 and T_3 were found as good general as well as specific combiners. L_{10} was a good general combiner and T_2 was a good specific combiner.

Forty six hybrids in S_1 , thirty three in S_2 and twelve in the pooled analysis exhibited significant positive relative heterosis. Thirty two hybrids in S_1 , twenty one in S_2 and ten in the pooled analysis evinced significant positive heterobeltiosis. Eighteen hybrids in S_1 , forty two hybrids in S_2 and twenty eight hybrids in the pooled analysis displayed significant positive standard heterosis. The observed high number of crosses showing positive standard heterosis and the highest magnitude of positive significant standard heterosis than any other traits under study as well as than the negative direction, indicated the possibility of getting success in heterosis breeding in sesame. Similar findings were reported by Pal (1945), Murty (1975), Chavan et al., (1982), Krishnaswami and Appadurai (1984), Singh et al., (1986), Padmavathi (1987) Jadon and Mehrotra (1988) and Omar Sheikh (1989).

5.8.4.15. Total drymatter production (Fig.30)

The estimates of sca variance was higher than the gca variance in both the seasons as well as in pooled analysis. This showed the predominance of non-additive gene action in conditioning the expression of this trait. This is in confirmity with Deenamani (1989).

Among the lines, L_{26} followed by L_3 and L_7 in S_1 , L_{24} followed by L_{12} and L_{10} in S_2 and L_{12} followed by L_{23} and L_7 in the pooled analysis exhibited highest positive and significant *gca* effects. T_3 in S_1 and T_2 in the S_2 and pooled analysis expressed maximum positive significant *gca* effects.

Among the hybrids, $L_{15} \times T_2$ followed by $L_6 \times T_3$ and $L_{21} \times T_3$ in S_1 , $L_{12} \times T_2$, followed by $L_2 \times T_2$ and $L_{24} \times T_3$ in S_2 and $L_{12} \times T_2$ followed by $L_6 \times T_3$ and $L_{23} \times T_3$ had maximum positive significant *sca* effects. The high magnitude of *sca* effects of $L_{12} \times T_2$ and $L_2 \times T_2$ (S_2) were reflected in the high *per se* performance of the hybrids and heterotic vigour. The parents L_{12} , L_{23} , L_{24} , T_2 and T_3 were found as good general and specific combiners.

Thirty three hybrids in S_1 , fourteen in S_2 and twenty three in the pooled analysis exhibited significant positive relative heterosis. Fifteen hybrids in S_1 , four in S_2 and fourteen in the pooled analysis expressed significant positive heterobeltiosis. Thirty hybrids in S_1 , twenty two in S_2 and twenty five in the pooled analysis showed positive significant standard heterosis for this trait. The observed high number of crosses with positive heterotic vigour and the extent of positive heterosis than the negative direction added a scope in utilizing this trait in heterosis breeding.

5.8.4.16. Harvest index (Fig.30)

The magnitude of **sca** variance was larger than that of **gca** variance in both the seasons as well as in the pooled analysis. Thus the importance of non-additive gene action in the expression of this trait was evidenced. Non-additive gene action for this trait was reported by Deenamani (1989). However, Singh et al., (1983) and Anitha (1988) observed the importance of additive gene action for this trait.

Among the lines, L_{23} followed by L_8 and L_{14} in S_1 , L_{27} followed by L_{10} and L_{18} in S_2 and L_{23} followed by L_{14} and L_{27} in the pooled analysis expressed highest positive and significant **gca** effects. T_3 in S_1 and pooled analysis and T_1 in S_2 showed significant positive **gca** effects.

Among the hybrids, $L_{10} \times T_2$ followed by $L_{24} \times T_3$ and $L_{14} \times T_2$ in S_1 , $L_1 \times T_2$ followed by $L_9 \times T_3$ and $L_{20} \times T_2$ in S_2 and $L_{10} \times T_2$ followed by $L_{14} \times T_2$ and $L_1 \times T_2$ showed high positive and significant **sca** effects. The high heterobeltiosis of $L_1 \times T_2$ (S_2) may be due to the high **sca** effects. The parents L_{14} and T_3 were found as both good general and specific combiners. T_2 was found as good specific combiner and L_{23} and L_{27} as good general combiner.

Thirty nine hybrids in S_1 , sixty two in S_2 and twelve in the pooled analysis showed significant positive relative heterosis. Twenty nine hybrids in S_1 , forty nine in S_2 and three in the pooled

analysis exhibited significant positive heterobeltiosis. Ten hybrids in S_1 , sixty two in S_2 and thirty one in the pooled analysis displayed significant positive standard heterosis for this trait. The observed high heterotic vigour and number of crosses showing positive heterosis and the extent and magnitude of positive heterosis than the negative direction indicated the usefulness of this trait in heterosis breeding. These findings enlight the possibility of exploiting the hybrid vigour for seed size, yield and their component characters of sesame by heterosis breeding technique, based on the combining ability study and gene action of the traits under inquiry and with the identified good combiners.

5.8.5. Per se performance, sca effect, heterobeltiosis and heterosis in individual seasons and pooled seasons.

From the correlation and causation studies it is evident that the characters viz., plant height, number of branches, flowers, capsules, 1000 seed weight, seed density, total dry matter production and harvest index evinced positive significant association with seed yield and among themselves consistantly over seasons and pooled seasons. Almost all the traits which exhibited positive significant genetic association with seed yield also displayed positive significant genetic association with 1000 seed weight. Seed yield and 1000 seed weight was also positively and significantly associated. Based on these characters sesame seed size and seed yield could be improved. With this view, the best three combinations based on per se performance sca effects, heterobeltiosis and standard heterosis of eight traits of importance

in the present investigation in individual as well as in pooled seasons are presented in Table 193.

Among the corss combinations listed in the Table 193 the following crosses which showed higher *per se* performance, positive and significant *sca* effect as well as heterobeltilosis for various traits are furnished below:

Traits of importance	Cross combinations			
1. Plant height at maturity	L ₃ x T ₃ L ₆ x T ₃	-	-	
2. Number of branches	L ₁₁ x T ₂ L ₁₆ x T ₂ L ₂₅ x T ₂	-	-	
3. Number of flowers	-	L ₂ x T ₂		
	L ₂₁ x T ₃ L ₂₃ x T ₃	L ₂₃ x T ₂	-	
4. Number of capsules	L ₂₃ x T ₃	-	-	
5. Weight of 1000 seeds	L ₈ x T ₁ L ₂₂ x T ₁	L ₂₅ x T ₃	-	
6. Density of seeds	-	L ₂ x T ₁	L ₂ x T ₁	
	-	L ₃ x T ₃	-	
7. Seed yield	L ₂₁ x T ₃ -	L ₁₂ x T ₁ L ₁₆ x TT ₁	L ₆ x T ₃ L ₁₃ x T ₂	
8. Total dry matter production	-	L ₂ x T ₂ L ₁₂ x T ₂	-	

Table 193. Per se performance, sca effect, heterobeltilosis and standard heterosis of best three combinations in individual and pooled seasons.

Characters	Per se			sca effects			Heterobeltilosis			Standard heterosis		
	S ₁	S ₂	P	S ₁	S ₂	P	S ₁	S ₂	P	S ₁	S ₂	P
Height of the plant at maturity	L ₃ xT ₃	L ₁₀ xT ₁	L ₃ xT ₃	L ₃ xT ₃	L ₁₀ xT ₁	L ₃ xT ₃	L ₃ xT ₃	L ₁₀ xT ₁	L ₁₃ xT ₃	L ₃ xT ₃	L ₁₀ xT ₁	L ₃ xT ₃
	L ₆ xT ₃	L ₂₄ xT ₃	L ₂₄ xT ₃	L ₁₈ xT ₂	L ₃ xT ₃	L ₆ xT ₃	L ₂₆ xT ₂	L ₁₂ xT ₂	L ₈ xT ₂	L ₆ xT ₃	-	L ₂₄ xT ₃
	L ₁₉ xT ₃	L ₃ xT ₃	L ₆ xT ₃	L ₆ xT ₃	L ₉ xT ₁	L ₁₈ xT ₂	L ₆ xT ₃	L ₁₇ xT ₂	L ₂₂ xT ₂	L ₁₉ xT ₃	-	L ₆ xT ₃
Number of branches	L ₁₆ xT ₂	L ₂₄ xT ₃	L ₁₆ xT ₂	L ₁₆ xT ₂	L ₁ xT ₂	L ₁₆ xT ₂	L ₁₆ xT ₂	L ₁₀ xT ₂	L ₁₁ xT ₃	L ₁₆ xT ₂	L ₂₄ xT ₃	L ₁₆ xT ₂
	L ₂₅ xT ₂	L ₂₅ x ₃	L ₂₅ xT ₂	L ₁₁ xT ₂	L ₂₇ xT ₁	L ₁₁ xT ₂	L ₂₅ xT ₂	-	L ₂₁ xT ₂	L ₂₅ xT ₂	L ₂₃ xT ₂	L ₂₅ xT ₂
	L ₁₁ xT ₂	L ₂₃ xT ₂	L ₁ xT ₃	L ₂₅ xT ₂	L ₂ xT ₁	L ₂₅ xT ₂	L ₂₂ xT ₂	-	L ₂₆ xT ₂	L ₁ xT ₃	L ₂₃ xT ₁	L ₁₁ xT ₂
Number of flowers	L ₂₃ xT ₃	L ₂₃ xT ₂	L ₂₃ xT ₃	L ₂₃ xT ₃	L ₂ xT ₂	L ₂₃ xT ₃	L ₂₃ xT ₃	L ₂ xT ₂	L ₈ xT ₂	L ₂₃ xT ₃	L ₂₃ xT ₂	L ₂₃ xT ₃
	L ₂₁ xT ₃	L ₁₆ xT ₁	L ₁₆ xT ₂	L ₂₁ xT ₃	L ₂₄ xT ₃	L ₂₁ xT ₃	L ₅ xT ₂	L ₂₅ xT ₂	L ₂₆ xT ₂	L ₂₁ xT ₃	L ₁₆ xT ₁	L ₁₆ xT ₂
	L ₆ xT ₃	L ₂₅ xT ₁	L ₂₁ xT ₃	L ₁₄ xT ₂	L ₂₃ xT ₂	L ₁₄ xT ₂	L ₂₁ xT ₃	L ₁₄ xT ₂	L ₂₀ xT ₂	L ₆ xT ₃	L ₂₅ xT ₁	L ₂₁ xT ₃

Table 193. Contd..

Characters	Per se			sea effects			Heterobeltiosis			Standard heterosis		
	S ₁	S ₂	P	S ₁	S ₂	P	S ₁	S ₂	P	S ₁	S ₂	P
Number of capsules	L ₂₃ xT ₃	L ₂₃ xT ₂	L ₂₃ xT ₃	L ₂₃ xT ₃	L ₂₄ xT ₁	L ₂₃ xT ₃	L ₂₃ xT ₃	L ₁₆ xT ₂	L ₈ xT ₂	L ₂₃ xT ₃	L ₂₃ xT ₂	L ₂₃ xT ₃
	L ₂₁ xT ₁	L ₁₆ xT ₁	L ₂₃ xT ₂	L ₂₁ xT ₃	L ₂₃ xT ₂	L ₂₁ xT ₃	L ₁₄ xT ₂	L ₂₄ xT ₂	L ₂₆ xT ₁	L ₂₁ xT ₃	L ₁₆ xT ₁	L ₂₃ xT ₂
	L ₆ xT ₃	L ₂₄ xT ₁	L ₁₆ xT ₂	L ₁₄ xT ₂	L ₁₀ xT ₂	L ₁₀ xT ₂	L ₂₁ xT ₃	L ₁₅ xT ₂	L ₂₆ xT ₂	L ₆ xT ₃	L ₂₄ xT ₁	L ₁₆ xT ₂
Weight of 1000 seeds	L ₂₂ xT ₁	L ₂₅ xT ₃	L ₈ xT ₁	L ₂₂ xT ₁	L ₂₅ xT ₃	L ₈ xT ₁	L ₂₂ xT ₁	L ₂₅ xT ₃	L ₂₃ xT ₂	L ₂₂ xT ₁	L ₂₅ xT ₃	L ₈ xT ₁
	L ₈ xT ₁	L ₂₆ xT ₃	L ₂₆ xT ₁	L ₈ xT ₁	L ₂₆ xT ₃	L ₁₀ xT ₂	L ₈ xT ₁	L ₁₄ xT ₂	L ₂₆ xT ₂	L ₈ xT ₁	L ₂₆ xT ₃	L ₂₆ xT ₁
	L ₂₆ xT ₁	L ₂ xT ₃	L ₁₉ xT ₁	L ₂₆ xT ₁	L ₁₂ xT ₂	L ₇ xT ₃	L ₂₆ xT ₁	L ₁₀ xT ₂	L ₁₈ xT ₁	L ₂₆ xT ₁	L ₂ xT ₃	L ₂₂ xT ₁
Density of seeds	L ₁₉ xT ₁	L ₂ xT ₁	L ₃ xT ₃	L ₄ xT ₃	L ₂ xT ₁	L ₄ xT ₃	L ₃ xT ₃	L ₂ xT ₁	L ₁₂ xT ₁	L ₁₉ xT ₁	L ₂ xT ₁	L ₃ xT ₃
	L ₁ xT ₁	L ₃ xT ₃	L ₂ xT ₁	L ₁ xT ₁	L ₁ xT ₂	L ₃ xT ₃	L ₁₉ xT ₃	L ₃ xT ₃	L ₂ xT ₁	L ₁ xT ₁	L ₃ xT ₃	L ₅ xT ₁
	L ₄ xT ₃	L ₃ xT ₁	L ₅ xT ₁	L ₂₁ xT ₁	L ₂₇ xT ₃	L ₂ xT ₁	L ₁₉ xT ₁	L ₃ xT ₁	L ₉ xT ₂	L ₄ xT ₃	L ₃ xT ₁	L ₁₉ xT ₁

Table 193. Contd..

Characters	Per se			sea effects			Heterobeltiosis			Standard heterosis		
	S ₁	S ₂	P	S ₁	S ₂	P	S ₁	S ₂	P	S ₁	S ₂	P
Seed yield	L ₂₃ xT ₃	L ₁₂ xT ₁	L ₂₃ xT ₃	L ₂₁ xT ₃	L ₁₃ xT ₂	L ₂₁ xT ₃	L ₂₁ xT ₃	L ₁₂ xT ₂	L ₂₃ xT ₂	L ₂₃ xT ₃	L ₁₂ xT ₁	L ₂₃ xT ₃
	L ₂₁ xT ₃	L ₁₆ xT ₁	L ₆ xT ₃	L ₂₃ xT ₃	L ₁₆ xT ₁	L ₁₃ xT ₂	L ₁ xT ₁	L ₁₂ xT ₁	L ₂₆ xT ₂	L ₂₁ xT ₃	L ₁₆ xT ₁	L ₆ xT ₃
	L ₆ xT ₃	L ₁₃ xT ₂	L ₁₃ xT ₂	L ₁₆ xT ₂	L ₁₂ xT ₁	L ₆ xT ₃	L ₆ xT ₃	L ₁₆ xT ₁	L ₂₆ xT ₁	L ₆ xT ₃	L ₁₃ xT ₂	L ₁₃ xT ₂
Total dry matter production	L ₆ xT ₃	L ₁₂ xT ₂	L ₁₂ xT ₂	L ₁₅ xT ₂	L ₁₂ xT ₂	L ₁₂ xT ₂	L ₄ xT ₂	L ₂₄ xT ₃	L ₂₂ xT ₂	L ₆ xT ₃	L ₁₂ xT ₂	L ₁₂ xT ₂
	L ₂₆ xT ₃	L ₂ xT ₂	L ₂₃ xT ₃	L ₆ xT ₃	L ₂ xT ₂	L ₆ xT ₃	L ₂₄ xT ₃	L ₁₂ xT ₂	L ₅ xT ₁	L ₂₃ xT ₃	L ₂ xT ₂	L ₂₃ xT ₃
	L ₂₃ xT ₃	L ₂₄ xT ₃	L ₆ xT ₃	L ₂₁ xT ₃	L ₂₄ xT ₃	L ₂₃ xT ₃	L ₁₂ xT ₂	L ₂ xT ₂	L ₁₃ xT ₁	L ₂₆ xT ₃	L ₂₄ xT ₃	L ₆ xT ₃
Harvest index	L ₂₃ xT ₃	L ₁ xT ₂	L ₁₀ xT ₂	L ₁₀ xT ₂	L ₁ xT ₂	L ₁₀ xT ₂	L ₂₃ xT ₃	L ₁ xT ₂	L ₂₀ xT ₁	L ₂₄ xT ₃	L ₁ xT ₂	L ₁₀ xT ₂
	L ₂₄ xT ₃	L ₁₂ xT ₁	L ₁₄ xT ₂	L ₂₄ xT ₃	L ₉ xT ₃	L ₁₄ xT ₂	L ₉ xT ₁	L ₁₂ xT ₁	L ₂₆ xT ₂	L ₂₃ xT ₃	L ₁₂ xT ₁	L ₁₄ xT ₂
	L ₁₄ xT ₂	L ₂₂ xT ₁	L ₆ xT ₃	L ₁₄ xT ₂	L ₂₀ xT ₂	L ₁ xT ₂	L ₅ xT ₁	L ₂₂ xT ₁	L ₂₃ xT ₂	L ₁₄ xT ₂	L ₂₂ xT ₁	L ₆ xT ₃

only a few specific combinations have registered highly significant *sca* effect, *per se* performance and heterobeltiosis in a particular season, contrary to the expectations that hybrids will perform better in varying seasons due to homogenous heterozygosity. This observation is corroborated by high *sca* x season interaction recorded in the present study. For example, the hybrid $L_2 \times T_2$ has recorded significant values for *sca* effects, heterobeltiosis and *per se* performance for number of flowers in S_1 . But in S_2 , it showed a similar trend for total dry matter production. Similarly, $L_3 \times T_3$ exhibited significant *sca* effects heterobeltiosis and *per se* performance for plant height in S_1 but for seed density in S_2 . For seed density, $L_2 \times T_1$ expressed significant *sca* effects, heterobeltiosis and *per se* performance in S_1 , but by $L_3 \times T_3$ in S_2 . $L_{21} \times T_3$ showed high *sca* affects, heterobeltiosis and *per se* performance for number of flowers and seed yield in S_1 thereby indicating their strong association between these two traits. A similar trend was registered by $L_{23} \times T_3$ for number of flowers and number of capsules in S_1 .

The present investigation lead to identify the best general combiners for the eight important traits and are listed below:-

Characters	Best general combiners
Height of the plant at maturity	L_3, T_3
Number of branches	L_{23}, T_2

Characters	Best general combiners
Number of flowers	L ₁₆ , L ₁₇ , L ₂₃ , T ₃
Number of capsules	L ₁₆ , L ₂₃ , L ₂₅ , T ₃
Weight of 1000 seeds	L ₁₉ , T ₃ , T ₁
Density of seeds	L ₂ , L ₃ , L ₁₉ , T ₁
Seed yield	L ₁₀ , L ₁₂ , L ₂₃ , T ₃
Total dry matter production	L ₇ , L ₁₂ , T ₂
Harvest index	L ₁₄ , L ₂₃ , L ₂₇ , T ₃

Note: These genotypes showed highest gca effects in any of the two analyses.

In the present investigations the best general and specific combiners were identified for the traits which showed positive significant association with seed size (1000 seed weight) and seed yield. Among them L₈ x T₁, L₂₂ x T₁ and L₂₅ x T₃ which showed high *per se* performance, positive significant *sca* effects and heterobeltiosis appears to be useful for increasing the seed size (1000 seed weight). The cross combinations *viz.*, L₁₂ x T₁, L₁₆ x T₁, L₁₃ x T₂, L₆ x T₃ and L₂₁ x T₃ exhibited high *per se* performance, positive significant *sca* effects and heterobeltiosis will be useful to enhance the seed yield potential. It is quite interesting to conceive that among the eight crosses suggested to improve seed size and seed yield, the parents involved were good general combiners and the cross L₂₂ x T₁ was a good specific combiner for days to maturity. So, it is possible to achieve high seed size, higher seed yield coupled with early maturity.

From line x tester analysis it was found that almost all the traits under the present inquiry showed predominant non-additive genetic control. So, the population improvement by recurrent selection and heterosis breeding might be useful for enhancement of seed size and seed yield in sesame.

5.8.6. Correlation studies

5.8.6.1. Correlation between per se performance of parents (lines and testers) and gca effects.

In S_1 , the correlation between per se performance and gca effects of the parents were highly significant for number of flowers and number of capsules and significant positive for seed length. In S_2 , it was negative and highly significant in number of seeds per capsule and significant positive in seed length. However, it was highly significant positive for all the other traits in the pooled analysis excepting seed breadth. This indicated that the choice of parents on the basis of per se performance may indicate their superior general combining ability on one hand, on the other hand, the it indicated that most of the traits are under additive genetic control in the parents. This is in accordance with Sharma and Chauhan (1985), also stated that the choice of parents on the basis of per se performance may be effective, if the character is unidirectionally governed by a set of additive genes.

5.8.6.2. Correlation between per se performance of hybrids and sca effects.

The association between per se performance and sca effects were highly positive and significant in individual as well as pooled seasons excepting capsule volume and seed yield in pooled season, where they evinced non-significant association. This indicated the reliability of sca effects in the choice of parents for hybridization.

5.8.7. Inter-relation between genetic diversity and combining ability

The results obtained from pooled analysis for diversity and combining ability were considered to find out the functional relationship between genetic diversity and combining ability for the traits which were positively and significantly associated with seed size and seed yield.

The best general combiners recorded for the traits of importance were almost observed to fall in a single cluster (I cluster) (Table 194) with a very rare exception for plant height one genotype was in III cluster, for 1000 seed weight one genotype was in V cluster and for seed density one genotype was in II cluster. This indicated that the highly diverged genotypes which fall in different clusters need not be good general combiners. Further insight into the origins of the genotypes which possessed high general combining ability revealed the eco-geographic diversity within the cluster I. Genotypes of Tamil Nadu origin showed high general combining ability for all the

nine traits of importance. Genotypes from Andhra Pradesh showed high general combining ability for 1000 seed weight and seed density. Genotype (G 49) from Gujarat showed high general combining ability for plant height, number of branches, flowers, capsules, seed yield, total dry matter production and harvest index.

Genotype, G37 from Israel exhibited high general combining ability for number of flowers and capsules. This indicated that the genotypes of Tamil Nadu has high general combining ability. As genetic diversity seemed to have practically no relevance with the general combining ability, it may be stated that the genotypes of different eco-geographic origin would result in better general combining ability. Singh and Joshi (1966), Joshi and Dhawan (1966) were also contended with a similar interpretation. In sesame, Shrivastava and Singh (1981) and Sharma and Chauhan (1985) concluded with a similar result. Further Sharma and Chauhan (1985) stated that the parents of distant origin having high additive x additive interaction effects are likely to result better genotypes with high yield in advanced generations.

The genotypes grouped in Cluster I showed high **sca** effects mostly. Rarely genotypes of different cluster showed high **sca** effects. One cross combination involving genotypes from different clusters showed high **sca** effects for plant height, number of capsules, seed density and harvest index (Table 194). Cross combinations involving genotypes of Tamil Nadu origin exhibited high **sca** effects for almost all the traits.

Table 194. Inter-relation between genetic diversity and combining ability (Based on pooled diversity and pooled Line x Tester analysis)

Character	Best general combiner	Cluster	Origin	Best specific combiners	Clusters	Origins
Height of the plant at maturity	G3 G49 G51 G59	I I III I	TN Guj NT TN	G3 x G59 G11 x G59 G51 x G59	I x I I x I III x I	TN x TN TN x TN NT x TN
Number of branches	G5 G49 G52 G40	I I I I	TN Guj TN TN	G37 x G40 G28 x G40 G52 x G40	I x I I x I I x I	Isr x TN TN x TN TN x TN
Number of flowers	G49 G37 G38 G59	I I I I	Guj Isr NT TN	G49 x G59 G47 x G59 G34 x G40	I x I I x I I x I	Guj x TN NT x TN TN x TN
Number of capsules	G49 G37 G52 G59	I I I I	Guj Isr TN TN	G49 x G59 G47 x G59 G22 x G40	I x I I x I V x I	Guj x TN NT x TN NT x TN
1000 seed weight	G42 G56 G9 G59	I V I I	AP TN NT TN	G15 x G20 G22 x G40 G12 x G59	I x II V x I I x I	TN x TN NT x TN TN x TN

Table 194. (Contd.)

Characters	Best general combiner	Cluster	Origin	Best specific combiners	Clusters	Origins
Seed density	G42	I	AP	G4 x G59	I x I	TN x TN
	G3	I	TN	G3 x G59	I x I	TN x TN
	G2	I	TN	G2 x G20	I x II	TN x TN
	G20	II	TN			
Seed yield	G49	I	Guj	G47 x G59	I x I	NT x TN
	G22	I	NT	G30 x G40	I x I	TN x TN
	G29	I	TN	G11 x G59	I x I	TN x TN
	G59	I	TN			
Total dry matter production	G29	I	TN	G29 x G40	I x I	TN x TN
	G49	I	Guj	G11 x G59	I x I	TN x TN
	G12	I	TN	G49 x G59	I x I	Guj x TN
	G40	I	TN			
Harvest index	G49	I	Guj	G22 x G40	V x I	NT x TN
	G34	I	TN	G34 x G40	I x I	TN x TN
	G60	I	NT	G5 x G40	I x I	TN x TN
	G59	I	TN			

Note: TN : Tamil Nadu
Guj : Gujarat
NT : Non-traceable

Genotype, G 49 originating from Gujarat in combination with genotype G 59 of Tamil Nadu expressed high sca effect for number of flowers, capsules and total dry matter production. Genotype, G 37, evolving from Israel in combination with genotype G 40 of Tamil Nadu showed high sca effect for number of branches. This again confirmed the fact that eco-geographical diversity of the genotypes would result in better general and specific combining abilities. In sesame, Shrivastava and Singh (1981) observed high sca effects among the parents selected from northern alluvial and South-eastern plains. The findings also brought out the general superiority of the genotypes hailing from Tamil Nadu in showing their higher pre-potency and imprinting.

5.8.8. Inter-relation between genetic diversity and heterosis

Heterosis has been frequently related to the degree of genetic diversity of the parents crossed (Griffing and Lindstrom, 1954; Moll et al., 1962; Paterniani and Lonnguist, 1963; Timothy, 1963). Bhatt (1973) suggested that the genetic variability in F_5 lines was proportional to the genetic divergence of the parents involved in a particular cross combination and that it may be possible to predict the performance of a cross in relatively advanced generation from the magnitude of the D^2 value of a parental combination (before making the actual cross).

The results from the pooled diversity and pooled heterosis were related to find out the relationship between the genetic diversity

and heterosis for the traits which were positively and significantly associated with seed size and seed yield. In the present study, both intra -and inter-cluster mating expressed heterotic vigour. However, crosses involving genotypes grouped in different clusters exhibited highest relative heterosis for number of flowers, total dry matter production and harvest index. For all the other traits of importance, crosses involving genotypes of a single cluster showed maximum heterosis. Heterobeltiosis was highest in crosses involving genotypes grouped in different clusters for seed density, total dry matter production and harvest index. For all the other characters of importance, genotypes grouped in a single cluster (Cluster I) showed highest heterobeltiosis (Table 195).

It is quite interesting to conceive that the cross combination(s) which exhibited highest heterosis had genotypes originating from Tamil Nadu as male or female parents. For plant height, number of branches, flowers, capsules and seed density, both the parents were of Tamil Nadu origin. For the other characters genotypes of Tamil Nadu served either as male or female parent. Genotypes originating from Rajasthan in cross combination with that of Tamil Nadu origin showed maximum relative heterosis and heterobeltiosis for plant height and total dry matter production. Genotypes evolved from Gujarat in cross combination with genotypes of Tamil Nadu origin expressed maximum relative heterosis and heterobeltiosis for 1000 seed weight, seed yield, and harvest index. The cross between genotype from Israel and Tamil Nadu showed maximum relative heterosis for plant height.

Table 195. Inter-relation between genetic diversity and heterosis

Characters	Best cross combinations	Clusters	Origins
Height of the plant at maturity	<u>di</u>		
	G30 x G59	I x I	TN x TN
	G48 x G40	IV x I	Raj x TN
	G37 x G59	I x I	Isr x TN
	<u>dii</u>		
	G30 x G59	I x I	TN x TN
	G15 x G40	I x I	TN x TN
	G48 x G40	IV x I	Raj x TN
	<u>di</u>		
	G47 x G40	I x I	NT x TN
	G28 x G59	I x I	TN x TN
	G56 x G40	V x I	TN x TN
Number of branches	<u>dii</u>		
	G28 x G59	I x I	TN x TN
	G47 x G40	I x I	NT x TN
	G56 x G40	V x I	TN x TN
	<u>di</u>		
	G56 x G40	V x I	TN x TN
	G15 x G40	I x I	TN x TN
	G56 x G20	V x II	TN x TN
	<u>dii</u>		
Number of flowers	G15 x G40	I x I	TN x TN
	G56 x G40	V x I	TN x TN
	G43 x G40	I x I	NT x TN

Contd...

Table 195 (Contd.)

Characters	Best cross combinations	Clusters	Origins
Number of capsules	<u>di</u>		
	G15 x G40	I x I	TN x TN
	G56 x G40	V x I	TN x TN
	G56 x G20	V x II	TN x TN
	<u>dii</u>		
	G15 x G40	I x I	TN x TN
	G56 x G20	V x II	TN x TN
	G56 x G40	V x I	TN x TN
	<u>di</u>		
	G43 x G40	I x I	NT x TN
	G49 x G40	I x I	Guj x TN
	G28 x G20	I x II	TN x TN
1000 seed weight	<u>dii</u>		
	G49 x G40	I x I	Guj x TN
	G56 x G40	V x I	TN x TN
	G39 x G20	I x II	NT x TN
Seed density	<u>di</u>		
	G30 x G59	I x I	TN x TN
	G29 x G20	I x II	TN x TN
	G2 x G20	I x II	TN x TN
	<u>dii</u>		
	G29 x G20	I x II	TN x TN
	G2 x G20	I x II	TN x TN
	G19 x G40	I x I	NT x TN

Contd..

Table 195 (Contd..)

Characters	Best cross combinations	Clusters	Origins
Seed yield	<u>di</u>		
	G49 x G40	I x I	Gu j x TN
	G56 x G40	V x I	TN x TN
	G56 x G20	V x II	TN x TN
	<u>dii</u>		
	G49 x G40	I x I	Gu j x TN
	G56 x G40	V x I	TN x TN
	G56 x G20	V x II	TN x TN
	<u>di</u>		
	G48 x G40	IV x I	Ra j x TN
	G9 x G20	I x II	NT x TN
	G30 x G59	I x I	TN x TN
Total dry matter production	<u>dii</u>		
	G48 x G40	IV x I	Ra j x TN
	G59 x G20	I x II	TN x TN
	G30 x G59	I x I	TN x TN
	<u>di</u>		
	G43 x G20	I x II	NT x TN
	G56 x G40	V x I	TN x TN
	G49 x G40	I x I	Gu j x TN
	<u>dii</u>		
	G43 x G20	I x II	NT x TN
	G56 x G40	V x I	TN x TN
	G49 x G40	I x I	Gu j x TN

di	:	Relative heterosis	Gu j	:	Gujarat
dii	:	Heterobeltiosis	Isr	:	Israel
TN	:	Tamil Nadu	NT	:	Non-traceable
Raj	:	Rajasthan			

On the over all basis, it is concluded that intra-cluster mating among genotypes of different eco-geographic diversity and more over among the genotypes of Tamil Nadu would result in high heterotic vigour. After utilizing the intra-cluster diversity, one can resort to inter-cluster diversity for heterosis or pedigree breeding. Preference may be given to the cross G 49 x G 40 which exhibited highest relative heterosis and heterobeltiosis for 1000 seed weight and seed yield.

In Sesame, Ricelli and Mazzani (1964) and Omar Sheik (1989) found that genotypes collected from different localities and of wide geographical diversity resulted in high heterotic vigour, which was in confirmity with our study. However, Murthy (1975), Rathnaswamy (1980), Djigma (1984), Dora and Kamala (1986), and Anitha (1988) stated that high heterosis was observed among the parents having wide genetic divergence.

5.8.9. Inter-relation between genetic diversity, combining ability and heterobeltiosis

The genotypes which were identified as best general combiners and the cross combinations which showed a good agreement between high specific combining ability, *per se* performance and heterosis for the traits which were positively associated with seed size and seed yield were considered here in conjunction with pooled diversity to assess the existing realities in the relationship among the three parameters viz., genetic diversity, combining ability and heterosis.

In general it was found in this study that the superior combinations involved at least one high general combining parent. Sharma and Chauhan (1985), Goyal and Sudhir Kumar (1988), Jadon and Mehrotra (1988) and Pawar *et al.*, (1990) also came out with such a result. However, for number of flowers, capsules, seed density and total dry matter production, the superior combinations had both the parents with high general combining ability (Table 196). It was also in confirmity with Sharma and Chauhan (1985), Goyal and Sudhir Kumar (1988) and Jadon and Mehrotra (1988).

Most of the cross combinations which showed good agreement between sca effects, *per se* performance and heterobeltiosis involved parents grouped in a single cluster and that too mostly from Cluster I. However, the identified crosses for 1000 seed weight, seed density and seed yield, involved parents which were grouped in different Clusters. While crosses involving genotypes of a single cluster showed a good agreement between sca effects, *per se* performance and heterosis, it posed the following questions of interest.

- i) What type of relationship does exist between divergence and specific combining ability?
- ii) Whether parental genetic divergence could speak for the observed heterobeltiosis or their specific combining ability is the cause for the heterobeltiosis?

Table 196. Inter-relation between genetic diversity, combining ability and heterobeltiosis

Characters	Seasons		
	S ₁	S ₂	P
Plant height	<u>G3</u> x <u>G59</u> (I x I) G11 x <u>G59</u> (I x I)	-	-
Number of branches	G28 x <u>G40</u> (I x I) G37 x <u>G40</u> (I x I) G52 x G40 (I x I)	-	-
Number of flowers	G47 x <u>G59</u> (I x I) <u>G49</u> x <u>G59</u> (I x I)	G2 x <u>G40</u> (I x I) <u>G49</u> x <u>G40</u> (I x I)	
Number of capsules	<u>G49</u> x <u>G59</u> (I x I)	-	-
Weight of 1000	G15 x <u>G20</u> (I x II) G48 x <u>G20</u> (IV x II)	G52 x <u>G59</u> (I x I)	-
Seed density	-	<u>G2</u> x <u>G20</u> (I x II) <u>G3</u> x <u>G59</u> (I x I)	<u>G2</u> x <u>G20</u> (I x II)
Seed yield	G47 x <u>G59</u> (I x I)	<u>G29</u> x G20 (I x II) G37 x G20 (I x II)	G11 x <u>G59</u> (I x I) G30 x G40 (I x I)
Total dry matter production	-	G2 x <u>G40</u> (I x I) G29 x <u>G40</u> (I x I)	-

Note: Genotypes underlined had high gca effects

Letters in the parantheses indicate the clusters in which the genotypes were grouped.

In the present study, there was no obvious relationship between genetic diversity and specific combining ability. The cross combinations which showed a good agreement between sca effects, *per se* performance and heterobeltiosis were mostly of intra-cluster origin. Thus, it obviously proved that the observed heterobeltiosis could be due to high specific combining ability *per se* of the cross combinations itself rather than the parental divergence. However, few crosses involving genotypes of different clusters also showed high sca effects and heterobeltiosis. Thus, the present study indicated that genotypes of different eco-geographic origin but grouped in a single cluster would result in better combining abilities and brought out that there is no obvious relationship between genetic divergence and combining ability.

5.8.10. Optimization of genetic divergence for the occurrence of heterosis

Heterosis is of direct relevance for developing hybrids in self-pollinated crops too. In view of the fact that large F₂ populations of every cross studied in F₁ cannot be screened for further breeding, the breeder is often constrained to select a few crosses in F₁. In that context, heterosis may be a key parameter for selection. Studies in groundnut (Pungle, 1983) showed that heterotic F₁'s generate a higher frequency of productive derivatives in F₅ and later generations when compared to non-heterotic F₁'s.

It is increasingly realized that crosses between divergent parents usually produce greater heterosis than those between closely

related ones as was pointed out by Hayes and Johnson (1939) and East and Hayes (1942). In practical situations, it can be reasoned that heterosis occurs because of parental divergence. But when divergent parents are crossed, heterosis is not found to occur always (Cress, 1966). It is essential therefore to explore the possible limits to parental divergence within which there are reasonably high chances for occurrence of heterosis (Arunachalam and Bandyopadhyay, 1984).

The present study is an attempt in this regard using the experimental results from pooled analysis. The experimental evidence provided in this study has suggested a definite relationship between parental divergence and F1 heterosis.

To take into account unequal number of crosses and heterotic ones, falling in various divergence classes, the percentage of heterotic crosses P (proportion of crosses showing positive values of heterosis) and q (the proportion of crosses showing a heterosis value greater than or equal to k - mean heterosis value of these crosses with positive value of heterosis for that character) were used as parameters in the decision process (Arunachalam and Bandyopadhyay, 1984). In addition, both the general level of heterosis (given by average heterosis value of those crosses showing positive heterosis) and a selected level (over a norm defined by overall mean heterosis) provided by the values x and y were considered in conjunction (Arunachalam and Bandyopadhyay, 1984). While the former would take into account the magnitude of F1 improvement over mid-parent value, however slight it might be, the latter would give weightage to those F1's showing substantial improvement

whose F2's a breeder would like to search on priority for desirable transgressive segregants (Pungle, 1983; Arunachalam and Bandyopadhyay, 1984).

The divergence class DC3 showed the lowest total score closely followed by DC1. According to Arunachalam and Bandyopadhyay (1984) DC3 will be the most desirable one with high frequency of heterotic crosses and high average magnitude of heterosis. Eventhough DC1 also showed lower score next to DC3, it consisted only a very few number of crosses and the average heterosis was less than DC3 or DC2. Next to DC3, the divergence class DC2 showed higher number of heterotic crosses and high average magnitude of heterosis. Thus the present results have brought out the definite syperiority of DC3 and DC2 over DC1 as far as occurrence of a high proportion of heterotic crosses or of high value of heterosis was concerned. Studies on triticales (Srivastava and Arunachalam, 1977) supported these results. The concept of that there are limits to parental divergence for optimum expression of heterosis was also set by past studies on crosses among divergent geographic races in maize (Moll et al., 1965).

From the correlation and causation studies it was evident that plant height at maturity, number of branches, number of flowers, number of capsules, thousand seed weight, seed density, total dry matter production and harvest index had consistent positive and significant association with seed size and seed yield. It was concluded that

primary importance must be given to total dry matter production and harvest index as they showed high positive direct effect towards seed size and seed yield. More over through these traits only all the other traits exerted maximum positive indirect effects towards seed size and seed yield. For plant height, number of branches, number of flowers, number of capsules, and seed density cross combinations in the divergence class DC 3 exhibited maximum relative heterosis. For the other traits DC3 ranked next to DC2. The divergence class DC2 expressed maximum relative heterosis for thousand seed weight, seed yield total dry matter production and harvest index. This explained that in sesame heterosis and yield improvement could well be made by selecting the cross combinations falling in DC2 and/or DC3. However, primary importance may be given to DC2 as they exhibited maximum positive relative heterosis and heterobeltiosis for 1000 seed weight, seed yield, total dry matter production and harvest index. Anitha and Stephen Dorai Raj (1990) also found the superiority of DC2 over other divergent classes.

The present study provides sufficient ground for conceiving those limits and for the hypothesis in general that - if 'm' and 's' are the mean and standard deviation of the values of divergence (given by D^2) among parents, the chances for the occurrence of a high frequency of heterotic crosses and with high values of heterosis are more when the parents are chosen to have their divergence in the interval (m-s, m+s) compared to the crosses between parents whose divergence falls outside that interval. This is in agreement with Arunachalam and Bandyopadhyay, (1984).

5.9. GENERATION MEAN AND VARIANCE ANALYSIS

Knowledge of gene action of yield and yield components is of paramount importance in deciding the breeding strategies. Biometrical techniques like line x tester and diallel mating designs are being extensively used in the combining ability analysis. Based on the combining ability the nature of gene action such as additive, dominance or epistasis can be determined. However, it can not explain the nature of epistasis.

The role of epistatic interactions in expressions of yield and their component characters could be understood only by generation mean and variance analysis technique. Added to that it partitions the epistatic effects from dominance effects. Hence, generation mean and variance analysis with first degree statistics was adopted to detect the non-allelic interactions components of the means of the phenotypic distributions.

Generation mean and variance analysis provides m (mean effects), $[d]$ (additive effects), $[h]$ (dominance effects), $[i]$ (additive x additive effects), $[j]$ (additive x dominance effects) and $[l]$ (dominance x dominance effects) more precisely. Such studies are very meagre in sesame.

With more than two interacting genes, cancellation of gene action can arise not only from dispersion but also because of the direction as inferred from the signs of the i 's, j 's and l 's, which may differ from one pair of interaction genes to another. This balancing action introduced by differences in sign is always likely to be encountered

in the contributions made to the expression of means and comparisons between them. Partitioning of variance into D, H and E_w (second degree statistics) was also followed in this study to provide further inference, partly or wholly.

As the quantitative traits are also influenced by the cytoplasmic effects and/or maternal genotype, delineating the one with the other and the extent to which these two factors affect the expression of quantitative traits of interest is also necessary while formulating an efficient breeding programme. Bearing this in mind, analysis of maternal and cytoplasmic effects were also done by comparing the means of F_2 populations of direct and reciprocal crosses as well as direct and reciprocal back cross progenies.

Thus the additive, dominance and epistatic genetic effects as assessed from the generation means approach and the variance components due to additive and dominance gene action and their modification due to cytoplasmic influence, the type of epistasis along with heterobeltiosis, degree of dominance and inbreeding depression are discussed in addition to the heritability and factor number estimates.

5.9.1. Per se performance

Among the three parents viz., P_1 , P_2 , and P_3 , P_1 ranked first for eight characters viz., capsule volume, number of seeds per capsule, seed length, seed breadth, 1000 seed weight, seed density, oil content and harvest index. But for seed yield it ranked third.

Parent P_2 ranked first for number of branches, flowers, capsules, seed yield and total dry matter production and stood second for most of the traits of interest. P_3 ranked first for early maturity, plant height and 1000 seed volume.

The high *per se* performance observed with P_1 for eight characters was also reflected in the hybrids having it as ovule or pollen parent for as many as seven out of eight traits. The superiority of P_1 for oil content was not reflected in any of its hybrids. Similarly the superiority of the parent P_2 was reflected in its hybrids, for all the five traits for which it ranked first. Similarly, the hybrids possessing the parent P_3 also reflected the superiority of P_3 for two out of the three traits for which it ranked first. All these put together, all the three parents viz., P_1 , P_2 and P_3 are seemingly good general combiners.

Among the hybrids, the F_1 's involving P_1 and P_2 recorded maximum *per se* performance for eleven out of sixteen traits, viz, days to maturity, number of branches, flowers, capsules, seeds per capsule, seed length, seed breadth, seed density, seed yield, total dry matter production, and harvest index. The hybrids possessing the parents P_1 and P_3 registered maximum for two characters viz., capsule volume and 1000 seed weight. For the remaining three traits, plant height, 1000 seed volume, and oil content, the hybrids of P_2 and P_3 expressed maximum. Thus the parents P_1 and P_2 are seemingly good specific combiners too.

There is ample evidence for good recombination and shuffling of genes. For example, for days to maturity the parent P_3 ranked first, P_1 second and P_2 third. But earlier maturity was recorded in hybrids involving P_1 and P_2 as parents.

About two thirds of all plant genera investigated show maternal inheritance of cytoplasmic traits (Tilney Bassett, 1975). Sivasubramanian (1988) reported about the effect of cytoplasm on quantitative traits in rice. Mosjidis and Yermanos (1984) found negligible cytoplasmic inheritance and maternal effects for oleic and linoleic acid contents in sesame. With that idea, the three parents were looked for its potentiality to use them as ovule parent. The superiority of the P_1 cytoplasm (with the assumption of uniparental inheritance of cytoplasm (Tilney-Bassett, 1975) was envisaged through the excelling performance of its hybrids having P_1 as ovule parent for five traits viz. days to maturity, number of seeds per capsule, seed breadth, seed density and harvest index. Similarly the superiority of the P_2 cytoplasm was evidenced from the superior performance of the hybrids having P_2 as ovule parent for as many as seven traits viz., number of branches, flowers, capsules, seed length, 1000 seed volume, seed yield and total dry matter production. For the traits, plant height, capsule volume, 1000 seed weight, and oil content, the hybrids having P_3 as cytoplasm (ovule parent) showed best performance. This indicated the definite role of cytoplasm in the expression of quantitative traits too. In fact this was supported and well evidenced from the obvious reciprocal differences found for

most of the traits under study. This necessitates the study of maternal and cytoplasmic effects on the expression of quantitative traits under inquiry along with the gene action and effects.

Heterobeltiosis (presented as percentage over better parent) was recorded to a maximum of -6.5 per cent and -4.64 per cent by $P_1 \times P_2$ and $P_3 \times P_1$ respectively for days to maturity. For plant height $P_3 \times P_2$ followed by $P_2 \times P_1$ expressed 29.94 and 16.27 per cents heterobeltiosis respectively. $P_1 \times P_2$ followed by $P_2 \times P_1$ exhibited 22.00 and 9.84 per cent heterobeltiosis respectively for number of branches. For number of flowers $P_2 \times P_1$ only showed heterobeltiosis (7.96 per cent), whereas for number of capsules, $P_3 \times P_1$ only showed heterobeltiosis (11.29 per cent). For capsule volume $P_3 \times P_1$ and $P_2 \times P_3$ respectively recorded 12.50 and 5.88 per cent heterobeltiosis. For number of seeds per capsule there was practically no heterobeltiosis. Negative heterobeltiosis were recorded for seed length and seed breadth. For 1000 seed weight only 1.98 per cent ($P_3 \times P_2$) heterobeltiosis was registered, whereas for 1000 seed volume, 9.81 and 8.80 per cent heterobeltiosis were obtained ($P_2 \times P_3$ and $P_3 \times P_2$ respectively). $P_3 \times P_2$ and $P_1 \times P_2$ recorded a maximum of 11.55 and 10.92 per cent heterobeltiosis for seed density. For oil content $P_3 \times P_2$ and their reciprocal cross evinced a maximum of 17.19 and 13.96 per cents heterobeltiosis respectively. For seed yield a maximum of 37.63 per cent heterobeltiosis was recorded by $P_2 \times P_3$. Parents P_2 and P_3 ranked first and second for mean seed yield. For total dry matter production

negative heterobeltiosis was recorded. A maximum of 10.91 and 5.22 per cents ($P_1 \times P_2$ and $P_3 \times P_1$ respectively) heterobeltiosis were registered for harvest index.

In general F_2 's performed better than their respective F_1 's. Inbreeding depression was rarely observed that too to a lesser extent.

Comparison of the means of B_1 's with their respective F_1 's indicated that the B_1 's of $P_1 \times P_2$ recorded maximum for seven traits. The cross $(P_1 \times P_2) \times P_1$ registered a maximum of 369.90 per cent seed yield over $P_1 \times P_2$. The B_1 's of the reciprocal cross of $P_1 \times P_2$ ($(P_2 \times P_1) \times P_2$) scored maximum for 1000 seed weight (40.53 per cent over F_1) and 1000 seed volume (40.99 per cent over F_1). For number of branches, and seed length the B_1 's of $P_1 \times P_3$ registered maximum over their F_1 's. The B_1 's of its reciprocal cross $(P_3 \times P_1) \times P_3$ recorded maximum oil content than its F_1 . For capsule volume, number of seeds per capsule, seed breadth and seed density the B_1 's of $P_2 \times P_3$ expressed maximum over their F_1 's.

Comparison of the means of B_2 's over their respective F_1 's indicated that B_2 's of $P_1 \times P_2$ exhibited maximum performance for days to maturity, plant height, number of branches, number of flowers, capsules, capsule volume and 1000 seed volume. The B_2 's of $P_1 \times P_3$ expressed maximum seed yield than their F_1 's (165.54 per cent). They also showed higher performance for 1000 seed weight, and total dry

matter production than their F_1 's. The B_2 's of the reciprocal cross ($P_3 \times P_1$) of $P_1 \times P_3$ registered maximum **per se** performance than their F_1 's for number of seeds per capsule, seed density and oil content. The B_2 's of $P_2 \times P_3$ showed maximum mean performance than their F_1 's for seed length and harvest index. The B_2 's of the reciprocal cross ($P_3 \times P_2$) of $P_2 \times P_3$ showed maximum **per se** performance than their F_1 's for seed breadth.

On considering the mean performance of B_1 's over their respective F_2 's revealed that the B_2 's of $P_1 \times P_2$ expressed a maximum of 153.4 per cent seed yield over their F_2 's. They also showed higher performance than their F_2 's for days to maturity plant height, number of branches, flowers, capsules, seeds per capsule, weight of 1000 seeds, total dry matter production and harvest index. The B_1 's of the reciprocal cross ($P_2 \times P_1$) of $P_1 \times P_2$ expressed higher performance than their F_1 's for capsule volume and 1000 seed volume. The B_1 's for the $P_1 \times P_3$ recorded maximum **per se** performance than their F_2 's for seed length and seed breadth. B_1 's of $P_2 \times P_3$ recorded maximum mean seed density than their F_2 's. The B_1 's of $P_3 \times P_3$ had maximum **per se** performance than their F_2 's for oil content.

Comparison of the B_2 's with their respective F_2 's revealed that the B_2 's of $P_1 \times P_2$ had 28.27 per cent higher seed yield than their F_2 's. The B_2 's of $P_1 \times P_2$ also showed higher mean performance than their F_2 's for days to maturity, plant height, number of branches,

flowers, capsules, capsule volume, weight of 1000 seeds, seed density, and total dry matter production. The B_2 's of the reciprocal cross ($P_2 \times P_1$) of $P_1 \times P_2$ showed higher *per se* performance for harvest index than their F_2 's. The B_2 's of $P_1 \times P_3$ showed higher mean performance than their F_2 's for seed length and breadth. The B_2 's of the reciprocal cross ($P_3 \times P_1$) of $P_1 \times P_3$ showed higher mean performance for number of seeds per capsule than their F_2 's. The B_2 's of $P_2 \times P_3$ had maximum 1000 seed volume than their F_2 's and the B_2 's of its reciprocal cross, $P_3 \times P_2$ had maximum oil content than their F_2 's.

On considering the B_1 mean and B_2 mean together in relation to their respective F_1 and F_2 mean, the back cross progenies of $P_1 \times P_2$ recorded maximum seed yield when either of them were used as recurrent parent. These two genotypes also maintained their superiority in recording higher B_1 and B_2 mean values over the F_1 and F_2 means for the maximum number of characters studied. The hybrids showing high heterobeltiosis were included any one of these parents either as ovule or pollen parent or both of them. Thus the parents P_1 and P_2 are potential donor for many of the traits of interest.

5.9.2. Analysis of maternal and cytoplasmic effects

5.9.2.1. Days to maturity

F_2 's, B_1 's and B_2 's of direct crosses differed from their respective reciprocal crosses for this trait indicating the presence of cytoplasmic inheritance for this trait. However, the similarities among B_1 's and

B_2 's of one direct crosses and in three reciprocal crosses indicated the maternal genetic control also. Bhagawan Dora and Kamala (1987) observed reciprocal difference for this trait.

5.9.2.2. Height of the plant at maturity

The presence of significant differences among the F_2 's of direct and reciprocal crosses, B_1 's of direct crosses and B_2 's of reciprocal crosses, B_2 's of direct crosses and B_1 's reciprocal crosses showed the presence of cytoplasmic inheritance for this trait. On the other hand the maternal genetic control on this trait was also evidenced from the non significant differences among the B_1 's and B_2 's of direct crosses as well as reciprocal crosses. Murthy (1975) and Anitha (1988) reported reciprocal difference for plant height.

5.9.2.3. Number of branches

Presence of significant reciprocal differences in the F_2 populations was also evidenced in the direct and reciprocal back cross progenies thereby confirmed the presence of cytoplasmic inheritance for this trait. However, maternal genetic control over this trait was seen in two direct and one reciprocal cross. Murthy (1975) and Anitha (1988) reported reciprocal differences for number of primary and secondary branches.

5.9.2.4. Number of flowers

F_2 's of direct crosses differed significantly from the F_2 's of reciprocal crosses only in $P_2 \times P_3$. However, such a difference

was not noticed in their back cross progenies. Comparison among the back cross progenies revealed the presence of significant difference only in the case of $P_1 \times P_2$ where the B_1 's of direct crosses and B_2 's of reciprocal crosses differed significantly, indicating the presence of cytoplasmic inheritance for this trait. Excepting one direct and one reciprocal crosses maternal genetic control was obvious.

5.9.2.5. Number of capsules per plant

Presence of cytoplasmic inheritance for this trait was evidenced only in one cross on the basis of significant reciprocal differences in the F_2 populations of the direct and reciprocal crosses of $P_2 \times P_3$. However, the comparisons of direct and reciprocal back crosses (B_1 's of direct crosses with B_2 's reciprocal crosses) indicated the presence of cytoplasmic inheritance in all the crosses. Maternal genetic control was obviously observed in one direct cross and two reciprocal crosses. Murthy (1975) reported reciprocal difference for this trait.

5.9.2.6. Volume of capsules

Cytoplasmic inheritance of this trait was evidenced for all crosses from the significant differences among the direct and reciprocal back cross progenies even though only one cross, $P_2 \times P_3$ showed significant difference in the comparison of F_2 populations of direct and reciprocal crosses. Whereas maternal genetic control was present in all the crosses except $P_2 \times P_1$.

5.9.2.7. Number of seeds per capsule

Significant differences among the direct and reciprocal F_2 populations of $P_1 \times P_3$, direct and reciprocal back cross progenies of $P_1 \times P_3$ and $P_2 \times P_3$ indicated the presence of cytoplasmic inheritance for this trait. Maternal genetic control was obvious in two direct and one reciprocal cross. Bhagawan Dora and Kamala (1987) reported reciprocal difference for this trait.

5.9.2.8. Length of seeds

Significant differences noticed among the F_2 's of direct and reciprocal crosses of $P_1 \times P_3$ and $P_2 \times P_3$. However, significant differences for this trait was noticed among the direct and reciprocal back cross progenies of $P_1 \times P_2$ and $P_1 \times P_3$ and not for $P_2 \times P_3$. So the difference observed in F_2 populations of the direct and reciprocal crosses of $P_2 \times P_3$ may be due to phenological or developmental or environment or one coupled with others. On the other hand, the differences present in the direct and reciprocal crosses of $P_1 \times P_3$ and $P_1 \times P_2$ may be due to cytoplasmic genetic factors. Maternal genetic control was obvious in one direct and three reciprocal crosses.

5.9.2.9. Breadth of seeds

Like that of length of seeds, significant reciprocal differences among the F_2 's of $P_1 \times P_3$ was observed for this trait. The comparison of the direct and reciprocal back cross progenies also conformed the presence of cytoplasmic inheritance in $P_1 \times P_3$ along with $P_1 \times P_2$. Maternal genetic control over this trait was obvious only in $P_2 \times P_3$.

5.9.2.10. Weight of 1000 seeds

F_2 's of direct and reciprocal crosses of $P_1 \times P_2$ showed significant difference. Such a significant difference was also noticed among the direct and reciprocal back cross progenies of $P_1 \times P_2$ and $P_2 \times P_3$. Maternal genetic control was evinced only in one cross ($P_1 \times P_3$). Anitha (1988) reported reciprocal difference for this trait.

5.9.2.11. Volume of 1000 seeds

Cytoplasmic inheritance was observed in only one cross $P_2 \times P_3$, from the significant differences among the B_2 's of direct and B_1 's of reciprocal crosses. Whereas maternal genetic control over this trait was obvious in all the crosses.

5.9.2.12. Density of seeds

Indication for the presence of cytoplasmic inheritance for this trait was evidenced for $P_1 \times P_2$, $P_1 \times P_3$ and $P_2 \times P_3$ from the significant differences among the direct and reciprocal back progenies. Maternal genetic control over this trait was observed for $P_1 \times P_2$, $P_1 \times P_3$, $P_2 \times P_1$ and $P_3 \times P_2$.

5.9.2.13. Oil content

There were no difference among the F_2 populations of direct and reciprocal crosses. However, significant differences were observed

among the direct and reciprocal back cross progenies indicating the presence of cytoplasmic inheritance. On the other hand, maternal genetic control over oil content was obvious in two direct and three reciprocal crosses. Reciprocal difference for oil content was reported by Bhagawan Dora and Kamala (1987) and Anitha (1988). Mosjidis and Yermanos (1984) found negligible cytoplasmic effect and detectable maternal effect for oleic and linoleic acids.

5.9.2.14. Seed yield

Significant differences among the direct and reciprocal back cross progenies indicated the presence of cytoplasmic inheritance in all the cross combinations. However, maternal genetic control was obvious in two direct and three reciprocal crosses. Bhagawan Dora and Kamala (1987) reported reciprocal difference for seed yield.

5.9.2.15. Total dry matter production

Presence of cytoplasmic inheritance for this trait was inferred from the differences among the direct and reciprocal back cross progenies, in all the crosses. Maternal genetic control over this trait was seen in $P_1 \times P_3$, $P_2 \times P_3$, $P_2 \times P_1$, and $P_3 \times P_1$.

5.9.2.16. Harvest index

Cytoplasmic inheritance of this trait was indicated by the cross $P_1 \times P_2$ only, where the B_1 's of direct and B_2 's of reciprocal crosses differed significantly. Whereas maternal genetic control over this trait was highly obvious in all the crosses.

The summary of the results on the analysis of maternal and cytoplasmic effects are presented in the Table 197. Comparisons of the means of F_2 populations of direct and reciprocal crosses, as well as the direct and reciprocal back cross progenies revealed the presence of cytoplasmic influence on the inheritance of the sixteen characters studied. On the other hand, the comparison of the B_1 's and B_2 's of direct crosses as well as reciprocal crosses indicated maternal genetic control over the expression of the traits of interest. This indicated the importance of nuclear x cytoplasmic interaction in the expression of quantitative traits. The cytoplasm of the parent P_1 differed from the cytoplasm of the parent P_2 for 14 characters and from the cytoplasm of P_3 for 12 characters. Similarly, the cytoplasm of P_2 differed from P_3 for 12 characters. This clearly indicated that the three parents under study has three different cytoplasm.

Dwivedi et al. (1989) in peanut observed strong influence of maternal and maternal interaction effects as well as genic effects in the expression of various pod and seed traits. They concluded that the presence of significant maternal interaction effects for several characters in many crosses revealed the importance of a combination of a nuclear, cytoplasm or physiological interplay between the pollen parent and the seed parent as suggested by Topham (1966).

5.9.3. Partitioning the gene effects

Generation mean and variance analysis were carried out to assess the fixable and non-fixable epistatic genetic effects on seed size, yield

Table 197. Summary of the results on the analysis of maternal and cytoplasmic effects.

Characters and combinations	Cytoplasmic control (c)															
	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆
D ₁ Vs. R ₁	C	C	C	C	C	C	-	C	C	C	-	C	C	C	C	C
D ₂ Vs. R ₂	C	C	-	C	C	C	C	C	C	-	-	C	C	C	C	-
D ₃ Vs. R ₃	C	C	-	C	C	C	C	-	-	C	C	C	C	C	C	-

Maternal genetic control (M)																
P ₁ xP ₂ (D ₁)	-	M	-	-	-	-	M	-	-	-	M	M	M	-	-	M
P ₁ xP ₃ (D ₂)	M	M	-	M	-	-	-	M	-	M	M	M	M	M	M	M
P ₂ xP ₃ (D ₃)	-	M	M	M	M	-	M	-	M	-	M	-	-	M	M	M
P ₂ xP ₁ (R ₁)	M	-	-	M	M	M	M	M	-	-	M	M	M	M	M	M
P ₃ xP ₁ (R ₂)	M	M	M	M	M	-	-	M	-	-	M	-	M	M	M	M
P ₃ xP ₂ (R ₃)	M	M	M	-	-	-	-	M	-	-	M	M	M	M	-	M

and their component characters. The results of mean and variance component analyses recorded on three direct and their reciprocal cross combinations are discussed below.

The simple additive-dominance model with three parameters viz., m , $[d]$, $[h]$ was adopted when it was adequate to explain the genetic variation (Mather and Jinks, 1971; 1977). When it was inadequate, that cross combinations were subjected to the analysis of digenic interaction model with the estimation of six parameters viz., m , $[d]$, $[h]$, $[i]$, $[j]$ and $[l]$.

5.9.3.1. Days to maturity

Additive, dominance and epistatic gene effects were significant in the direct crosses viz., $P_1 \times P_2$, $P_2 \times P_3$ and their reciprocal combinations. In the direct and reciprocal crosses of $P_1 \times P_3$, dominance and epistasis were found significant. In all the crosses, dominance effect was predominant over dominance x dominance, which was in turn mostly higher magnitude than other epistatic effects. Thus, even though this trait is governed by all the three genetic effects, is predominantly controlled by dominance effect. Non-additivity was recorded to play predominant role for days to maturity in sesame was earlier reported by Yermanos and Kotecha (1978) and Dora and Kamala (1987). Whereas Padmavathi (1987), Khorgade et al. (1988) and Anitha (1988) reported the importance of additivity for this trait. On the other hand Pathak and Dixit (1988) and Deenamani (1989) realized the importance of both additivity and non-additivity for this trait.

The [h] and [l] effects had opposite signs in all the cross combinations indicating mainly a duplicate dominant epistasis (Mather and Jinks, 1971). Similarly in all the crosses, [i] and [l] had the opposite signs indicating the predominantly dispersed alleles at the interacting loci (Jinks and Jones, 1958).

Variance component due to dominance was higher than that of additivity in all the cross combinations. The dominance ratio was more than unity in only one cross, $P_3 \times P_2$, indicating predominance of dominance effect.

5.9.3.2. Height of the plant at maturity (Fig.31)

Dominance, additive x additive and dominance x dominance epistatic effects were found significant in two direct and three reciprocal cross combinations. In $P_2 \times P_3$, additive x dominance was significant. In all the crosses except $P_2 \times P_3$, dominance effect was higher in magnitude than dominance x dominance which was mostly higher than additive x additive epistatic effects. Such higher dominance effect than additivity was reported by Murthy and Hashim (1974) and Chavan et al. (1983). Predominance of non-additive gene action for this trait was observed by Shrivastava and Singh (1981), Djigma (1984), Godawat and Gupta (1985) and Krishnadoss et al. (1987). However, predominance of additive gene action for plant height in sesame was reported by Nafie (1980), Rathinaswamy (1980), Shrivastava and Singh (1981), Reddy et al. (1982), Singh et al. (1983), Rathinaswamy and Jagathesan (1984),

Padmavathi (1987) and Anitha (1988). But, Deenamani (1989) had reported additive, dominance, and epistatic gene effects for this trait. Pathak and Dixit (1988) observed the importance of both additive and non-additive gene effects.

In almost all the crosses, [i], and [l] had opposite signs indicating the predominantly dispersed alleles at the interacting loci (Jinks and Jones, 1958). The presence of duplicate dominant epistasis was evidenced in all the crosses, indicated by the opposite signs of [h] and [l]. Two direct and three reciprocal crosses showed additive x additive interaction effect along with duplicate epistasis. This duplicate gene action coupled with [i] type interaction indicates the possibility of plants taller than either of the parents (Kulkarni et al. 1978). Duplicate epistasis for this trait was also reported by Chavan et al. (1981) and Godawat and Gupta (1985).

The dominance variance was higher than the additive variance in five out of six crosses. In one reciprocal cross, $P_x \times P_1$, D component was higher than H. Dominance ratio was more than unity in $P_2 \times P_1$ indicating the predominance of dominant gene action in this cross.

5.9.3.3. Number of branches (Fig.32)

In one cross, $P_2 \times P_3$, both additivity and dominance effect were recorded with dominance being predominant. Additive and epistatic effects were significant in $P_2 \times P_1$ and $P_2 \times P_3$. In $P_1 \times P_3$ and its reciprocal cross, epistatic effect alone was significant whereas

the importance of additive, dominance and epistatic effects was observed in $P_1 \times P_2$. Dominance and/or dominance x dominance expressed higher magnitude wherever they present, followed by additive x dominance effect. Dixit (1976a) and Deenamani (1989) reported all the three types of gene action for this trait. Whereas, significance of additive gene action was observed by Murty (1975), Gupta (1981), Chaudhari et al. (1984), Anitha (1988) and Khorgade et al. (1988). Non additivity has been found to govern this character as reported by Dora and Kamala (1987), Reddy et al. (1982) and Singh et al. (1983).

All the cross combinations showed duplicate dominant epistasis for this trait, which is again in confirmity with Dixit (1976a) and Deenamani (1989). In most of the crosses [i] and [l] had opposite signs.

The non-additive component of variance H was of greater magnitude than the additive component in all the crosses. The dominance ratio was more than unity in $P_2 \times P_1$ indicating the presence of dominance gene action.

5.9.3.4. Number of flowers (Fig.33)

Dominance and epistatic gene effects were found significant in $P_1 \times P_2$ and $P_3 \times P_2$. Dominance was predominant in these two crosses. Dominance x Dominance alone was significant in three cross combinations. In one cross, $P_1 \times P_3$, additive x dominance and dominance x dominance interaction was significant. In that cross also [l] showed

higher magnitude than [j]. So, this trait is mostly governed by either dominance and/or dominance x dominance epistatic gene action. The opposite signs of [h] [l] in the two crosses $P_1 \times P_2$ and $P_3 \times P_2$ indicated the presence of duplicate dominant epistasis. The H component of variance was higher than D component in four crosses. In two crosses viz., $P_2 \times P_3$ and $P_3 \times P_1$, D component was higher than H component. The dominance ratio was more than unity in $P_2 \times P_1$ and $P_3 \times P_2$ conforming the predominance of dominant gene action for this trait.

5.9.3.5. Number of capsules (Fig.34)

Only one cross, $P_3 \times P_1$ recorded significant additive effect alone. In two crosses viz., $P_2 \times P_3$ and $P_2 \times P_1$ both additive and additive x additive interaction effect was significant. Predominance of additivity for this trait was also reported by Rathinaswamy (1980), Fatteh et al. (1982), Singh et al. (1983), Rathinaswamy and Jagathesan (1984), Padmavathi (1987), Khorgade et al. (1988), Anitha (1988) and Deenamani (1989). In two crosses viz., $P_1 \times P_2$ and $P_3 \times P_2$ all the gene effects, additive, dominance and epistasis were significant. However, dominance showed higher magnitude followed by dominance x dominance in both the crosses. In the cross, $P_1 \times P_3$, dominance and epistasis were significant. In this cross also dominance showed higher magnitude followed by dominance x dominance interaction. Higher magnitude of dominance with epistasis interactions were also reported by Dixit (1976a) and Deenamani (1989). Out of the six crosses, additive and additive x additive interaction was significant in three crosses and additive, dominance and epistatic gene effects with predominance

of dominance gene action were significant. Predominance of non-additivity for this character was reported by Shrivastava and Singh (1981), Reddy et al. (1982), Djigma (1984), Godawat and Gupta (1985), Dora and Kamala (1987), Krishnadoss et al. (1987) and Deenamani (1989). Pathak and Dixit (1988) observed the importance of both additive and non-additive gene effects for this trait.

Five out of the six crosses showed opposite signs among [h] and [l] indicating mainly a duplicate dominant gene action. In the remaining one cross, $P_3 \times P_1$, the sign was same among [l] and [h] indicated the presence of recessive epistasis-complementary gene action for this trait. Dixit (1976a) and Deenamani (1989) recorded duplicate epistasis for this trait.

Partitioning of variance revealed that H component of variance was greater than D component in four crosses. The dominance ratio was more than unity in $P_1 \times P_3$ and $P_2 \times P_1$. These indicated the predominance of dominance gene action. However, in two crosses viz. $P_2 \times P_3$ and $P_3 \times P_1$, D component was higher than H component and the dominance ratio was less than unity indicating the presence of additive gene effects in them.

5.9.3.6. Volume of capsules

Additive, dominance, and epistasis were significant in $P_1 \times P_2$, $P_1 \times P_3$ and their reciprocal crosses. In all these crosses dominance

effect was predominant which was closely followed by dominant x dominant epistatic effect. In $P_2 \times P_3$, dominance and epistatic effects were significant. Here also, dominance showed higher magnitude followed by dominance x dominance interaction effect. In the reciprocal cross of $P_2 \times P_3$, additive x additive and Additive x dominance were significant. Additive interaction was predominant than additive x dominance. Predominance of dominance gene action for this trait was also reported by Deenamani (1989). Similarly, Anitha (1988) found the predominance of epistasis for this trait. However, additivity was also reported to be predominance for both length and breadth of capsule by Dora and Kamala (1987) and Padmavathi (1987) and for capsule length by Kotecha and Yermanos (1978), Rathinaswamy (1980), Chaudhari *et al.* (1984), Rathinaswamy and Jagadesan (1984), Djigma (1984), and Khorgade *et al.* (1988).

It was found that capsule volume was predominantly governed by dominance gene action followed dominance epistasis. The [i] and [l] effects were recorded in five out of six crosses. It may be due to the fact that like alleles are predominantly dispersed at the interacting loci (Jinks and Jones, 1958). Similarly, in five out of six crosses, [h] and [l] had opposite signs indicating the presence of duplicate dominant epistasis for this trait. However, the sign was same in $P_3 \times P_2$ indicating the presence of recessive epistasis, complementary gene action for this trait.

The dominance variance [h] was higher in magnitude than additive variance [D] in five out of six crosses, conforming the predominance of dominance gene action for this trait. However, in the cross $P_3 \times P_2$ [D] was higher than [H] conforming the presence of additive gene action also. This is in conformity with Deenamani (1989).

5.9.3.7. Number of seeds per capsule

Three cross combinations showed significant additive, dominance and epistatic effects. Invariably in all the cases, dominance was in higher magnitude which was followed by dominance x dominance interaction effect. Dominance and dominance x dominance interaction effect was significant in $P_2 \times P_3$ whereas in its reciprocal cross additive x dominance and dominance x dominance were significant. In $P_2 \times P_3$ dominance was higher in magnitude than dominance x dominance whereas in its reciprocal cross dominance x dominance was higher in magnitude. In $P_1 \times P_3$, additive and additive x dominance interaction was significant. Additive x dominance was in higher magnitude than additive alone. All put together, dominance followed by dominance x dominance interaction effects were predominantly governed this trait. Higher magnitude of dominance for this trait was also reported by Chavan *et al.* (1981) and Deenamani (1989). However, predominance of both additive and non-additive gene effects were reported by Anitha (1988), and additivity alone was reported by Chaudhari *et al.* (1984) and Padmavathi (1987). On the other hand, Tyagi (1975), Singh *et al.* (1983), Dora and Kamala (1987) reported non-additivity for this trait. Pathak and Dixit (1988)

observed the importance of both additive and non additive gene effects for this trait.

Invariably in all the cross combinations opposite signs among [h] and [l] were obvious. This indicated the presence of duplicate dominant epistasis for this trait, giving a clue for the possibility increasing this trait. Chavan et al. (1981) and Shivaparakash (1986) have also reported duplicate dominant epistasis for this trait.

The partitioning of the variance indicated the presence of higher magnitude of dominance variance than additive variance in all the cross combinations. The dominance ratio was more than unity in $P_1 \times P_3$ and $P_3 \times P_1$ conforming the predominance of dominance gene action for this trait.

5.9.3.8. Length of seeds

In the cross combinations viz., $P_1 \times P_3$, $P_3 \times P_1$ and $P_3 \times P_2$, significant additive, dominance and epistatic effects were envisaged. Among them dominance followed by dominance x dominance were predominant. In $P_2 \times P_1$, dominance and epistatic effects were predominant. Here also [h] followed by [l] showed higher magnitude. In $P_1 \times P_2$, additive x additive and additive x dominance were significant. Additive x additive was predominant. In $P_2 \times P_3$ additive and additive x dominance were significant. Additive x dominance was in greater in magnitude. In toto, this trait was governed by dominance and epistatic gene actions.

Dora and Kamala (1987) also found the predominant role of non-additive gene influence on this trait.

In all the crosses [h] and [l] had opposite signs showing the presence of dominant duplicate epistasis. Similarly in all the crosses [i] and [l] had opposite signs.

Partitioning of the variance revealed the higher magnitude of additive variance than dominance variance in four out of six crosses. The dominance ratio was less than unity in $P_2 \times P_1$ explaining the role of additivity in the expression of this trait. However, in the remaining two crosses, H component was higher than D component, indicating the presence of dominance in the expression of this trait.

5.9.3.9. Breadth of seeds

Additive, dominance and epistatic effects were significant in two direct and three reciprocal crosses. In three crosses dominance was in higher magnitude followed dominance x dominance, and by additive x additive, additive x dominance respectively in one cross. This indicated the predominant role of dominance in the expression of this trait. Dora and Kamala (1987) found the importance of non-additive gene action in the expression of this trait. However, in one cross, $P_1 \times P_3$, additive and additive x additive gene effects were significant, with a higher magnitude of additive x additive effects.

Presence of duplicate dominant epistasis was evidenced from the opposite signs of [h] and [l] in all the crosses. The [i] and [l] effects were also showed opposite signs.

Dominance variance was higher than additive variance in five out of six crosses. The dominance ratio was higher than unity in $P_1 \times P_3$ conforming the predominant role of dominance in the expression of this trait. However, in $P_2 \times P_1$, D component was higher than H component indicating the presence of additivity for this trait.

5.9.3.10. Weight of 1000 seeds (Fig.35)

In three out of six crosses, additive, dominance and epistatic effects were significant. In these three crosses dominance was in higher magnitude followed by dominance x dominance interaction effect. In the remaining three crosses, additive and epistatic effects were significant, with a higher magnitude of additive x dominance and dominance x dominance interaction effect. All put together, additive and epistatic gene effects were important in the expression of this trait. This finding is in conformity with Deenamani (1989). Non-additive gene action for this trait was reported by Tyagi (1975), Singh *et al.* (1983), Dora and Kamala (1986) and Padmavathi (1987). Additivity for this trait was also reported by Dixit (1976a) Fatteh *et al.* (1982), Djigma (1984), Anitha (1988) and Khorgade *et al.*, (1988).

Weight of 1000 seeds was governed by duplicate dominant epistasis in all the crosses as inferred from the opposite signs of

[h] and [l]. The [i] and [l] effects were also showed opposite signs in five out of the six crosses.

Partitioning of the variance showed greater dominance variance than additive variance in five out of six crosses. The dominance ratio was more than unity in $P_1 \times P_2$, conforming the predominance of dominance gene action for this trait. However, in $P_3 \times P_2$ H and D variance were equal and the dominance ratio was also unity. All these trend led to infer that dominance, additive and epistasis were important in the expression of this trait.

5.9.3.11. Volume of 1000 seeds

In four crosses showed non significant additive, dominant and epistatic gene effects. In two crosses simple additive-dominant model was adequate. However, both additivity and dominance showed non-significant effect. Duplicate dominant epistasis governed this trait in four out of six crosses, as inferred from the opposite signs of [h] and [l] effects. In these crosses [i] and [l] also showed opposite signs.

Partitioning of the variance indicated the presence of greater dominance variance than additive variance in four crosses. This indicated the predominance of dominance in the expression of this trait. However, in two crosses, viz., $P_2 \times P_1$ and $P_3 \times P_1$, additive variance was greater than dominance variance, indicating the presence of additive genetic control on this trait.

5.9.3.12. Density of seeds (Fig.36)

Simple additive dominance model was adequate for $P_2 \times P_3$ where both additive and dominance were significant. Dominance was predominant. Additive and epistasis were significant in $P_1 \times P_3$ and its reciprocal cross. In both the crosses, dominance x dominance was higher in magnitude. In $P_1 \times P_2$ and $P_3 \times P_2$, dominance and epistatic effects were significant with higher magnitude of dominance followed by dominance x dominance interaction effect. In $P_2 \times P_1$ all the effects were non-significant. So, it may be concluded that this trait is predominantly controlled by dominance and dominance x dominance gene effects, i.e. non-additive gene action.

Duplicate dominant epistasis governed this trait as inferred from the opposite signs of [h] and [l]. Similarly, [i] and [l] took opposite signs in four out of six crosses.

Partitioning of the variance revealed the higher magnitude of dominance variance than additive variance in all the crosses. The dominance ratio was also more than unity in $P_2 \times P_1$ and $P_3 \times P_1$ again conforming the predominant dominance genetic control over this trait.

5.9.3.13. Oil content

Additive and additive x additive interaction effects were significant in $P_1 \times P_2$ and its reciprocal cross. While additive epistasis was higher in magnitude in the direct cross, simple additive was higher

in its reciprocal cross. This is in conformity with Mosjidis (1982), Reddy et al. (1982) and Anitha (1988). In the remaining four crosses additive, dominance and epistatic interaction effects were significant. Dominance effect was higher in magnitude followed by dominance x dominance interaction effect.

Preponderance of dominance for this trait was also reported by Uzo and Oziake (1981), Tyagi (1975), Murty (1975), Fatteh et al. (1982), Singh et al. (1983), Dora and Kamala (1987) and Padmavathi (1987) reported non-additivity for this trait.

The [i] and [l] took opposite signs in all the crosses. Similarly [h] and [l] took opposite signs in all the crosses, indicating the duplicate dominant type of epistasis. This is in conformity with Reddy et al. (1986).

The partitioning of the variance component, the H component was higher than D component in all the crosses, conforming the presence of dominance gene action. The dominance ratio was more than unity in $P_3 \times P_1$ and $P_3 \times P_2$ assured the presence of dominance gene action.

5.9.3.14. Seed yield (Fig.37)

Additive x additive interaction alone was significant in two crosses combinations viz., $P_2 \times P_3$ and $P_3 \times P_1$. Predominance of additivity was also reported by Chaudhari et al. (1984), Rathinaswamy and Jagathesan (1984), Padmavathi (1987) and Anitha (1988). In three

crosses, dominance and epistatic interaction effects were significant. In all these crosses, dominance was higher in magnitude followed by dominance x dominance interaction effect. A similar finding of higher magnitude of dominance governing seed yield was reported by Dixit (1976a) in Sesame. Uzo and Ojiake (1981) and Deenamani (1989) also observed dominance and interactions for this trait. Chavan et al. (1981) and Shivaprakash (1986) reported less magnitude of interaction effects. Non-additivity was also reported for this trait by Djigma (1984), Godawat and Gupta (1985), Anandakumar and Sree Rangasamy (1987) Dora and Kamala (1987), Krishnadoss et al. (1987). IN, $P_2 \times P_1$ all the effects were non-significant.

Five out of the six crosses showed H opposite signs among the [h] and [l]. This indicated the presence of duplicate dominant epistasis in the inheritance of seed yield. This is in corroboration with the results of Dixit (1976a) Chavan (1981), Reddy et al. (1986), Shivaprakash (1986) and Deenamani (1989). However, in one cross, $P_2 \times P_1$ the [h] and [l] had same sign, showing the recessive epistasis (complementary) too in the inheritance of this trait.

The H component was higher than D component in all the crosses. The dominance ratio was higher than unity in $P_1 \times P_3$. These conformed the preponderance of dominance gene action in the expression of seed yield.

5.9.3.15. Total dry matter production (Fig.38)

Additive, additive x additive interaction effects were significant in $P_2 \times P_1$, where additive x additive was predominant. In $P_3 \times P_1$, additive, dominance and additive x additive interactions were significant, but dominance was predominant. In $P_3 \times P_2$, additive and non-additive epistasis were significant with preponderance of dominance x dominance interaction effect. In $P_1 \times P_3$, additive, dominance and dominance x dominance interactions effects were significant, with pre-dominance of dominance effect. In $P_1 \times P_2$, and $P_2 \times P_3$, additive, dominance and interaction effects were significant with predominance of dominance effect. Thus this trait was mostly governed by dominance and dominance x dominance epistatic effect predominantly which is in conformity with Deenamani (1989).

On considering the opposite signs of [h] and [l] in all the crosses, the presence of duplicate dominant epistasis was evidenced. Similarly, [i] and [l] also took opposite signs in all the crosses.

Partitioning of the variance showed the preponderance of H component than 'D'. The dominance ratio was more than unity in $P_1 \times P_3$, $P_3 \times P_1$ and $P_2 \times P_3$ conforming the preponderance of dominance gene action for this trait.

5.9.3.16. Harvest index (Fig.39)

In three crosses simple additive-dominance model was adequate. However, both additive and dominance were non-significant. In the other

crosses interaction was present but non significant excepting $P_1 \times P_2$ where dominance x dominance alone was significant. This is partly in conformity with Deenamani (1989). However, this does not agree with the findings of Singh et al. (1983) and Anitha (1988) who reported predominance of additivity for this trait.

In $P_1 \times P_2$ and $P_3 \times P_2$, the [h] and [l] took opposite sign, showing the presence of duplicate dominant epistasis in the inheritance of this trait. However, in $P_1 \times P_3$ [h] and [l] took the same sign indicating the presence of recessive complementary epistasis too for the trait. The [i] and [l] took opposite sign only in the two cross combinations.

In partitioning the variance component, H was higher than D in all the cross combinations conforming the involvement of dominance gene action in the expression of this trait.

For most of the characters, [i] and [l] type of interactions took opposite signs showing thereby that like alleles are predominantly dispersed at these interacting loci (Jinks and Jones, 1958). The negative sign of F in most of the combinations indicates the direction of dominance deviation for this character (Mather and Jinks, 1977). The negative estimate of D may be due to sampling error (Sandhu and Khehra, 1976).

5.9.4. Summary of the results on gene effects

The scaling tests indicated the inadequacy of the data to a simple additive - dominance model for all the characters and crosses in general with a few exceptions. Simple additive-dominance model was adequate in the direct cross, $P_2 \times P_3$, for number of branches, density of seeds and harvest index. For its reciprocal cross it was inadequate for the same traits. The adequacy in both direct and reciprocal crosses ($P_2 \times P_3$, $P_3 \times P_2$) was found for volume of 1000 seeds. It was also adequate in the reciprocal crosses viz., $P_2 \times P_1$ and $P_3 \times P_1$ for harvest index and inadequate in their direct crosses for the same trait. The lack of adequacy of this simple model in the reciprocal cross of $P_2 \times P_3$ i.e. in $P_3 \times P_2$ for number of branches, seed density and harvest index as well as in the direct crosses of the reciprocal crosses viz., $P_2 \times P_1$ and $P_3 \times P_1$ i.e. in $P_1 \times P_2$ and $P_1 \times P_3$ indicated the existence of reciprocal differences for these traits.

The existence of simple additive-dominance model indicated the prevalence of dominance effect for these traits in the respective crosses. Devoiding these cross combinations, all other crosses were subjected to the additive-dominance model with digenic interaction. The overall genetic situation obtained for the sixteen traits of interest in different cross combinations is summarized in Tables 198 and 199.

For days to maturity additive, dominance and epistatic effects were significant in most of the crosses with predominance of dominance

gene action. This was again conformed by the preponderance of dominance variance than the additive variance. The dominance ratio was also more than unity. Duplicate type of epistasis was present in all the crosses.

Dominance and epistatic effects were significant for plant height at maturity. Dominance was predominant. Dominance variance was higher than additive variance. Duplicate dominant epistasis was present in all crosses.

On overall basis, additive, dominance and epistatic effects were present for number of branches with predominance of non-additive epistatic effect. H was higher in magnitude than D component and the dominance ratio was more than unity. Dominant duplicate epistasis was observed in all crosses.

Dominance x dominance epistatic effect was preponderant for number of flowers. D was higher than H in four crosses and the reverse was true in two crosses. The dominance ratio was more than unity in two crosses. Duplicate dominant epistasis was present in all the crosses.

For number of capsules per plant, additive, dominance and epistatic effects were significant. Of these, dominance and additive x additive epistatic effects were important. H was higher in magnitude

in five crosses and the dominance ratio was more than unity in two crosses. D was higher than H in two crosses and dominance ratio was less than unity in two crosses, conforming the prevalence of both dominance and additive x additive epistatic effects. Five crosses showed duplicate dominant epistasis and one cross showed complementary recessive epistasis.

Additive, dominance and epistatic effects were significant for volume of capsules. However, dominance and dominance x dominance epistatic effects were preponderant. H was higher than D in five crosses. In one cross D was more than H. Dominance Ratio was less than unity in one cross. Dominant duplicate epistasis was present in five crosses. In one cross, recessive epistasis was present.

Dominance followed dominance x dominance interaction effect were preponderant even though all the three effects were significant for number of seed per capsule. H was higher than D in all the crosses. The dominance ratio was more than unity in two crosses. Duplicate dominant epistasis was present in all the crosses.

For seed length, additive, dominance and epistatic effects were significant with predominance of dominance and dominance x dominance interaction effect. However, D was higher than H in four crosses and H was higher than D in two crosses. Dominance ratio was less than unity in two crosses indicating the importance of additivity too. Duplicate dominant epistasis was present in all the crosses.

Additive, dominance and epistatic effects were significant. For seed breadth, dominance was higher in magnitude. H was more than D in five crosses. D was more than H in only one cross. Dominance ratio was more than unity in one cross. Duplicate dominant epistasis was present in all the crosses.

Additive, dominance and epistatic effects were prevalent for weight of 1000 seeds. Dominance was higher in magnitude. H was more than D in five crosses and H was equal to D in one cross. Dominance ratio was more than unity in one cross and unity in one cross indicating the presence of additivity too. Duplicate dominant epistasis was present in all the crosses.

For 1000 seed volume all the effects were non-significant. H was higher than D in four crosses and D was higher than H in two crosses, indicating the importance of both dominance and additivity. Four crosses showed duplicate dominant epistasis.

Dominance x dominance interaction effect was important in the expression of seed density even though additivity, and dominance were also observed. Dominance was higher than additive variance in all the crosses. Dominance ratio was more than unity in two crosses. Five crosses showed duplicate dominant epistasis.

For oil content, additive, dominance and epistatic effects were significant. Dominance was higher in magnitude. Dominance was higher

than additive variance in all the crosses. Dominance ratio was more than unity in two crosses. In all the crosses duplicate dominant epistasis was present.

For seed yield, dominance and epistatic effects were significant. Dominance was higher in magnitude. Additive x additive interaction effect was alone significant in two crosses. Dominance variance was higher than additivity in all the crosses. The dominance ratio was more than unity in one cross. Duplicate dominant epistasis was present in five crosses and recessive complementary epistasis was present in one cross.

Additive, dominance and epistatic interaction effects were significant for total dry matter production. Dominance and dominance x dominance interaction effect was prevalent. In one cross, additive and additive epistasis was alone significant. H was higher than D in all the crosses. Dominance ratio was more than unity in three crosses. Duplicate dominant epistasis was present in all the crosses.

For harvest index, dominance x dominance interaction effect alone was significant that too in only one cross. Other crosses showed non-significant genetic effects. D was higher than H in all the crosses. Both duplicate and dominant (two crosses) and complementary recessive epistasis was present.

Table 198. Overall genetic situation obtained in the number of crosses for different traits .

Characters significant gene effects	Number of crosses															
	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆
i	-	-	-	-	1	-	-	-	-	-	-	-	-	2	-	-
j	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-
l	-	-	-	3	-	-	-	-	-	-	-	-	-	-	-	1
dh	-	-	1 ^s	-	-	-	-	-	-	-	-	1 ^s	-	-	-	-
di	-	-	-	-	2	-	-	-	1	-	-	-	2	-	1	-
dj	-	-	1	-	-	-	1	1	-	1	-	-	-	-	-	-
dl	-	-	1	-	-	-	-	-	-	-	-	1	-	-	-	-
hl	1	-	-	-	-	-	1	-	-	-	-	-	-	2	-	-
ij	-	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-
jl	-	-	1	1	-	-	1	-	-	-	-	-	-	-	-	-
dhl	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-
dhj	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-
dhl	-	-	-	-	-	-	1	-	-	1	-	-	1	-	1	-
hil	1	5	-	-	-	-	-	-	-	-	-	2	-	-	-	-
dij	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-
djl	-	-	-	-	-	-	-	-	-	1	-	1	-	-	1	-
hjl	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
dhil	1	-	-	-	1	1	1	-	-	1	-	-	-	-	1	-
dhjl	-	-	-	-	1	-	-	-	1	1	-	-	1	-	-	-
hijl	-	-	-	2	-	1	-	1	-	-	-	-	-	-	-	-
dhijl	3	-	1	-	1	3	1	3	2	-	-	-	2	1	1	-
dhijl All NS	-	-	-	-	-	-	-	-	-	-	4	1	-	1	-	2
Simple modle NS	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	3

S = Superscript indicate simple additive-dominance model

Table 199. Types of epistasis for different characters

Code No.	Characters	Total No. of crosses	Numbers of crosses					H/D more than unity	H/D less than unity	Number of crosses (or) pairs of crosses	Cytoplasmic effect (C)	Maternal genetic effect (M)
			Simple additive dominance mode	Type of epistasis		D greater than H						
				D	C	H greater than D	D greater than H					
X ₁	Days to maturity	6	-	6	-	6	-	1	-	3	4	
X ₂	Height of the plant at maturity	6	-	6	-	5	1	-	-	3	5	
X ₃	Number of branches	6	1	5	-	6	-	1	-	1	3	
X ₄	Number of flowers	6	-	6	-	4	2	2	-	3	4	
X ₅	Number of capsules	6	-	5	1	4	2	2	2	3	3	
X ₆	Volume of capsules	6	-	5	1	5	1	-	1	3	1	
X ₇	Number of seeds per capsule	6	-	6	-	6	-	2	-	2	3	
X ₈	Length of seeds	6	-	6	-	2	4	-	1	2	4	
X ₉	Breadth of seeds	6	-	6	-	5	1	1	-	2	1	
X ₁₀	Weight of 1000 seeds	6	-	6	-	5*	-	1	-	2	1	
X ₁₁	Volume of 1000 seeds	6	2	4	-	4	2	-	-	1	6	
X ₁₂	Density of seeds	6	1	5	-	6	-	2	-	3	4	
X ₁₃	Oil content	6	-	6	-	6	-	2	-	3	5	
X ₁₄	Seed yield	6	-	5	1	6	-	1	-	3	5	
X ₁₅	Total dry matter production	6	-	6	-	6	-	3	-	3	4	
X ₁₆	Harvest index	6	3	2	1	6	-	-	-	1	6	

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Note: * In one cross H = D.

D= Duplicate dominant epistasis

C = Complementary recessive epistasis

5.9.5. Cytoplasmic influence on gene effects

From the analysis of maternal and cytoplasmic effects it was obvious that the cytoplasm of the three parents used in this part of study viz., P_1 , P_2 and P_3 differed from each other for most of the traits of interest. P_1 differed from P_2 for 14 traits, from P_3 for 12 traits. P_2 differed from P_3 for 12 traits. This necessitated to study the influence of the cytoplasm on the estimates of nuclear gene effects.

5.9.5.1. Days to maturity

Dominance and dominance x dominance interaction effects were significant in the direct cross $P_1 \times P_3$. Added to [h] and [l], [i] effects was also significant in its reciprocal cross, $P_3 \times P_1$. Similarly in $P_2 \times P_3$, [d], [h], [i] and [l] were important. But for its reciprocal cross [d], [h], [i], [j] and [l] were significant. In the direct crosses, [h] was in higher magnitude, followed by [l] whereas in the reciprocal cross [h] followed by [i] were in higher magnitude.

5.9.5.2. Height of the plant at maturity

For $P_2 \times P_3$, [j] effect alone was significant. Whereas for its reciprocal cross $P_3 \times P_2$, [h], [i] and [l] effects were significant. In $P_2 \times P_3$, [i] and [l] had same sign whereas in its reciprocal cross [i] and [l] had opposite sign.

Dominance variance was higher in $P_1 \times P_3$, whereas additive variance was higher in its reciprocal cross, $P_3 \times P_1$.

5.9.5.3. Number of branches

Effects of [d], [h], [i], [j] and [l] were important in $P_1 \times P_2$ whereas [d] and [j] alone were important in $P_2 \times P_1$. For $P_1 \times P_3$, [j] and [l] effects were significant, but for $P_3 \times P_1$ [j] effect alone was significant. $P_2 \times P_3$ fits well to the simple additive-dominance model and [d] and [h] effects were significant. Whereas in its reciprocal form, [d] and [l] interaction effects were significant and had digenic interaction. In $P_1 \times P_2$, [i] and [l] effects had opposite sign, whereas it was same sign in its reciprocal cross.

5.9.5.4. Number of flowers

For $P_1 \times P_2$, [h], [i], [j] and [l] effects were significant. But for $P_2 \times P_1$, [l] effect alone was significant. For $P_1 \times P_3$, [j] and [l] effects were significant. For its reciprocal cross [l] effect alone was significant. For $P_2 \times P_3$, [l] effect alone was significant, but [h], [i], [j] and [l] effects were significant for its reciprocal cross. [i] and [l] effects had opposite sign in $P_1 \times P_2$ but same sign in $P_2 \times P_1$. $P_2 \times P_3$ had same sign but $P_3 \times P_2$ had opposite sign.

H component was higher than D component of variance for $P_1 \times P_3$ and $P_3 \times P_2$ whereas D was higher than H in $P_3 \times P_1$ and $P_2 \times P_3$.

In breeding vigour was high in $P_1 \times P_2$ and $P_1 \times P_3$ comparatively less in $P_2 \times P_1$, and $P_3 \times P_1$. It was comparatively high in $P_3 \times P_2$ and $P_2 \times P_3$.

5.9.5.5. Number of capsules

Gene effects [d], [h], [i], [j] and [l] were significant in $P_1 \times P_2$, whereas [d] and [i] effects alone significant in $P_2 \times P_1$. For $P_1 \times P_3$, [h], [j] and [l] were important but [i] alone important for $P_3 \times P_1$. Additive and additive x additive interaction effects were significant for $P_2 \times P_3$ but [d], [h], [j] and [l] effects were significant for $P_3 \times P_2$. [i] and [l] had opposite sign in $P_1 \times P_3$ but had same sign in $P_3 \times P_1$. Similarly, $P_1 \times P_3$ showed opposite sign for [h] and [l] but $P_3 \times P_1$ showed same sign for [h] and [l].

Dominant variance was higher than D variance in $P_1 \times P_3$ and $P_3 \times P_2$. But the reverse was true in their reciprocal and direct crosses respectively.

5.9.5.6. Volume of capsules

For $P_1 \times P_2$, [d], [h], [i], [j] and [l] were significant. But for $P_2 \times P_3$ [d], [h], [i] and [l] were significant. For $P_2 \times P_3$, [h], [i], [j] and [l] were significant. But for $P_3 \times P_2$ [i] and [j] alone were significant. For $P_2 \times P_3$, [h] and [l] had opposite sign, but for $P_3 \times P_2$ [h] and [l] had same sign. $P_2 \times P_3$ showed opposite signs of [i] and [l] whereas $P_3 \times P_2$ showed same sign.

Dominance component of variance was higher than additive component in $P_2 \times P_3$, but D was higher than H in its reciprocal cross.

5.9.5.7. Number of seeds per capsule

Gene effects [d], [h] and [l] were significant for $P_1 \times P_2$ whereas [d], [h], [i], [j] and [l] were significant for $P_2 \times P_1$. For $P_1 \times P_3$, [d] and [j] alone were significant. But for $P_3 \times P_1$, [d], [h], [i] and [l] were significant. For $P_2 \times P_3$ [h] and [l] were significant but for its reciprocal cross ($P_3 \times P_2$), [j] and [l] were significant.

5.9.5.8. Length of seeds

For the cross $P_1 \times P_2$, [i] and [j] effects were significant. But for its reciprocal cross ($P_2 \times P_1$), [h] [i], [j] and [l] effects were significant. Similarly for the cross $P_2 \times P_3$, [d] and [j] were significant. But for the reciprocal cross, $P_3 \times P_2$, all the effects were significant.

5.9.5.9. Breadth of seeds

Gene effects [d], [h], [j] and [l] were significant for $P_1 \times P_2$, whereas for its reciprocal cross all the effects including [i] were significant. For $P_1 \times P_3$ [d] and [i] were significant. But for $P_3 \times P_1$ [d], [h], [i], [j] and [l] were significant. Similarly for $P_2 \times P_3$, [d], [h] and [i] were significant. But for $P_3 \times P_2$, [d], [h] and [j] were significant.

H was higher than D in $P_1 \times P_2$, but D was higher than H in $P_2 \times P_1$.

5.9.5.10. Weight of 1000 seeds

For the cross, $P_1 \times P_2$, [d], [h], [i] and [l] were significant, but for its reciprocal cross, $P_2 \times P_1$ [d], [h], [j] and [l] were important. But for $P_3 \times P_1$, [d] and [j] alone were important. Similarly, [d], [h], and [l] effects were significant in $P_2 \times P_3$ but [d], [i] and [j] were significant for $P_3 \times P_2$. [i] and [l] had opposite sign in $P_3 \times P_1$, but had same sign in $P_1 \times P_3$.

H was higher than D in $P_2 \times P_3$ whereas both were equal in its reciprocal cross.

5.9.5.11. Volume of 1000 seeds

In all the cross combinations, all the gene effects were non significant. Dominant component of variance was higher than additive component in $P_1 \times P_2$ and $P_1 \times P_3$. Whereas in $P_2 \times P_1$ and $P_3 \times P_1$, D was higher than H.

5.9.5.12. Density of seeds

For $P_1 \times P_2$, [h], [i] and [l] were significant. But all the effects were non-significant in its reciprocal cross. For $P_1 \times P_3$, [d] and [l] were significant, but added to these effects [j] were also significant in its reciprocal cross. Simple additive and dominance were significant in $P_2 \times P_3$, whereas dominant and non-additive epistasis were significant in $P_3 \times P_2$. $P_3 \times P_1$ showed [i] and [l] opposite sign but $P_1 \times P_3$ showed same sign.

5.9.5.13. Oil content

Gene effects, [d], [h], [i], [j] and [l] were significant in $P_1 \times P_3$ whereas [d], [h] and [l] were significant in $P_3 \times P_1$. For $P_2 \times P_3$, [d], [h], [i], [j] and [l] were significant in $P_2 \times P_3$ whereas [i] was non-significant in its reciprocal cross, $P_3 \times P_2$.

5.9.5.14. Seed yield

Dominance and epistatic effects were significant in $P_1 \times P_2$ whereas all effects were non-significant in $P_2 \times P_1$. $P_1 \times P_3$ showed significance for [h] and [l] effects, whereas $P_3 \times P_1$ showed significance for [i] effect alone. Similarly while $P_2 \times P_3$ showed significance for [i] effect alone, its reciprocal cross $P_3 \times P_2$ showed non-significant [i] effect and significant [h] and [l] effects. [h] and [l] expressed opposite sign in $P_1 \times P_2$, but showed same sign in $P_2 \times P_1$. For $P_1 \times P_2$ [i] and [l] had opposite sign. But for $P_2 \times P_1$ it had same sign.

5.9.5.15. Total dry matter production

Gene effects [d], [h], [i], [j] and [l] were significant for $P_1 \times P_2$, whereas [d] and [i] effects alone were significant in its reciprocal cross. For $P_1 \times P_3$, [d], [h] and [l] effects were significant. But, [d], [h] and [i] effects were significant in $P_3 \times P_1$. Additive, dominance, additive x additive and dominance x dominance interaction effects were significant in $P_2 \times P_3$ whereas simple additive and non-additive epistasis were significant in its reciprocal cross, $P_3 \times P_2$.

5.9.5.16. Harvest index

Digenic interaction effect [1] was significant in $P_1 \times P_2$ whereas non-significant simple additive and dominance were observed in $P_2 \times P_1$. While $P_1 \times P_3$ showed non-significant interaction effect, $P_3 \times P_1$ exhibited non-significant simple additive and dominance effect. Similar trend was also observed in $P_2 \times P_3$ and $P_3 \times P_2$.

Summary of the cytoplasmic influence on gene effects are presented in Table 200. The difference in the gene effects among the direct and reciprocal crosses were highly obvious in fifteen out of sixteen traits. In one trait, volume of 1000 seeds all the gene effects were non-significant in direct as well as reciprocal crosses. However, this difference in the gene effects among direct and reciprocal crosses, was not able to change the type of epistasis excepting the shift from duplicate dominant epistasis to complementary recessive epistasis in $P_1 \times P_2$ and $P_2 \times P_1$ for seed yield, $P_1 \times P_3$ and $P_3 \times P_1$ for capsule number, and $P_2 \times P_3$ and $P_3 \times P_2$ for capsule volume. This clearly explained the existence of different cytoplasm and its influence in the genetic expression of quantitative traits as well.

Table 200. Summary of the cytoplasmic influence on gene effects

Characters/ Crosses/ Significant + Gene effects	X_1						X_2					
	D_1	R_1	D_2	R_2	D_3	R_3	D_1	R_1	D_2	R_2	D_3	R_3
i												
j											✓	
l												
dh												
di												
dj												
dl												
hl			✓									
ij												
jl												
dhi												
dhj												
dhl												
hil				✓			✓	✓	✓	✓		✓
dij												
djl												
hjl												
dhil					✓							
dhjl												
hijl												
dhijl	✓	✓				✓						
dhijl All NS												
Simple NS												
No. of crosses with reciprocal difference	----- 2/3 -----						----- 1/3 -----					
Type of epistasis	D	D	D	D	D	D	D	D	D	D	D	D
	$D_1 = P_1 \times P_2$			$D_2 = P_1 \times P_3$			$D_3 = P_2 \times P_3$					
	$R_1 = P_2 \times P_1$			$R_2 = P_3 \times P_1$			$R_3 = P_3 \times P_2$					

Table 200. Contd..

Characters/ Crosses/ Significant + Gene effects	X_3						X_4					
	D_1	R_1	D_2	R_2	D_3	R_3	D_1	R_1	D_2	R_2	D_3	R_3
i												
j				✓								
l								✓		✓	✓	
dh					✓							
di												
dj		✓										
dl						✓						
hl												
ij												
jl			✓						✓			
dhi												
dhj												
dhl												
hil												
dij												
djl												
hjl												
dhil												
dhjl												
hijl							✓					
dhijl	✓											✓
dhijl All												
Simple												
No. crosses with												
reciprocal difference					3/3					3/3		
Type of epistasis	D	D	D	D	D	D	D	D	D	D	D	D

$$D_1 = P_1 \times P_2$$

$$R_1 = P_2 \times P_1$$

$$D_2 = P_1 \times P_3$$

$$R_2 = P_3 \times P_1$$

$$D_3 = P_2 \times P_3$$

$$R_3 = P_3 \times P_2$$

Table 200. Contd..

Characters/ Crosses/ Significant + Gene effects	X ₅						X ₆					
	D ₁	R ₁	D ₂	R ₂	D ₃	R ₃	D ₁	R ₁	D ₂	R ₂	D ₃	R ₃
i				✓								
j												
l												
dh												
di		✓			✓							
dj												
dl												
hl												
ij												✓
jl												
dhi												
dhj												
dhl												
hil												
dij												
djl												
hjl			✓									
dhil								✓				
dhjl					✓							
hijl											✓	
dhijl	✓						✓		✓	✓		
dhijl All NS												
Simple NS												
No. crosses with reciprocal difference	----- 3/3 -----						----- 2/3 -----					
Type of epistasis	D	D	D	D	D	D	D	D	D	D	D	D

$$D_1 = P_1 \times P_2$$

$$R_1 = P_2 \times P_1$$

$$D_2 = P_1 \times P_3$$

$$R_2 = P_3 \times P_1$$

$$D_3 = P_2 \times P_3$$

$$R_3 = P_3 \times P_2$$

Table 200. Contd..

Characters/ Crosses/ Significant + Gene effects	X_7						X_8					
	D_1	R_1	D_2	R_2	D_3	R_3	D_1	R_1	D_2	R_2	D_3	R_3
i												
j												
l												
dh												
di												
dj												
dl			✓								✓	
hl					✓							
ij							✓					
jl						✓						
dhi												
dhj												
dhl	✓											
hil												
dij												
djl												
hjl												
dhil					✓							
dhjl												
hijl								✓				
dhijl		✓							✓	✓		✓
dhijl All NS												
Simple NS												
No. crosses with reciprocal difference	----- 3/3 -----						----- 2/3 -----					
Type of epistasis	D	D	D	D	D	D	D	D	D	D	D	D

$$D_1 = P_1 \times P_2$$

$$R_1 = P_2 \times P_1$$

$$D_2 = P_1 \times P_3$$

$$R_2 = P_3 \times P_1$$

$$D_3 = P_2 \times P_3$$

$$R_3 = P_3 \times P_2$$

Table 200. Contd..

Characters/ Crosses/ Significant + Gene effects	X ₉						X ₁₀					
	D ₁	R ₁	D ₂	R ₂	D ₃	R ₃	D ₁	R ₁	D ₂	R ₂	D ₃	R ₃
i												
j												
l												
dh												
di			✓									
dj										✓		
dl												
hl												
ij												
jl												
dhi					✓							
dhj						✓						
dhl											✓	
hil												
dij									✓			✓
djl												
hjl												
dhil							✓					
dhjl	✓							✓				
hijl												
dhijl		✓		✓								
dhijl All	NS											
Simple	NS											
No. crosses with												
reciprocal difference	----- 3/3 -----						----- 3/3 -----					
Type of epistasis	D	D	D	D	D	D	D	D	D	D	D	D

$$D_1 = P_1 \times P_2$$

$$R_1 = P_2 \times P_1$$

$$D_2 = P_1 \times P_3$$

$$R_2 = P_3 \times P_1$$

$$D_3 = P_2 \times P_3$$

$$R_3 = P_3 \times P_2$$

Table 200. Contd..

Characters/ Crosses/ Significant + Gene effects	X_{11}						X_{12}					
	D_1	R_1	D_2	R_2	D_3	R_3	D_1	R_1	D_2	R_2	D_3	R_3
i												
j												
l												
dh											✓	
di												
dj												
dl									✓			
hl												
ij												
jl												
dhi												
dhj												
dhl												
hil							✓					✓
dij												
djl										✓		
hjl												
dhil												
dhjl												
hijl												
dhijl												
dhijl All NS	✓	✓	✓	✓	✓	✓		✓				
Simple NS												
No. crosses with reciprocal difference	----- 3/3 -----						----- 3/3 -----					
Type of epistasis	D	D	D	D	D	D	D	D	D	D	D	D

$$D_1 = P_1 \times P_2$$

$$R_1 = P_2 \times P_1$$

$$D_2 = P_1 \times P_3$$

$$R_2 = P_3 \times P_1$$

$$D_3 = P_2 \times P_3$$

$$R_3 = P_3 \times P_2$$

Table 200. Contd..

Characters/ Crosses/ Significant + Gene effects	X_{13}						X_{14}					
	D_1	R_1	D_2	R_2	D_3	R_3	D_1	R_1	D_2	R_2	D_3	R_3
i										✓	✓	
j												
l												
dh												
di	✓	✓										
dj												
dl												
hl									✓			✓
ij												
jl												
dhi												
dhj												
dhl				✓								
hil												
dij												
djl												
hjl												
dhil												
dhjl						✓						
hijl							✓					
dhijl			✓		✓							
dhijl All NS												
Simple NS									✓			
No. crosses with reciprocal difference	----- 2/3 -----						----- 3/3 -----					
Type of epistasis	D	D	D	D	D	D	D	D	D	D	D	D

$$D_1 = P_1 \times P_2$$

$$R_1 = P_2 \times P_1$$

$$D_2 = P_1 \times P_3$$

$$R_2 = P_3 \times P_1$$

$$D_3 = P_2 \times P_3$$

$$R_3 = P_3 \times P_2$$

Table 200. Contd..

Characters/ Crosses/ Significant + Gene effects	X ₁₅						X ₁₆					
	D ₁	R ₁	D ₂	R ₂	D ₃	R ₃	D ₁	R ₁	D ₂	R ₂	D ₃	R ₃
i												
j												
l							✓					
dh												
di		✓										
dj												
dl												
hl												
ij												
jl												
dhi				✓								
dhj			✓									
dhl												
hil												
dij												
djl						✓						
hjl					✓							
dhil												
dhjl												
hijl												
dhijl	✓											
dhijl All NS									✓			
Simple NS							✓			✓		
No. crosses with reciprocal difference												
Type of epistasis	D	D	D	D	D	D	D	D	D	D	D	D

$$D_1 = P_1 \times P_2$$

$$R_1 = P_2 \times P_1$$

$$D_2 = P_1 \times P_3$$

$$R_2 = P_3 \times P_1$$

$$D_3 = P_2 \times P_3$$

$$R_3 = P_3 \times P_2$$

SUMMARY AND CONCLUSION

6. SUMMARY AND CONCLUSION

The present investigation was formulated to evaluate the breeding values of the sesame genotypes and to identify the potential parents to conceptualize the breeding strategies based on the genetic informations on seed size, yield and their component characters. Informations on the nature and magnitude of genetic variability, extent of heritable differences (genetic determination), genetic gain that can be made by selection, genetic correlations of the component traits with 1000 seed weight and seed yield as well as among the component traits, were generated. Aside the causal basis of such relationship, phenotypic stability of the traits of interest, the genetic diversity among the genotypes, the character contribution towards genetic diversity, the prepotency, combining ability and yielding capacity of the genotypes, the exploitable maximum heterosis, the type of predominant gene action governing their expression, and the possible interplay of cytoplasmic and/or maternal influence in the expression of quantitative traits were obtained by adopting the well-established biometrical genetic approaches, such as variability, heritability, genetic advance, correlation, path analysis, stability analysis, mahalanobis' D^2 , line x tester analysis and generation mean and variance analysis. The reliability of the genetic information obtained in a single season was tested by conducting the experiments in varying seasons and doing pooled analysis.

Altogether 16 morphological and economic plant traits namely, days to maturity, height of the plant at maturity, number of branches,

number of flowers, number of capsules, volume of capsules, number of seeds per capsule, length of seeds, breadth of seeds, weight of 1000 seeds, volume of 1000 seeds, density of seeds, oil content, seed yield, total dry matter production and harvest index were studied.

Univariate and multivariate analyses were done in three seasons with sixty genotypes of diverse eco-geographic origin. The experiments were done in three seasons viz., September 1988, January 1989 and June 1989. Line x Tester analyses were done with 27 lines and 3 testers in two seasons viz., January 1989 and July 1989. Three genotypes viz., P1 P2 and P3 were involved in the generation mean and variance analysis. Six generations were obtained from direct and reciprocal crosses among the three parents.

6.1. MEAN PERFORMANCE

Fourteen genotypes viz. G7, G11, G12, G16, G26, G27, G30, G31, G32, G34, G39, G44, G50 and G58 showed mean seed yield more than six grams in any of the two out of the three seasons. These genotypes also showed consistently higher mean performance than the grand mean in all the three seasons for 11 out of 15 component characters. So, they can also be used as potential donor for the component traits.

The analysis of variance for individual seasons and pooled over seasons indicated significant differences among the 60 genotypes for all the 16 characters studied excepting for plant height in SI and

pooled analysis. This indicated the existence of sufficient variability among the genotypes studied for almost all the traits of interest.

6.2. GENETIC PARAMETERS

Genotypic variance and genotypic coefficient of variation were higher for number of flowers, number of capsules, total dry matter production and harvest index. Genotypic variance alone was higher for height of the plant at maturity and GCV alone was higher for seed yield. This explained their remarkable share to the total variability. These characters could be reasonably relied upon for successful isolation of desirable recombinants and segregants.

High heritability estimates were consistently observed for all the characters studied excepting for plant height which exhibited low to high values. The genetic advance as percentage over mean was high for seed yield, number of capsules, 1000 seed volume, harvest index, number of flowers, total dry matter production, seed density and capsule volume.

High heritability estimates coupled with high genetic advance as percentage over mean was observed for most of the traits namely, number of flowers, number of capsules, volume of capsules, volume of 1000 seeds, density of seeds, seed yield, total dry matter production and harvest index. High heritability coupled with medium genetic advance as percentage over mean was observed for number of branches, and 1000 seed weight. High heritability coupled with low genetic advance as

percentage over mean was observed for days to maturity, number of seeds per capsule, seed length, seed breadth and oil content. Low heritability coupled with low genetic advance as percentage over mean and high heritability coupled with high genetic advance as percentage over mean was observed for height of the plant at maturity.

High genotypic coefficient of variation, coupled with high heritability and high genetic advance as percentage over mean was observed for number of flowers, number of capsules, seed yield, total dry matter production and harvest index. This clearly explained the existence of additive genetic variability and the pre-dominance of additive gene action in the expression of these traits. This suggested that quick improvement can be expected in a short time for these characters in the breeding programme.

6.3. Correlation and causation

Seed yield exhibited significant positive association with height of the plant at maturity, number of branches, number of flowers, number of capsules, weight of 1000 seeds, density of seeds, total dry matter production and harvest index. Seed yield expressed consistently positive significant association with number of flowers, number of capsules, weight of 1000 seeds and harvest index in all the analyses. With remaining four traits it showed positive significant association mostly i.e. in three out of four analyses. These eight traits may be considered as the most important yield attributing traits dependable for selection for

the yield improvement of sesame. Days to maturity and length of seeds evinced positive significant association in only one season (SII) evidencing the vulnerability of this association to seasonal changes to a greater extent.

Seed size (weight of 1000 seeds) exhibited consistently positive and significant association with number of capsules and seed yield in all the analyses, whereas with height of the plant at maturity, number of branches, number of flowers, density of seeds, total dry matter production and harvest index it showed positive significant association (mostly) in three out of the four analyses. With seed length it had positive significant association in SI and pooled analysis. With days to maturity (SI), seed breadth (SI), volume of 1000 seeds (SII) and oil content (SIII) it had positive significant association in one season only. Thus, seed size had positive and significant association with all the traits which showed positive significant association with seed yield. The *inter se* correlation among the component traits were also positive significant or non-significant (neutral) excepting plant height and total dry matter production with harvest index in SI and SII respectively. This indicated that improvement in any of the eight traits which were positively and significantly associated with seed yield, will result in automatic improvement in seed size and *vice-versa*. Most of the characters which showed positive significant association with seed yield and seed size also exhibited a positive significant association with oil content. So, oil content, seed size and seed yield can be improved simultaneously. As days to maturity had mostly non-significant association with seed yield, there is also a possibility for incorporating earliness along with higher seed size, oil content and seed yield.

From the path coefficient analysis (seed yield as dependent variable) it was concluded that among the traits studied, total dry matter production and harvest index showed high positive and consistent direct effects towards seed yield (which were close to the genetic correlation coefficient with seed yield) and through these traits only the other major yield components exhibited their indirect positive effects towards seed yield. Among the eight traits which were positively and significantly associated with seed yield, total dry matter production and harvest index exhibited consistent positive and high direct effects. Among the other, traits which were positively and significantly associated with seed yield, number of flowers, weight of 1000 seeds and density of seeds exhibited mostly positive direct effects towards seed yield. Number of capsules mostly showed high negative direct effects towards seed yield. The only character which showed negative significant correlation with seed yield, namely, number of seeds per capsule also showed mostly negative direct effect towards seed yield. Among the other traits which did not exhibit significant association with seed yield, seed breadth showed mostly positive direct effect and oil content had mostly negative direct effect towards seed yield. Even though the direct effects of the traits, other than total dry matter production and harvest index, were less positive and high negative, the overall effect towards seed yield was positive due to their high positive indirect effects evidenced mostly through total dry matter production and harvest index. So, the traits viz., total dry matter production and harvest index must be given primary importance in sesame yield improvement programme through crop breeding.

From the path coefficient analysis (weight of 1000 seeds as dependent variable), it was concluded that the traits viz., days to maturity and oil content showed consistently positive direct effects. Among the traits which were positively and significantly associated with 1000 seed weight, the traits viz., height of the plant at maturity, number of capsules and total dry matter production exhibited positive direct effects mostly. But the other traits viz., density of seeds and seed yield evinced negative direct effects mostly. Volume of 1000 seeds which was positively and significantly associated with weight of 1000 seeds in only one season (SII) also expressed positive direct effects mostly. Number of seeds per capsule which showed non-significant association with 1000 seed weight evidenced positive direct effects mostly. Even though the traits which were positively and significantly associated with 1000 seed weight showed positive and/or negative direct effects towards 1000 seed weight the overall effect was positive due to the high positive indirect effects made mainly through capsule number, oil content and total dry matter production and to a considerable extent through harvest index too. Among these three traits primary importance may be given to capsule number, total dry matter production and harvest index as they witnessed positive significant association with weight of 1000 seeds.

From the correlation and causation studies *in toto*, it was found that eight traits viz., height of the plant at maturity, number of branches, flowers, capsules, weight of 1000 seeds, density of seeds,

total dry matter production and harvest index which showed positive significant association with seed yield also showed positive significant association among themselves. This indicated that an exclusive improvement programme either for seed size (weight of 1000 seeds) or seed yield will improve both the traits. Or in a more perspective manner, it can be also stated that selection for any of the eight traits which were positively and significantly associated with seed yield will improve both seed size and seed yield. It was suggested to give primary importance to number of capsules and total dry matter production and harvest index for enhancement in seed yield. As capsule number showed negative direct effect towards seed yield, it is earnestly advised to rely strongly upon total dry matter production and harvest index to hopefully improve both seed size and seed yield, as these two traits expressed their excellency by having high positive direct effects (equal to genetic correlation coefficient) towards seed yield consistently and towards seed size mostly. Moreover, through these traits only, all other characters showed their maximum positive indirect effects. As a direct selection for harvest index is difficult, a concurrent selection for seed yield, total dry matter production and harvest index will be of immense use. It is also evidenced to not to go in for a direct selection for seed density as they might have a negative impact on seed size, due to their negative direct effects (mostly) towards seed size.

The causal factors determining the genetic correlations do depend on season and that genotype x season interactions affect the

expression as well as the contribution of the causal factors towards dependent variable, which in turn reflects on the direction and magnitude of genetic correlations. The differential contribution of different component traits in different seasons towards the same dependent variables were well evidenced from the differences in the magnitude and direction of genetic correlations among themselves as well as with dependent variables.

6.4. STABILITY ANALYSIS

From the assessment of genotype x season interaction and stability analysis the following conclusions were made.

Significant differences existed among the genotypes for all the characters studied excepting height of the plant at maturity in SI and pooled analysis.

The seasons chosen for the study varied significantly in respect of all the characters studied. Third season (SIII) appears to be the best season as it exhibited higher mean performance for as many as six traits including number of flowers, weight of 1000 seeds, seed yield and harvest index.

Genotype x season interaction was significant for all the characters excepting for plant height at maturity indicating that different genotypes responded differently to changes in the season.

Genotype x season interaction component of variance was predominant than that of genotypic component for days to maturity, number of branches, flowers, capsules, capsule volume, number of seeds per capsule, seed breadth, 1000 seed weight, oil content, seed yield, total dry matter production and harvest index indicating that these traits were highly influenced by seasonal changes. For plant height and 1000 seed volume, the share of the genotypic component was more than that of genotype x season interaction component. This indicated that these two traits were least sensitive to seasonal changes comparatively. The share of the genotypic component was equal for seed length and seed density to that of the genotype x season interaction component indicating the importance of both genotype as well as genotype x season interaction in the expression of these traits.

A major portion of the variance attributed to genotype x season interaction was accounted for by the linear component (variance due to regression) for all the characters excepting capsule volume and total dry matter production. Preponderance of linear portion over non-linear portion was suggestive of possibilities of prediction of the performance of the genotypes across the seasons. Days to maturity, plant height, number of seeds per capsule, weight of 1000 seeds, volume of 1000 seeds and seed yield were the most predictable. For number of branches, flowers, capsules, seed length, breadth, seed density, oil content and harvest index the prediction with precision was comparatively less possible. The prediction with precision was hardly possible

capsule volume (linear and non-linear component was more or less equal) and total dry matter production (linear component was less than non-linear component).

The genotypes included in the present study did not exhibit uniform stability and responsiveness pattern for all the characters and all the genotypes showed differential stability and differential responsiveness for different characters. The stability/responsiveness levels of particular genotype appeared to be specific for individual characters and not common for all the characters. Similarly, the stability/responsiveness levels to different characters appeared to be specific for individual genotypes and not common for all the sixty genotypes of the present study.

The frequency of genotypes not interacting with seasons was maximum for number of flowers followed by number of branches, seed breadth and plant height showing that a large majority of genotypes had stability for this character. None of the genotypes showed unpredictable interaction with season for number of flowers. The frequency of genotypes not interacting with seasons was minimum for seed yield. But for seed yield, capsule volume, oil content and harvest index, a maximum number of genotypes exhibited unpredictable interaction with season indicating that a vast majority of the genotypes were unstable for these four characters. Similar trend was also observed for number of seeds per capsule, weight of 1000 seeds, volume of 1000 seeds and total dry matter production.

Stability ($\bar{S}_d^2$) and responsiveness (b) of seed yield were not associated with those of the traits which were positively and significantly associated with it. On the other hand, the responsiveness of the days to maturity and capsule volume was significantly and negatively associated with that of seed yield. Thus, it was found that mean productivity, production response and production stability were relatively independent of each other. Interestingly, the stability of weight of 1000 seeds was positively and significantly associated with the stability of number of capsules and volume of 1000 seeds and negatively and significantly associated with the stability of number of branches. Number of branches and capsules had positive significant association with 1000 seed weight. Eventhough, selection for stability of capsule number will simultaneously enhance the mean 1000 seed weight and stability and vice-versa, its negative direct effect on seed yield may hinder the seed yield improvement and hence is not advisable. But the selection for stability of number of branches will destabilize weight of 1000 seeds, even though it may increase the mean 1000 seed weight. It may be concluded that stability for seed size or seed yield might be achieved either through stability and/or plasticity of their component characters. The observed correlations among the responsiveness of seed yield, capsule volume and days to maturity and the correlation among the stability of seed size, number of branches capsule number and volume of 1000 seeds pointed to the fact that variability in the responsiveness and stability of these component characters of seed size and seed yield could well be successfully utilized in imparting homeostasis for seed size and seed yield.

Genotypes viz., G3, G12, G27 and G30 showed high mean, average responsiveness and high stability for seed yield. Genotypes viz., G6, G9, G12, G20, G27, G32 and G38 showed high mean, average responsiveness and high stability for 1000 seed weight. These genotypes also showed high mean, average responsiveness and high stability for most of the traits which were positively and significantly associated with seed size and seed yield. Genotypes viz., G12 and G27 showed high mean, average responsiveness and high stability both for 1000 seed weight and seed yield. Genotypes viz., G11, G12, G24, G27, G30, G52, G58 and G59 for total dry matter production, and G5, G11, G12, G22, G35 and G44 for harvest index exhibited high mean, average responsiveness and high stability. These genotypes can very well be used as the source material for the exploitation with assured possibility of developing high yielding stable varieties of sesame.

Thus the present study indicated the necessity for testing the genotypes in varied seasons.

6.5. GENETIC DIVERSITY

D^2 analysis of the sixty genotypes based on sixteen characters confirmed the presence of high diversity among the types by their resolution into twelve clusters in SI, six clusters in SII and pooled analysis and eight clusters in SIII. Genotypes of different eco-geographic origins were grouped in a single cluster as well as in different clusters. Thus, the pattern of clusters demonstrated that the genetic diversity was

not fully related to geographical diversity.

Selection of parents has been suggested in three ways i.e. on the basis of (a) genetic divergence exhibited under the best season, (b) consistent values of divergence over all the seasons and (c) divergence exhibited in the pooled analysis.

Using the first criterion, the following cross combinations involving high yielding stable and high yielding responsive genotypes are found suitable for future breeding programmes.

EC. 137935 (G45) x S.00028 (G3)
 x Si 1150 (G12)
 x PDK.8 (G27)
 x S.0516 (G30)

Using first and second criteria, the following genotypes are useful for future breeding programme.

EC.137935 (G45) x Si.1088 (G10)
 x IS.212 (G23)
 x N.36950 (G26)
 x A.T.9 (G41)
 x CO 1 (G44)
 x H.T.6 (G46)

The divergence of above crosses was also confirmed by the third criterion, i.e., on the basis of pooled analysis and hence and above six crosses can also be utilized in breeding programme. However, when we consider high seed yield coupled with high mean performance of the traits which were positively associated with seed yield and seed size, priority is to be given to the two crosses:

EC.137935 (G45) x N.36950 (G26)
x Co.1 (G44)

These three genotypes showed high mean seed yield. Further, G26, exhibited **high per se** performance for number of branches and flowers, and G44 expressed high **per se** performance for number of flowers, capsules, seed density and harvest index. These cross combinations are identified based on genetic divergence and high mean coupled with high stability and average responsiveness, and so, heterosis for both seed yield and responsiveness can be expected.

For obtaining the high yielding hybrids, showing heterotic effects due to sets of genes responsible for the seed yield and not for response, crossing among the divergent varieties within the cluster is advisable. The twelve genotypes *viz.*, G21, G27, G29, G32, G37, G39, G40, G47, G52, G55 and G58, which were grouped consistently in all the analyses in cluster I were found to be good. Among them G27, G32, G35, G39 and G40 showed high mean seed yield and high mean performance for most of the characters that were positively and signifi-

cantly associated with seed yield and seed size. By crossing among these iso-responsive genotypes high yielding genotypes with a response similar to parents are likely to be obtained.

Volume of 1000 seeds followed by oil content contributed maximum towards genetic diversity. In general, the traits which showed high genotypic variance and genotypic coefficient of variation showed less contribution towards genetic diversity. The only character which showed high genotypic coefficient of variation and contributed maximum towards genetic diversity was volume of 1000 seed thereby indicating that the genotypes showing high variability for volume of 1000 seeds might be genetically divergent. Thus, the possibility of using traits with high genetic polymorphism as a morphological marker for genetic diversity was identified.

6.6. LINE x TESTER ANALYSIS

Hybrids, lines, and line x tester interactions were significant for eleven out of sixteen characters studied in S_1 and S_2 . Capsule volume, seed length, seed breadth, 1000 seed weight and seed density exhibited non-significant variances. Additionally, the variance due to line x tester interaction was non-significant for number of branches in S_2 . The variance due to testers was also significant for eleven out of sixteen traits studied. Capsule volume, seed length, seed breadth and seed density displayed non-significant variances both in S_1 and S_2 . Apart from these traits, 1000 seed volume in S_1 and oil content S_2 showed non-significant variation.

The pooled analysis of variance over seasons revealed the presence of significant variation among hybrids, lines, line x tester interaction, line x season interaction and (line x tester) x season interaction for eleven out of sixteen characters studied. Capsule volume, seed length, seed breadth, 1000 seed weight and seed density exhibited non-significant variances. The variance due to testers, season and tester x season interaction was significant for twelve out of sixteen characters studied. Capsule volume, seed length, seed breadth, and seed density displayed non-significant variances. This indicated that lines, testers and hybrids were influenced by the seasons. The non-significant variances may at least partially be due to the narrow genetic bases. The significant interaction with the seasons brought out the need for multi-seasonal testing for obtaining reliable and precise estimates for various characters.

The *sca* variance was higher than the *gca* variance for all the characters in individual analyses. This indicated the predominance of non-additive gene action for all the traits studied. The high *gca:sca* ratio also confirmed the importance of non-additive gene influence on the expression of the characters. In the pooled analysis all the traits excepting seed density showed negative variances and so were not comparable. For seed density, the variance due to *gca* was higher than *sca* indicating the importance of both additive and non-additive gene action in the expression of seed density.

The component of variance due to specific combining ability for seed yield, seed size and most of the characters which were positively and significantly associated with them were relatively larger than that

due to general combining ability. Thus, non-additive type of gene action appeared to be important in lines or testers which might have selected directly for seed yield and/or indirectly for seed size and the components of seed size and seed yield. When the lines or testers were relatively unselected, (for example, selection for seed density), the opposite was true (Sprague and Tatum, 1942, Rojas and Sprague, 1952 and El-Itriby et al., 1981).

The sca x season interaction variances were higher than gca x season interaction variances for all the traits analysed. This indicated that the hybrids had interacted more than parents with the seasons, i.e., non-additive variation interacted more with the season than that of additive component, necessitating for multiseasonal evaluation of hybrids for obtaining reliable estimates of genetic variance. This also indicated the possibility of identifying best hybrids for a particular season.

The proportional contribution of lines x testers interaction to the total variance was higher than that of lines and testers for almost all the characters studied. This clearly explained the importance of hybrid vigour or non-additive gene action.

The general combining ability of the parents in general was not consistent over seasons in the present study. The parents exhibiting highest gca effects in any of the two out of three analyses for the traits which showed positive significant association with seed size and

seed yield will be of immense use in pedigree breeding programme. The parents viz., L_3 and T_3 for plant height; L_{23} and T_2 for number of branches; L_{16} , L_{17} , L_{23} and T_3 for number of flowers; L_{16} , L_{23} , L_{25} and T_3 for number of capsules; L_{19} , T_3 and T_1 for weight of 1000 seeds; L_2 , L_3 , L_{19} and T_1 for seed density; L_{10} , L_{12} , L_{23} and T_3 for seed yield, L_7 , L_{12} and T_2 for total dry matter production and L_{14} , L_{23} , L_{27} and T_3 for harvest index, were identified as best general combiners.

Among the 81 hybrids evaluated, the hybrids $L_3 \times T_3$ and $L_6 \times T_3$ for plant height; $L_{11} \times T_2$, $L_{16} \times T_2$ and $L_{25} \times T_2$ for number of branches; $L_2 \times T_2$, $L_{23} \times T_2$, $L_{21} \times T_3$ and $L_{23} \times T_3$ for number of flowers; $L_{23} \times T_3$, number of capsules, $L_8 \times T_1$, $L_{22} \times T_1$ and $L_{25} \times T_3$ for weight of 1000 seeds, $L_2 \times T_1$ and $L_3 \times T_3$ for seed density, $L_{12} \times T_1$, $L_{16} \times T_1$, $L_{13} \times T_2$, $L_6 \times T_3$ and $L_{21} \times T_3$ for seed yield and $L_2 \times T_2$ and $L_{12} \times T_2$ for total dry matter production recorded high *per se* performance, specific combining ability effects and heterotic expression. These traits were also positively and significantly associated with seed yield. It is quite interesting to conceive that among the eight crosses suggested to improve seed size and seed yield, the parents involved were good general combiners and the cross $L_{22} \times T_1$ was a good specific combiner for days to maturity. So, it is possible to achieve high seed size, higher seed yield coupled with early maturity.

There was good agreement among *per se* performance, sca effects, heterosis and heterobeltiosis in all the cross combinations mentioned above indicating the

reliability of these parameter for exploitation of hybrid vigour in sesame

In general, it was found that the superior combinations involved atleast one high general combining parent. However, for number of flower, capsules, seed density and total dry matter production, the superior combinations had both the parents with high general combining ability.

Heterosis, heterobeltiosis and standard heterosis were worked for all the characters. A maximum of 764.00 per cent relative heterosis for seed yield was recorded by $L_{21} \times T_3$ (S_1). This cross combination also showed a maximum heterobeltiosis of 532.97 per cent and standard heterosis of 303.74 per cent in S_1 . But, the standard heterosis was maximum with $L_{23} \times T_3$ (341.35 per cent). Thus, the superiority of T_3 (TMV 6) in production of best hybrids was identified. In the pooled analysis also this hybrids combination showed its excellence (standard heterosis was 241.07 per cent). For weight of 1000 seeds, maximum relative heterosis was observed with $L_8 \times T_1$ (129.29 per cent in S_1). However, the heterobeltiosis and standard heterosis was maximum with $L_{22} \times T_1$ in S_1 (125.97 and 128.09 per cents respectively). Thus, the superiority of T_1 (TMV 3) for weight of 1000 seeds was brought out.

For seed yield, relative heterosis has maximum in the crosses viz., large x small (seed size based on 1000 seed weight) medium x large, small x large, small x medium, large x large, and small x small. Heterobeltiosis was maximum in all the crosses except in large x medium

and medium x small. Whereas standard heterosis was maximum in large x small, medium x large, medium x medium and small x small. For 1000 seed weight, maximum relative heterosis was recorded in all the crosses except large x medium and medium x small. Heterobeltiosis was maximum in the crosses viz., small x large, small x medium, large x large medium x medium and small x small. Standard heterosis was maximum in only four cross combinations viz., large x small, small x large, large x large and small x small. So, to get maximum standard heterosis for seed yield and seed size simultaneously, large x small and small x small cross combinations might be preferred.

For the other traits which were positively and significantly associated with seed size and seed yield, relative heterosis was ranging from 71.18 per cent (number of flowers in S_1) to 290.12 per cent (harvest index in S_1) and heterobeltiosis ranging from 58.78 per cent (seed density in S_1) to 301.03 per cent (number of capsules in S_1).

It is quite interesting to note that the cross combination which showed high standard heterosis for seed yield also expressed maximum relative heterosis and heterobeltiosis for number of flowers and harvest index and maximum standard heterosis for number of flowers and capsules. This clearly explained the possibility of getting maximum heterosis for seed yield by way of adjusting and manipulating the traits which were positively and significantly associated with seed yield.

A critical perusal of the occurrence of heterobeltiosis for seed yield brought and following points of interest (Table 201).

In S_1 , $L_{21} \times T_3$ expressed maximum heterobeltiosis for seed yield. This cross combination showed significant positive heterobeltiosis for plant height, number of flowers, capsule, 1000 seed weight and total dry matter production, with a significant negative heterobeltiosis for number of branches, seed density and harvest index. So, the increased seed yield was obtained with a simultaneous increase in total dry matter production. But, the harvest index was significantly reduced, indicating that heterobeltiosis for seed yield was realized by a reduction in the partitioning efficiency.

On the contrary, $L_9 \times T_1$ (S_1) expressed maximum heterobeltiosis for seed yield with a concurrent positive significant heterobeltiosis for total dry matter production and harvest index. Number of branches was the only trait which showed negative significant heterobeltiosis. The other traits which were positively and significantly associated with seed yield remained constant (non-significant positive or negative heterobeltiosis).

A similar, but, with a small change was observed behind the maximum heterobeltiosis for seed yield, obtained with $L_6 \times T_3$ (S_1). This cross combination exhibited significant positive heterobeltiosis

Table 201. Behaviour of the cross combinations which showed maximum positive significant heterobeltiosis for seed yield

Character	S ₁			S ₂			P		
	L ₂₁ ×T ₃	L ₉ ×T ₁	L ₆ × T ₃	L ₁₂ ×T ₂	L ₁₂ ×T ₁	L ₁₆ ×T ₁	L ₂₃ ×T ₂	L ₂₆ ×T ₂	L ₂₆ ×T ₁
Plant height	27.80**	0.37 ^{NS}	56.16**	18.59**	8.37	10.72	3.23	-26.08**	-24.80**
Number of branches	-15.91**	-12.28*	9.09	-20.11*	-42.53**	6.42	-42.84**	76.46**	-7.67
Number of flowers	49.54*	10.00	44.12**	9.05	-27.43**	36.51**	7.22	52.52	30.36**
Number of capsules	55.84**	-15.08	43.15**	34.40**	-37.32**	47.76**	18.25**	-26.99**	-10.26
Weight of 1000 seeds	14.60**	-7.24	5.45	27.10**	-3.25	-17.62**	27.72**	26.36**	-18.34**
Seed density	-10.85**	-3.76	71.28**	-18.79**	2.55	14.01*	-23.58**	40.51**	33.83**
Total dry matter production	73.33**	40.20**	89.45**	82.72**	8.41	16.43	39.16**	28.06*	21.22
Harvest index	-63.52**	276.18**	93.11**	12.25	113.32**	92.79**	40.65**	46.03**	-5.91

* : Significant at P:5%

** : Significant at P:1%

for all the traits which were positively and significantly associated with seed yield excepting number of branches and weight of 1000 seeds which remained unaltered.

In S_2 , $L_{12} \times T_2$ expressed maximum heterobeltiosis for seed yield. This hybrid showed significant positive heterobeltiosis for plant height at maturity, number of flowers, weight of 1000 seeds and total dry matter production and negative significant heterobeltiosis for number of branches and seed density. Number of flowers and harvest index remained unaltered. This explained the possibility that increased seed yield could be achieved with a simultaneous increase in total dry matter production, by keeping the harvest index constant (unaltered).

$L_{12} \times T_1 (S_2)$ which showed maximum heterobeltiosis for seed yield also expressed significant positive heterobeltiosis for harvest index and significant negative heterobeltiosis for number of branches, flowers and capsules. The other traits, viz., plant height, 1000 seed weight, seed density and total dry matter production remained unaltered. This brought out the other possibility of increasing the seed yield. that is increased seed yield and harvest index could be achieved by keeping total dry matter production constant (unaltered), by enhancing the partitioning efficiency.

A more or less similar trend was observed with $L_{16} \times T_1 (S_2)$. Here also maximum heterobeltiosis for seed yield was obtained with a significant positive heterobeltiosis for harvest index and non-

significant heterobeltiosis for total dry matter production. This cross combination also showed significant positive heterobelitosis for number of flowers, capsules and seed density and negative significant heterobeltiosis for 1000 seed weight. Plant height and number of branches remained unaltered along with total dry matter production (non-significant heterobeltiosis).

In the pooled analysis, maximum heterobeltiosis observed with $L_{23} \times T_2$, $L_{26} \times T_2$ and $L_{26} \times T_1$.

The hybrids viz., $L_{23} \times T_2$ and $L_{26} \times T_2$ showed significant positive heterobeltiosis fo total dry matter production and harvest index, confirming the fact, that increased seed yield could be achieved with a concurrent increase in total dry matter production and harvest index.

Interestingly, total dry matter production and harvest index remained unaltered (constant) in $L_{26} \times T_1$ which expressed maximum heterobeltiosis for seed yield. This may be due to a complex compro made among the inversely proportional characters viz., total dry matter production and harvest index.

From the foregoing analysis, there exists the following five options to increase the seed yield in sesame.

- A. Increasing the seed yield and total dry matter production but reducing the harvest index.
- B. Simultaneous increases in seed yield, total dry matter production and harvest index.

- C. Enhancing both seed yield and total dry matter production with an unchanged harvest index
- D. Increasing seed yield and harvest index leaving total dry matter production unaffected.
- E. Increasing the seed yield leaving total dry matter production and harvest index relatively unaffected (involving small changes).

Among these five options, the first four options (viz., A, B, C and D) may be given primary importance as they are proven techniques in cereal breeding (Donald and Hamblin, 1976; Bhatia and Mitra, 1988).

Increasing the harvest index by B and D approaches demands the least increment in photosynthates and nutrient inputs over the baseline, whereas other alternatives necessitate a steep rise in demand for photosynthates and nutrients. The fertilizer requirements are also higher for the other options (A and C). This clearly shows the need for the additional inputs of fertilizer to increase the productivity of sesame. This follows the suggestion offered by Bhatia and Mitra (1988) for cereal breeding. The large difference in the energy content of the residue and seed in oilseed crops further increases the requirement for additional photosynthates associated with improved harvest index (Sinha *et al.*, 1982; Bhatia and Mitra, 1988). This is perhaps one of the main reasons why substantial progress in increasing the harvest index could not yet be made in oilseed crops (Bhatia and Mitra, 1988) and specifically in sesame too.

A critical analysis of the crosses which showed maximum heterobeltiosis for weight of 1000 seeds also expressed significant positive heterobeltiosis for seed yield and for most of the traits which were positively and significantly associated with weight of 1000 seeds as well as seed yield. Noteworthy is the positive significant heterobeltiosis observed for total dry matter production and/or harvest index among the crosses which displayed maximum heterobeltiosis for seed size. So, selection and manipulation for total dry matter production and harvest index will have a concurrent increase in seed yield and seed size and vice-versa.

6.7. GENETIC DIVERSITY AND COMBINING ABILITY

The best general combiners recorded for the nine traits of importance were almost observed to fall in a single cluster (Cluster-I). This indicated that the highly diverged genotypes which fall in different clusters need not be good general combiners. In fact, genotypes of different eco-geographic origin resulted in better general combining ability. Genotypes of Tamil Nadu origin showed high general combining ability effects for all the nine traits of importance. Genotypes from Andhra Pradesh showed high general combining ability effects for 1000 seed weight and seed density. Genotype (G 49) from Gujarat expressed high general combining ability effects for plant height, number of branches, flowers, capsules, seed yield, total dry matter production and harvest index. Genotype (G37) from Israel exhibited high general combining ability effects for number of flowers and capsules.

The genotypes grouped in cluster I showed high sca effects mostly. Cross combinations involving genotypes of Tamil Nadu origin exhibited high sca effects for almost all the nine traits of interest. Genotype, G 49, originating from Gujarat in combination with genotype, G 59 of Tamil Nadu expressed high sca effect for number of flowers, capsules and total dry matter production. Genotype, G 37, evolving from Israel in combination with genotype, G 40 of Tamil Nadu showed high sca effect for number of branches. This again confirmed the fact that eco-geographical diversity of the genotypes would result in better general and specific combining abilities and genetically highly divergent genotypes need not be good combiners. The findings also brought out the general superiority of the genotypes hailing from Tamil Nadu in showing their higher pre-potency and imprinting.

6.8. GENETIC DIVERSITY AND HETEROSIS

Both intra-and inter-cluster mating expressed high heterotic vigour. Crosses involving genotypes grouped in different clusters exhibited highest relative heterosis for number of flowers, total dry matter production and harvest index. For all the other traits of importance, crosses involving genotypes of a single cluster showed maximum heterosis. Heterobeltiosis was highest in crosses involving genotypes grouped in different clusters for seed density, total dry matter production and harvest index. For all the other traits of importance, genotypes grouped in a single cluster (Cluster-I) showed highest heterobeltiosis. Cross combination (s) which exhibited highest heterosis had genotypes originating from

Tamil Nadu as male or female parents. For plant height, number of branches, flowers, capsules and seed density both the parents were of Tamil Nadu origin. For the other characters genotypes of Tamil Nadu served either as male or female parent. Genotypes originating from Rajasthan in cross combination with that of Tamil Nadu origin showed maximum relative heterosis and heterobeltiosis for plant height and total dry matter production. Genotypes evolved from Gujarat in cross combination with genotypes of Tamil Nadu origin expressed maximum relative heterosis and heterobeltiosis for 1000 seed weight, seed yield and harvest index. The cross between genotypes from Israel and Tamil Nadu showed maximum relative heterosis for plant height. On the over all basis, it is concluded that intra-cluster mating among genotypes of different eco-geographic diversity and more over among the genotypes of Tamil Nadu would result in high heterotic vigour.

6.9. GENETIC DIVERSITY, COMBINING ABILITY AND HETEROBELTIOSIS

The cross combinations which showed a good agreement between **sca** effects, **per se** performance and heterobeltiosis were mostly of intra-cluster origin. Thus, it obviously proved that the observed heterobeltiosis might be due to high specific combining ability **per se** of the cross combinations and geographic diversity rather than the genetic divergence. The observed positive and significant association between **sca** effects and **per se** performance of the hybrids also confirmed this fact. However, few crosses involving genotypes of different clusters also showed high **sca** effects and heterosis. Thus, the present study

indicated that genotypes of different eco-geographic origin but grouped in a single cluster would result in better combining ability and heterobeltiosis.

6.10. OPTIMIZATION OF GENETIC DIVERGENCE FOR THE OCCURRENCE OF HETEROSIS

The present study have also brought out the definite superiority of divergence class 3 (DC 3) and 2 (DC 2) over DC 1 as far as occurrence of a high proportion of heterotic crosses or of high value of heterosis was concerned. Cross combinations in DC 3 expressed maximum relative heterosis for plant height, number of branches, number of flowers, number of capsules, and seed density. Cross combinations in DC 2 expressed maximum relative heterosis for thousand seed weight seed yield, total dry matter production and harvest index. The primary importance may be given to DC 2 as they exhibited maximum relative heterosis for the four important traits. Thus, the study provides sufficient ground for conceiving those limits and for the hypothesis in general that-if 'm' and 's' are the mean and standard deviation of the values of divergence (given by D^2) among parents, the chances for the occurrence of a high frequency of heterotic crosses and with high values of heterosis are more when the parents are chosen to have their divergence in the interval (m-s, m+s) compared to the crosses between parents whose divergence falls outside that interval.

6.11. GENERATION MEAN AND VARIANCE ANALYSIS

The mean performance of the parents has brought out the superiority of the parent P_2 for seed yield and most of the characters which were positively associated with seed yield and seed size viz., number of branches, flowers, capsules and total dry matter production. The parent P_1 showed highest performance for capsule volume, number of seeds per capsules, seed length, seed breadth, 1000 seed weight, seed density, oil content and harvest index. P_3 expressed early maturity, highest mean plant height and 1000 seed volume. This indicated that all the three genotypes can be utilized for the hybridization programme for seed yield and seed size.

The cross combination, $P_2 \times P_3$ recorded the maximum heterobeltiosis for seed yield (37.63 per cent), $P_3 \times P_2$ for plant height, 1000 seed weight, seed density, and oil content, $P_1 \times P_2$ for number of branches, $P_2 \times P_1$ for number of flowers, $P_3 \times P_1$ for number of flowers and $P_1 \times P_2$ for harvest index. Negative heterobeltiosis were recorded for seed length and breadth and total dry matter production. For number of seeds per capsule there was practically no heterobeltiosis.

In general F_2 's performed better than their respective F_1 's. Inbreeding depression was rarely observed, that too to a lesser extent.

The B_1 's of $P_1 \times P_2$ showed the maximum of 369.90 per cent seed yield over their F_1 's. The B_1 's of $P_2 \times P_1$ scored maximum 1000 seed weight (40.53 per cent) over F_1 's.

The B_1 's of $P_1 \times P_2$ expressed a maximum of 153.40 per cent seed yield over their F_2 's. They also showed higher mean performance than their F_2 's for days to maturity, plant height, number of branches, flowers, capsules, seeds per capsule, weight of 1000 seeds, total dry matter production and harvest index.

The B_2 's of $P_1 \times P_3$ expressed the highest seed yield than their F_1 's (165.54 per cent). They also showed higher performance for 1000 seed weight and total dry matter production than their F_1 's.

The B_2 's of $P_1 \times P_2$ had 28.27 per cent higher seed yield than their F_2 's. They also exhibited higher than performance than their F_2 's for days to maturity, plant height, number of branches, flowers, capsules, capsule volume, weight of 1000 seeds, seed density and total dry matter production.

On considering the B_1 mean and B_2 mean together in relation to their respective F_1 and F_2 mean, the back cross progenies of $P_1 \times P_2$ recorded maximum seed yield when either of them were used as recurrent parent. These two genotypes also maintained their superiority in recording higher B_1 and B_2 mean values over the F_1 and F_2 means for the maximum number of characters studied. The hybrids showing high heterobeltiosis were included any of these parents either as ovule or pollen parent or both of them. Among these two parents P_1 ($G_3=L_3$) and P_2 ($G_{28}=L_{11}$), P_1 seemed to be a potential donors as it showed

high mean and stability for seed yield and many of the traits which were positively and significantly associated with seed yield and seed size.

Comparisons of the means of F_2 populations of direct and reciprocal crosses, as well as the direct and reciprocal back cross progenies revealed the presence of cytoplasmic influence on the inheritance of the sixteen quantitative characters studied. On the other hand, the comparison of the B_1 's and B_2 's of direct crosses as well as reciprocal crosses indicated the maternal genetic control over the expression of the traits of interest. In toto, this indicated the nuclear x cytoplasmic interactions in the expression of quantitative traits. The cytoplasm of the parent P_1 different from the cytoplasm of the parent P_2 for 14 characters and from the cytoplasm of P_3 for 12 characters. Similarly, the cytoplasm of P_2 differed from P_3 for 12 characters. This clearly indicated the possibility for the existence of three different cytoplasm, in the three parents viz., P_1 , P_2 and P_3 of the study.

The simple additive-dominance model was adequate in one cross ($P_2 \times P_3$) for number of branches, two crosses ($P_2 \times P_3$ and $P_3 \times P_2$) for volume of 1000 seeds, one cross ($P_2 \times P_3$) for seed density and three crosses ($P_2 \times P_3$, $P_2 \times P_1$ and $P_3 \times P_1$) for harvest index. For the remaining cross combinations, it was inadequate. In general, all the characters showed the presence of epistatic interactions.

A few cross combinations that emerged as unique with significant additive x additive interaction effects alone were, $P_3 \times P_1$ for number of capsules and seed yield and $P_2 \times P_3$ for seed yield alone. Additive and additive x additive interaction effects were significant in $P_2 \times P_3$ for number of capsules, $P_2 \times P_1$ for number of capsules, oil content and total dry matter production, $P_1 \times P_3$ for seed breadth and $P_1 \times P_2$ for oil content. Considering the magnitude of additive gene effects, recombination breeding with selection of recombinant inbreds will be effective for the improvement of the traits concerned, involving the specific cross combinations.

The traits which were positively and significantly associated with seed size and seed yield were governed predominantly by dominance followed by dominance x dominance interaction effect in addition to one or more of the different types of epistasis. A similar type of gene action was also observed for oil content and days to maturity. H component of variance was greater than the D component in almost all the crosses for all the characters. This indicated the preponderance of dominance genetic variation. However, one cross for height of the plant, volume of capsules, and breadth of seeds, two crosses for number of flowers and capsules and volume of 1000 seeds and four crosses for length of seeds showed higher values of D component than H. This indicated that additive or dominance variation for a particular character is cross specific.

The dominance ratio was more than unity (where it was estimable) for seed yield, total dry matter production, harvest index and for all

the other traits which were positively and significantly associated with seed yield and seed size with a very rare exception, indicating the presence of over dominance for all the traits of interest.

Almost in all the crosses and in all the traits over dominance was associated with duplicate dominant epistasis.

Comparisons of the means of F_2 populations of direct and reciprocal crosses, as well as the direct and reciprocal back cross progenies revealed the presence of cytoplasmic influence on the inheritance of 16 quantitative characters studied. On the other hand, the comparison of the B_1 's and B_2 's of direct crosses as well as reciprocal crosses indicated the maternal genetic control over the expression of the 16 quantitative traits. In toto, this indicated the nuclear x cytoplasmic interactions in the expression of the 16 quantitative traits. The cytoplasm of the parent P_1 differed from the cytoplasm of the parent P_2 for 14 traits and from the cytoplasm of P_3 for 12 traits. Similarly, the cytoplasm of P_2 differed from P_3 for 12 traits. This clearly indicated that the three parents viz., P_1 , P_2 and P_3 has three different cytoplasm. This was well evidenced from the observed differences in the gene effects among direct and reciprocal crosses.

For fifteen out of sixteen traits there were obvious differences in the gene effects among the direct and reciprocal crosses. In one trait, volume of 1000 seeds all the gene effects were non-significant

in direct as well as reciprocal crosses. However, this difference in the gene effects among direct and reciprocal crosses was not able to change the type of epistasis excepting the shift from duplicate dominant epistasis to complementary recessive epistasis in $P_1 \times P_2$ and $P_2 \times P_1$ for seed yield, $P_1 \times P_3$ and $P_3 \times P_1$ for capsule number and $P_2 \times P_3$ and $P_3 \times P_2$ for capsule volume.

The different magnitudes of positive and negative heterosis for the different characters in the F_1 over the parental means indicated the overall dominance of positively acting genes. On line with Francis Minvielle (1987) statement, the observed positive heterosis might be due to the random assortment of poorer and better alleles among the parents of a specific cross, and negative heterosis due to the more frequency of better alleles in only one parent of a particular cross. In addition to the one locus-dominance hypothesis and the multilocus epistasis hypothesis (Prichner, 1983), Francis Minvielle (1987) proposed a two-locus additive gene model, the non-additive interaction between additive genes. In the present study as inferred from generation mean and variance analysis, heterobeltiosis may be attributed to the duplicate dominant epistasis. Whatever might be the hypothesis, heterosis is the result of complementation (Gallais, 1988a).

Problems in the estimation of genetic parameters are often associated with the presence of large proportion of non-fixable epistatic variation. Other assumptions for the genetic analysis are that the parental

lines are highly inbred, that there are no reciprocal effects and that the genes effecting the traits measured are not linked. In the present study, all parents were highly inbred. But the parents were not tested for linkage. Effect of cytoplasm on the expression of quantitative traits was also observed. Genetic estimates were generally consistent with earlier studies. Within plant and between plant variation (Mosjidis and Yermanos, 1985) imposes a common limitation to genetic studies and to reciprocal back crosses. The indeterminant flowering pattern of sesame results in a period of several weeks between the set of first and last capsules which in turn are affected by environmental and internal factors. The contradictory results from reciprocal crosses might be due to minor differences in vegetative growth periods of the parental lines, as pointed out by Dani and Kohel, (1989).

6.12. BREEDING STRATEGIES

6.12.1. Selection of the characters

Out of the sixteen morphological traits the following traits viz., height of the plant at maturity, number of branches, flowers and capsules, weight of 1000 seeds, seed density, total dry matter production and harvest index were positively and significantly associated with seed yield as well as 1000 seed weight over seasons. The inter se correlation among these traits were also positive and significant over seasons. Even though a negative significant association of plant height and total dry matter production with harvest index was observed, each in one but different season, in the other seasons and pooled analysis they showed neutral association (non-significant).

From the path analysis, it was inferred that the traits viz., total dry matter production and harvest index showed highest positive direct effects towards seed yield (direct effects more or less equal to genetic correlation coefficients) and through these traits only all the other positive traits had their maximum positive indirect effects. These two traits also evinced a considerable positive direct effects towards seed size to a considerable level though not equal to the genetic correlation coefficients, and also positive indirect effects, so, a direct selection for these two traits can well improve the seed yield and seed size.

But the question is how to rely upon these two traits and how to select for harvest index. Eventhough there will be a small practical problem in uprooting the entire plant and finding the dry weight of it, total dry matter production can be selected directly. But, being a ratio of seed yield to total dry matter production, harvest index can not be selected directly. On the other hand it necessitates to look in for a trait which showed positive significant genetic association due to a high or moderate direct effect towards seed yield and seed size.

A perusal of the direct effects of the positively and significantly associated traits with seed yield showed that number of flowers and 1000 seed weight exhibited positive direct effects. But the effects were less. So, instead of selecting a component trait to increase the seed yield and thereby to increase the harvest index, a direct selection

for seed yield and total dry matter production can well improve the harvest index. In toto, seed yield total dry matter production are the two and selection criteria.

From the critical analysis of the occurrence of heterobel-tiosis five options were brought out to increase seed yield in sesame.

- A. Increasing the seed yield and total dry matter production but reducing the harvest index.
- B. Simultaneous increases in seed yield, total dry matter production and harvest index.
- C. Enhancing both seed yield and total dry matter production with an unchanged harvest index.
- D. Increasing seed yield and harvest index leaving total dry matter production unaffected.
- E. Increasing the seed yield leaving both total dry matter production and harvest index relatively unchanged (involving small changes).

Among these five options, the first four may be given primary importance due to their functional excellence in cereal breeding.

6.12.2. Genetic variability and heritability of the identified traits

The high genotypic coefficient of variation coupled with high heritability and high genetic advance (percentage over mean) observed

for seed yield, total dry matter production and harvest index, indicated the existence of adequate genetic (additive) variability, and sufficient heritability to obtain desired improvement for these traits in the progenies coupled with high genetic gain. As these traits were mostly positively and significantly associated with the other traits which showed positive significant association with seed yield as well as seed size, the question of component compensation and correlated response in the negative direction appeared not to occur.

6.12.3. Stability for the identified traits

The responsiveness and stability of 1000 seed weight and seed yield showed non-significant association with the responsiveness and stability of total dry matter production and harvest index, as well as with the other traits which were positively and significantly associated with them (excepting the stability of number of branches which had negative correlation with that of 1000 seed weight). This indicated that the mean productivity, production response and production stability were independent from that of total dry matter production and harvest index and can be manipulated to increase the seed yield. Genotypes viz., G3, G12, G27 and G30 for seed yield, G11, G12, G24, G27, G30, G52, G58 and G59 for total dry matter production and G5, G11, G12, G22, G35, and G44 for harvest index exhibited high mean, average responsiveness and high stability and thus suitable for all seasons. Among these, genotypes G12, G27, and G30 expressed high mean, average responsiveness and high stability for seed yield and total dry matter

production whereas G12 was good for seed yield, total dry matter production and harvest index. Interestingly, G12, G27 and G30 also exhibited high mean, average responsiveness and high stability for most of the traits which were positively and significantly associated with seed yield and 1000 seed weight and 1000 seed weight itself. These genotypes can well be utilised in direct selection (mean seed yield is above six grams) as well as in cross breeding programme.

6.12.4. Genetic nature of the identified traits

The variances due to specific combining ability were higher than that due to general combining ability for seed yield, total dry matter production harvest index and all the characters which were positively and significantly associated with seed yield and seed size. Partitioning of the gene effects through generation mean and variance analysis showed that seed yield, total dry matter production, harvest index and the other traits which were positively and significantly associated with seed yield and seed size were pre-dominantly controlled by dominance followed by dominance x dominance interaction effects, besides one or more of the different types of epistasis. Partitioning of the variance also indicated a higher magnitude of dominance variance than the additive variance for these traits. The dominance ratio was more than unity (where it was estimable) indicating the presence of over dominance for seed yield, total dry matter production and harvest index. However, incomplete (for number of capsules) and complete dominance (for 1000 seed weight) were also found to operate in certain cross combinations. The overdominance was associated with the duplicate dominant epistasis ([h] and [l] opposite signs) in most of the crosses for seed yield, total dry matter production,

harvest index and for the other traits which were positively and significantly associated with seed yield and seed size. Both cytoplasmic and maternal genetic control were found to control these traits indicating the importance of nucleo-cytoplasmic interaction in the expression of these traits.

6.12.5. Combining ability and heterosis for the identified traits

Among the stable genotypes identified for seed yield, the genotypes viz., G12 (L_7 07) and G 30 (L_{13}) were also found as good general combiners (pooled analysis). Similarly, among the stable genotypes identified for total dry matter production G12 (L_7) was found as good general combiner (pooled analysis). For harvest index, among the stable genotypes, G11 (L_6), G22 (L_{10}) and G35 (L_{15}) were found as good general combiners (pooled analysis). These genotypes, viz., G12 (L_7) and G30 (L_{13}) can well be utilized for pure line selection and/or pedigree selection or for developing synthetics as they showed high mean, average responsiveness, high stability and good general combining ability for seed yield and total dry matter production.

The stable genotype G30 (L_{13}) in combination with G40 (T_2) expressed high mean, high sca effect and high standard heterosis for seed yield (Pooled analysis). For total dry matter production the stable genotype G11 (L_6) in combination with G59 (T_3) (stable) exhibited high per se performance, sca effects and standard heterosis (pooled analysis). Similarly, for harvest index the stable genotypes G5 (L_1) and G22 (L_{10})

in combination with G40 (T_2) expressed high *per se* performance and standard heterosis (pooled analysis).

These genotypes were mostly grouped in cluster I and the suggested cross combinations included in DC 3. As these genotypes were iso-responsive, crosses among these genotypes will result in high yielding genotypes (variety or hybrid) with a response similar to that of the parents. So, these cross combinations, *viz.*, G5 (L_1), x G40 (T_2); G11 (L_6) x G59 (T_3); G22 (L_{10}) x G40 (T_2) and G30 (L_{13}) x G40 (T_2) along with the other cross combinations listed in Table 193 can be included in the future breeding programme.

6.12.6. Choice of the breeding method

Sesame breeders has the choice between lines, hybrids, and synthetics. Synthetics can be considered as a passing phase in sesame, until a well established genic-or cytoplasmic genic male sterile systems become available. Single crosses can be more justified at the beginning and lines can be justified later if all the heterosis were fixable. As the present study revealed the preponderance of non-additivity and the non-fixable dominance effect [h] and dominance x dominance [l] interaction effect, the improvement for seed yield or total dry matter production or harvest index by simple pedigree selection (commonly followed) or modified pedigree selection may not be possible. Hence, yield improvement can be expected by delaying the selection to later generations, when the dominance and epistatic gene actions disappear

and resorting to intermating of segregants followed by recurrent selection. Anderson (1939), Al-Jibouri et al. (1958), Jensen (1970), Hallauer (1981; 1986), Ramage (1981), Frey (1984), and Delogu et al. (1988) suggested recurrent selection as a basic breeding approach in autogamous crops. Diallel selective mating design as suggested by Jensen (1970) can also be adopted.

However, in a comprehensive strategy of varietal development, it is necessary to combine population improvement and varietal development.

To have short time efficiency it requires high selection intensity with direct varietal development of the breeding material. However, this will lead to the loss of variability and to a very restricted recombination between loci. Favourable genes linked to unfavourable will be eliminated and hence the probability of detecting them will be low, due to the large environmental and/or seasonal effect on the low frequencies of favourable genes. So maximum genetic advance can not be expected by varietal development.

Maximum genetic advance can only be expected at long term by the accumulation during several cycles of selection followed by intercrossing and with a low selection intensity. Therefore, there is a conflict between short term efficiency and long term efficiency. Resolving this conflict requires a strategy where these two objectives are separated.

Long term advance must be preceded by population improvement by recurrent selection to enhance the ability of the population to give good varieties. Short term efficiency can be satisfied by the derivation of varieties from the breeding material at any cycle of recurrent selection (Gallais, 1988a).

The aim of the population improvement is to improve the varietal ability of the population. This will be achieved through the increase of frequencies of favourable genes or associations of genes (favourable in the varietal situation). The aim of the varietal development will be extract the best possible varieties from a given generation of the breeding population(s). Population improvement increases the mean of the population of varieties and varietal development exploits the variance among varieties of a given type within a generation of the breeding material. So in a single time one can harvest a total genetic advance of two components viz., the expected genetic advance due to population improvement and that due to varietal development.

To develop lines, it will be necessary to improve the line value' of the population, that is to say the expected value of all lines which can be derived from the population. The test must be based upon the line value of one genotype. If haplodiploidization will be well controlled it is easy to show that the best recurrent selection will be recurrent selection on the phenotype of the doubled haploid line with only one line per plant (Gallais, 1988b). If haplodiploidization will not be controlled well, testing S_1 can be used very efficiently.

To develop hybrids in the absence of overdominance, the best scheme of recurrent selection for a character with low heritability, will be a recurrent selection on general combining ability (the mean of crosses of all lines which can be derived from the plant). At the beginning of the selection the best lines could be inferior to the best crosses, but after several cycles of recurrent selection, the best lines could be better than the best single crosses. Such a situation is expected in autogamous plants where there is generally high additivity and low heterosis (Gallais, 1988a).

As at the level of the whole genome, over dominance and partial or complete dominance will coexist, the best way will be to select simultaneously on line value and on combining ability according to an index. So, it will be possible to use different types of variation.

In the presence of overdominance, the best recurrent scheme to develop hybrids will be a reciprocal recurrent scheme (R.R.S). The advantage of reciprocal recurrent selection is that hybrid development is almost an end product or by product of population improvement. Moreover, with the same amount of means it is more efficient than within population improvement to limit genetic drift. The other advantage of reciprocal recurrent selection over other systems is the harnessing of cytoplasmic genes due to the reciprocal crossing among the two populations.

To conclude, haplodiploidisation can be an efficient system for line breeding but also for hybrid breeding. In the absence of haplodiploidisation system, resorting to S_1 family selection can be employed. Recurrent selection must be developed for line breeding as well as hybrid breeding, as it is the most efficient way to fix heterosis. To develop hybrids, reciprocal recurrent selection will be the most efficient method, but it must be organized in a way to have continuity between population improvement and varietal development [Figs. 40 and 41].

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ILLUSTRATIONS

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Plate 1. Sesame flower(Co.1)



Plate 2. Heterosis and combining ability studies - S_1 -Field view



Plate 3. Heterosis and combining ability studies
S₂- Field view



Plate 4. Co.1



6. Plate 6. TMV.4



5. Plate 5. TMV.3

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Plate 8. IS.299



Plate 7. TMV.6



Plate 9. F₁'s IS.299xTMV.6



Plate 10. F_1 s of Si.3175xTMV.4



Plate 11. Generation mean and variance analysis-
Field view



Plate 12.P_I: S.00028



Plate 13.P₂: S.0327



Plate 14. F₁'s of S.00028xs.0327

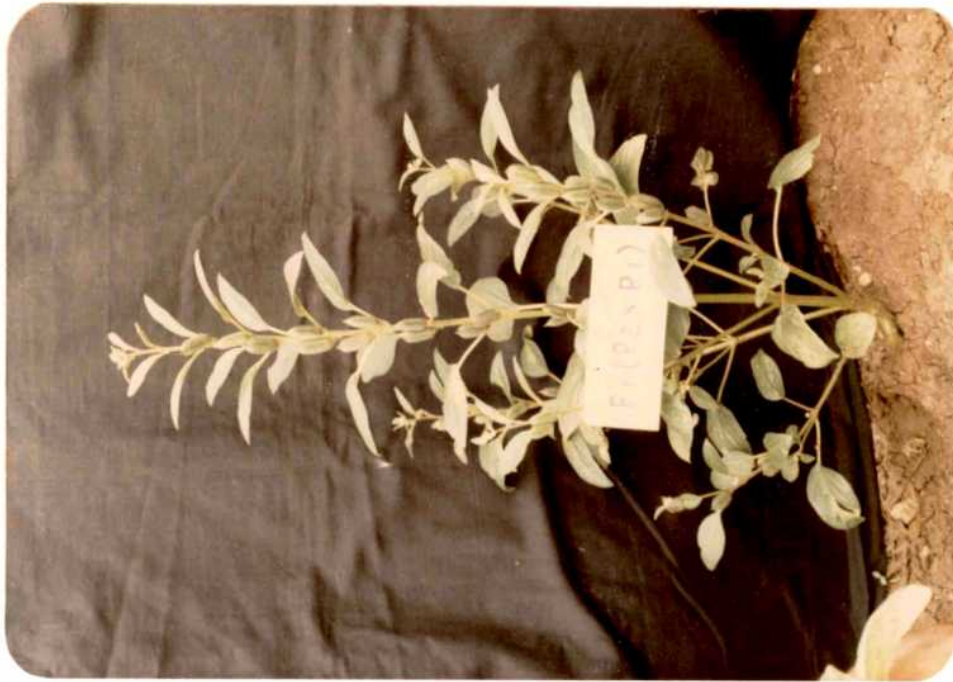


Plate 15. F₁'s of S.0327xs.00028



Plate 16. F_2 's of S.00028xs.0327



Plate 17. F_2 's of S.0327xs.00028



Plate.18 B₁'s of S.00028xS.0327



Plate 19.B'₂'s of S.0327xS.00028



Plate 20. B₂'s of S.00028xS.0327



Plate 21. B₁'s of S.0327xS.00028

Fig.1. Frequency Distribution of Genotypes
Evaluated for 1000 Seed Weight and Seed
Size Grouping (First Evaluation)

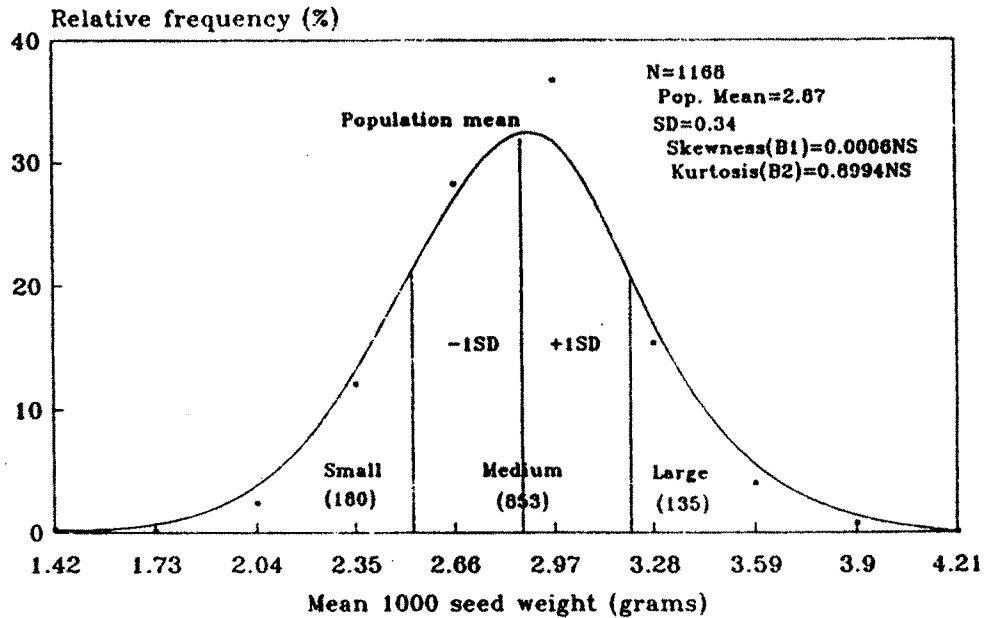


Fig.2. Frequency Distribution of Genotypes
Evaluated for 1000 Seed Weight and Seed
Size Grouping (Second Evaluation)

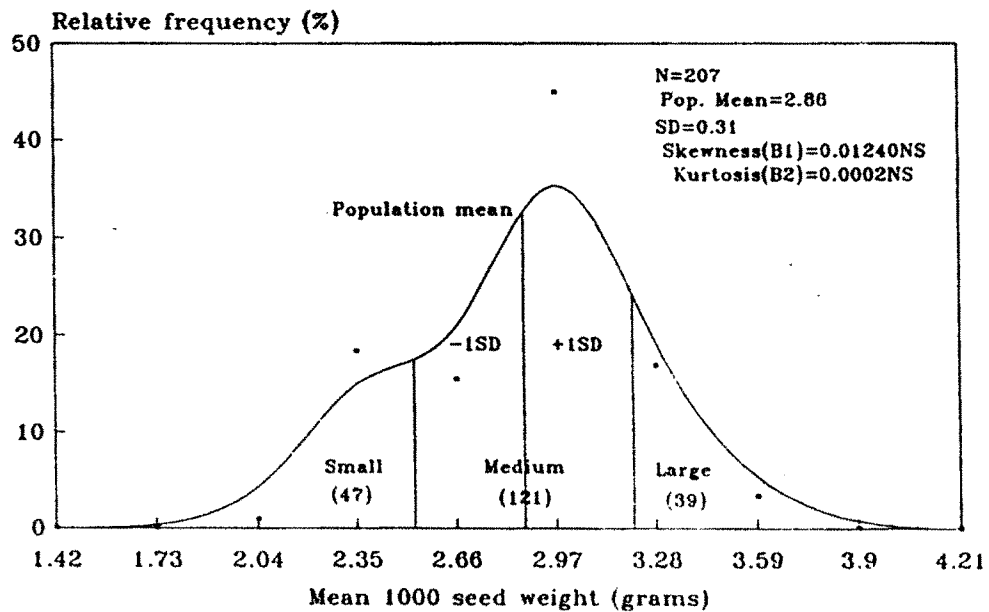


FIG. 3. PCV, GCV, HERITABILITY (%) AND GENETIC ADVANCE OVER PERCENTAGE OF MEAN FOR THE IMPORTANT TRAITS - POOLED ANALYSIS.

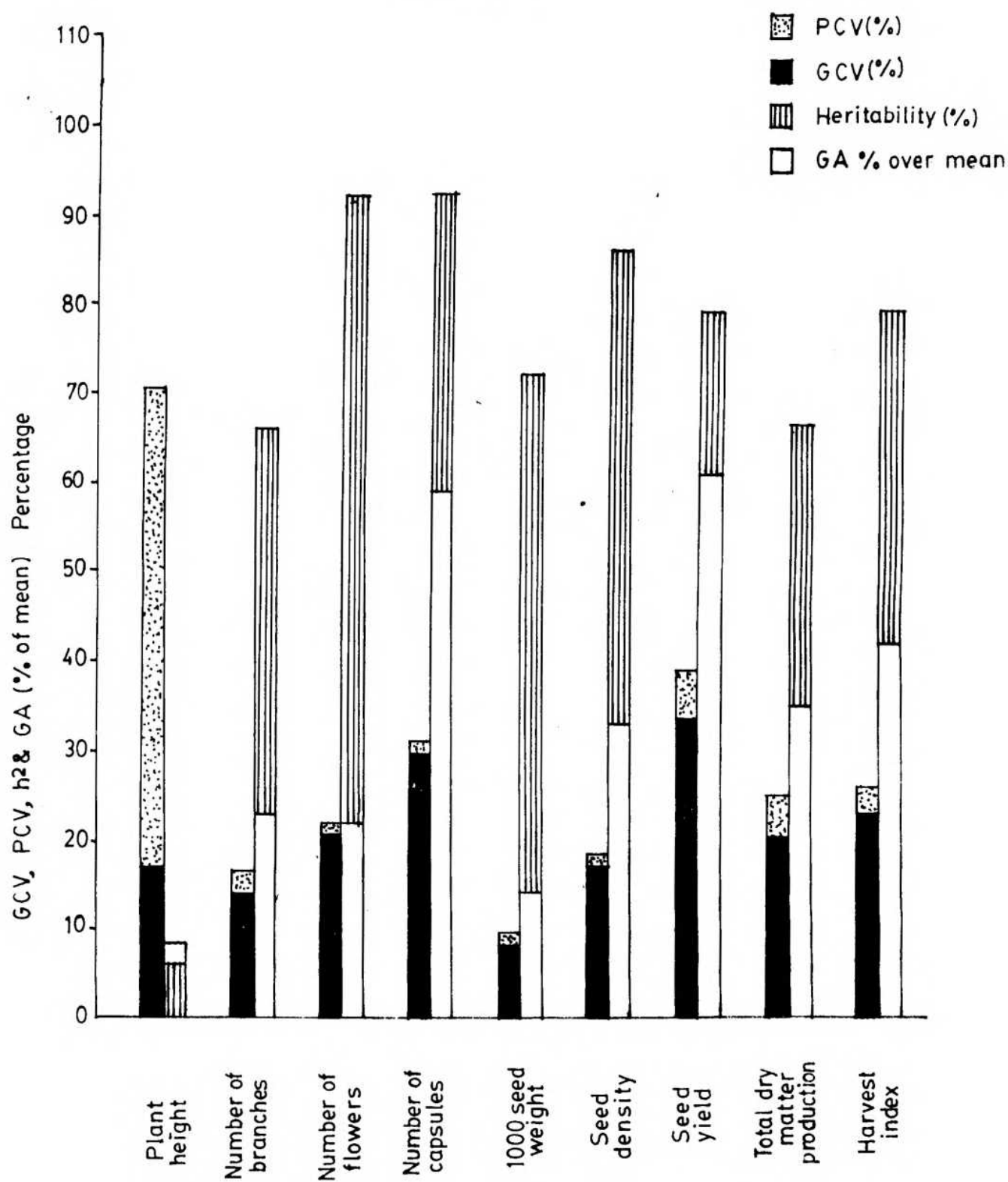


FIG. 4 PATH DIAGRAM SHOWING COEFFICIENT OF FACTORS INFLUENCING THE 1000-SEED WEIGHT IN
SESAME - S I

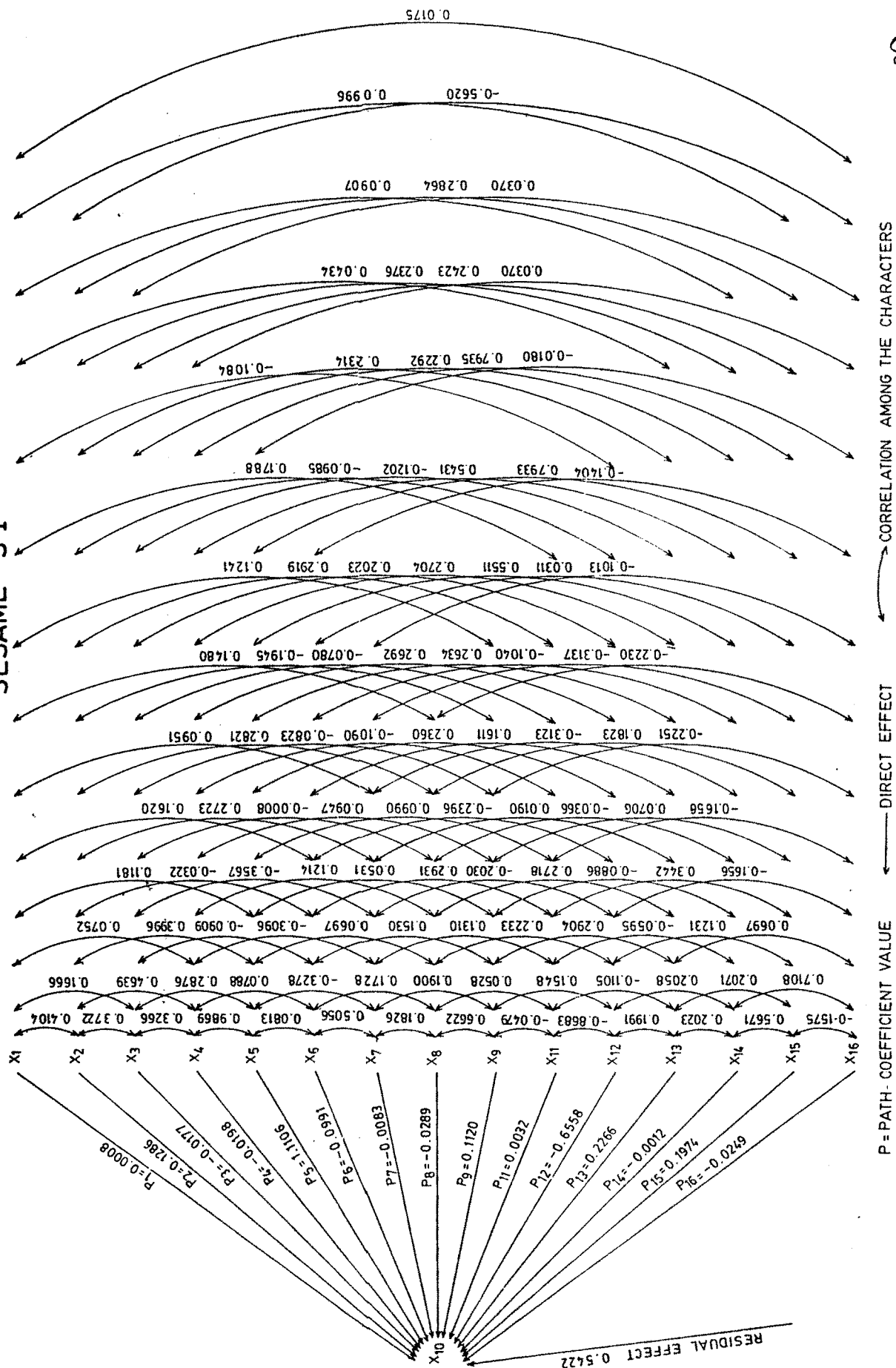


FIG.5 PATH DIAGRAM SHOWING COEFFICIENT OF FACTORS INFLUENCING THE 1000-SEED WEIGHT IN SESAME - S II

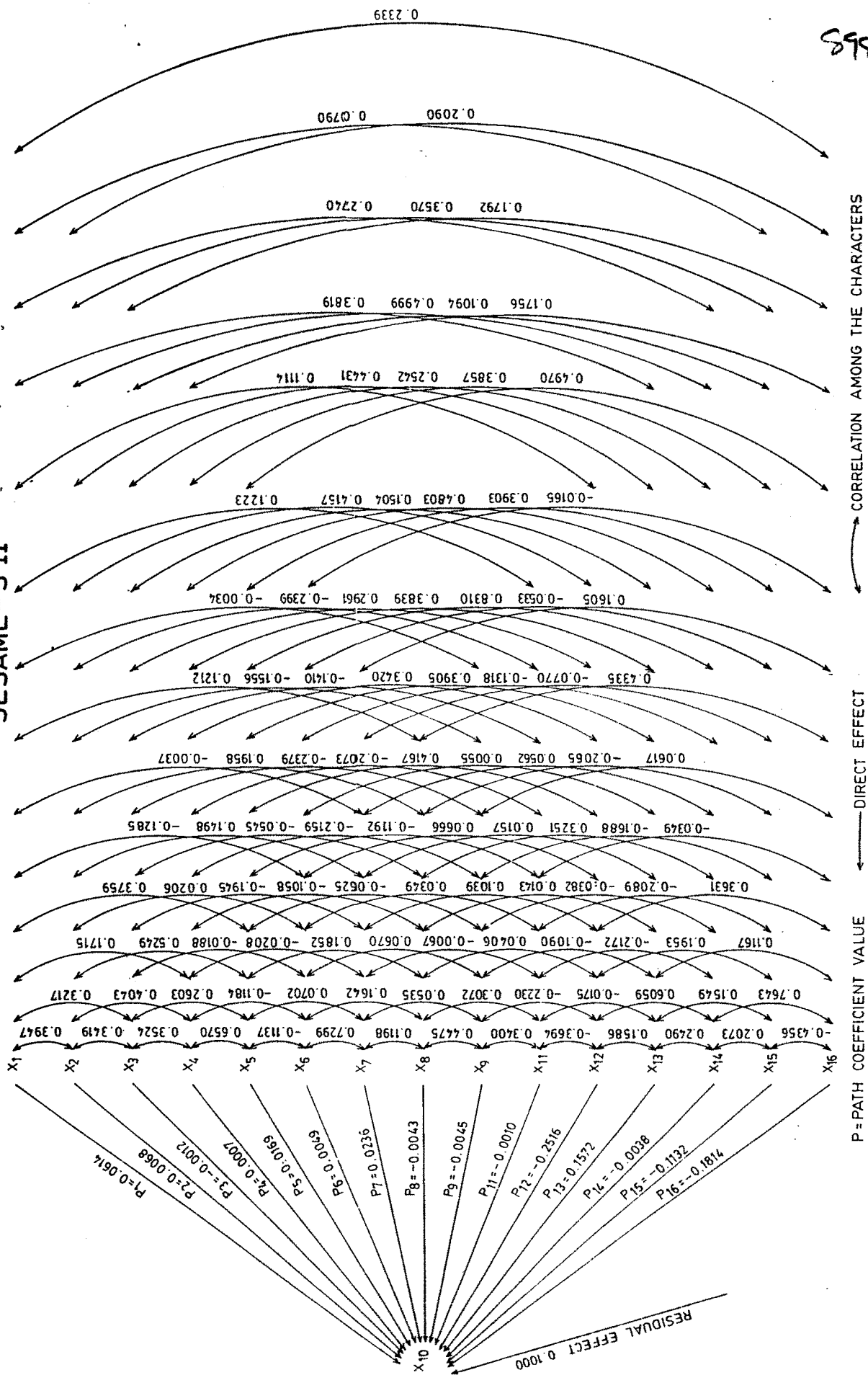


FIG.6 PATH DIAGRAM SHOWING COEFFICIENT OF FACTORS INFLUENCING THE 1000-SEED WEIGHT IN SESAME-S III

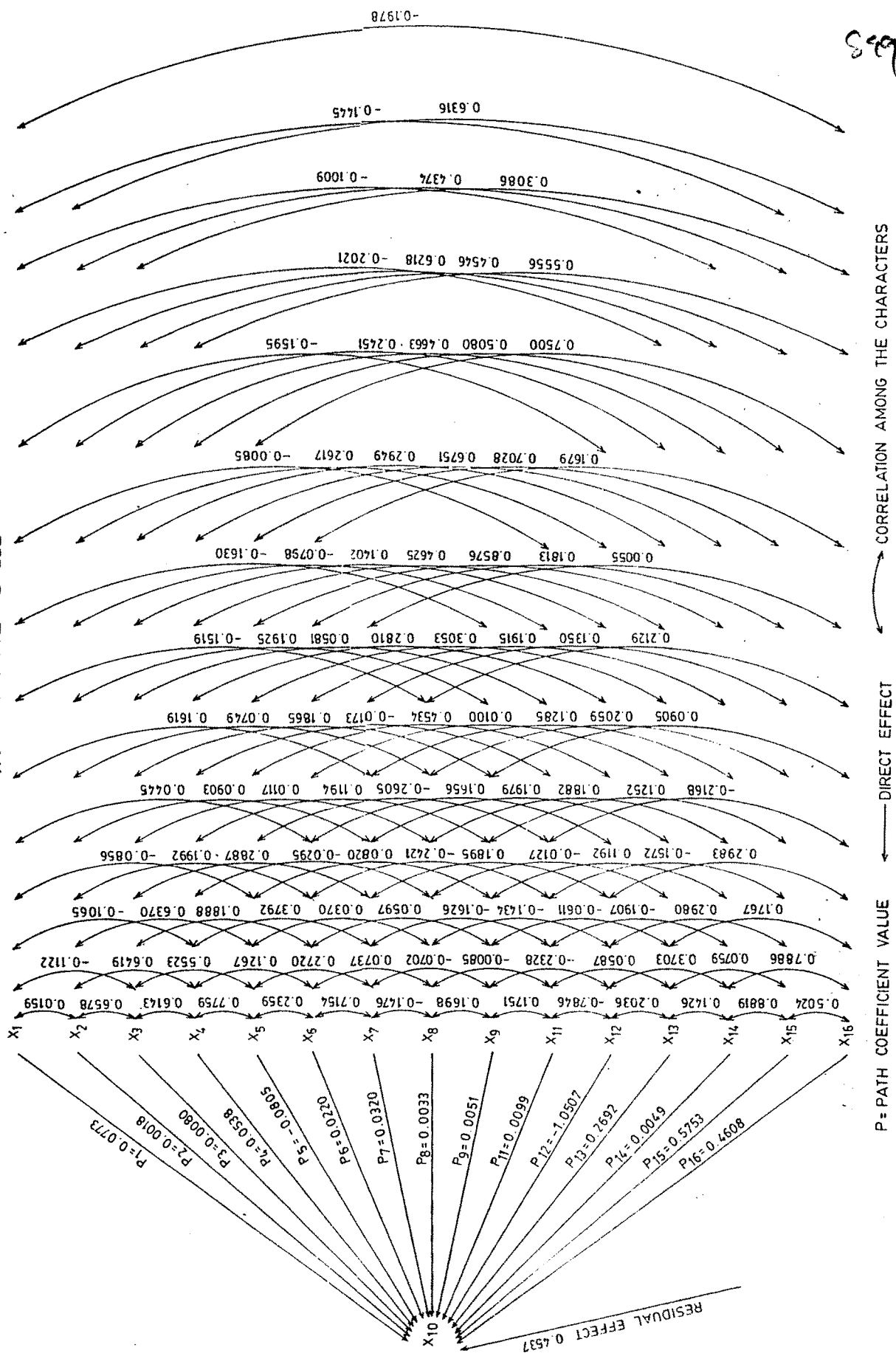


FIG. 7 PATH DIAGRAM SHOWING COEFFICIENT OF FACTORS INFLUENCING THE 1000-SEED WEIGHT IN SESAME POOLED

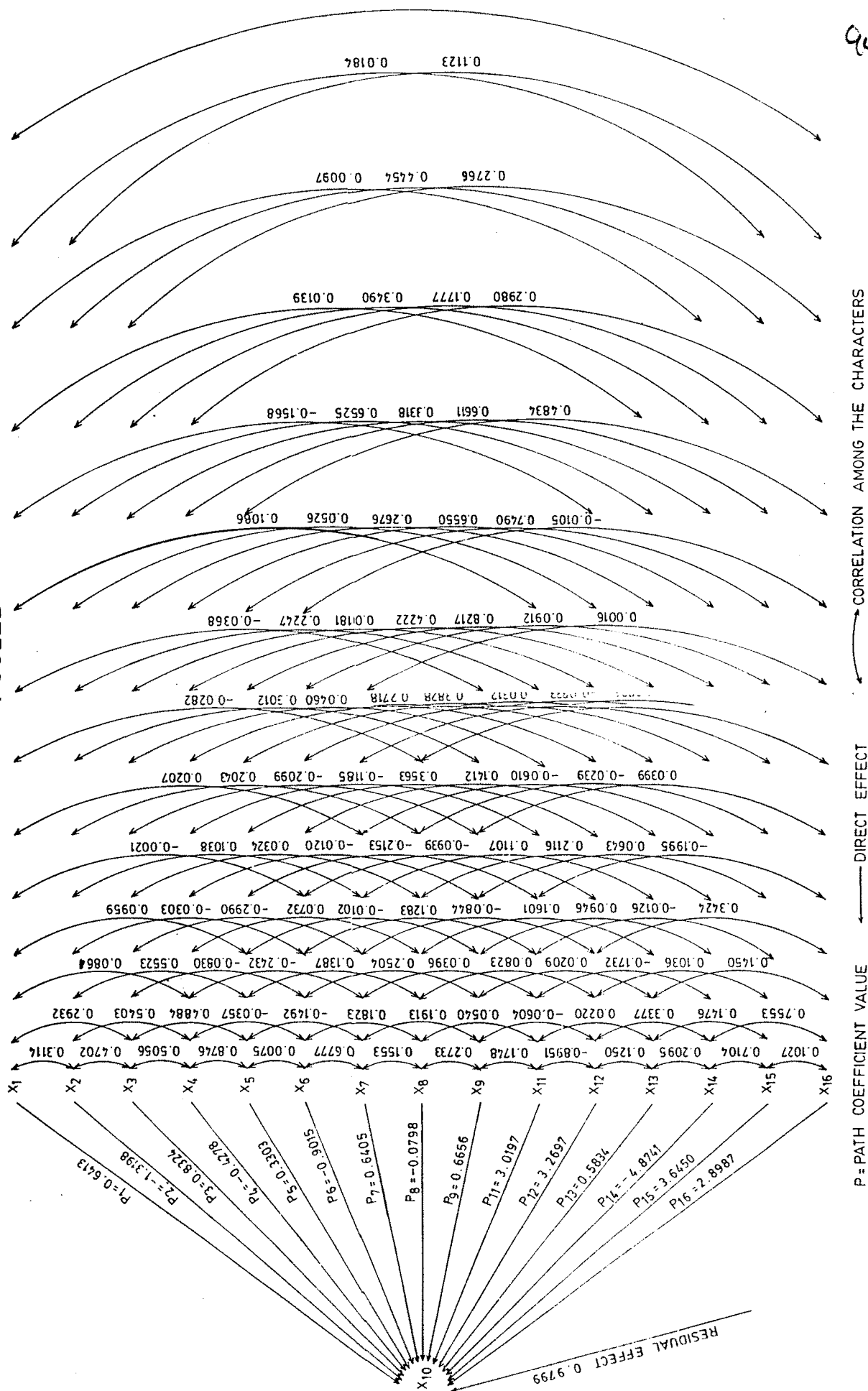


FIG. 8 PATH DIAGRAM SHOWING COEFFICIENT OF FACTORS INFLUENCING THE YIELD IN SESAME-SI

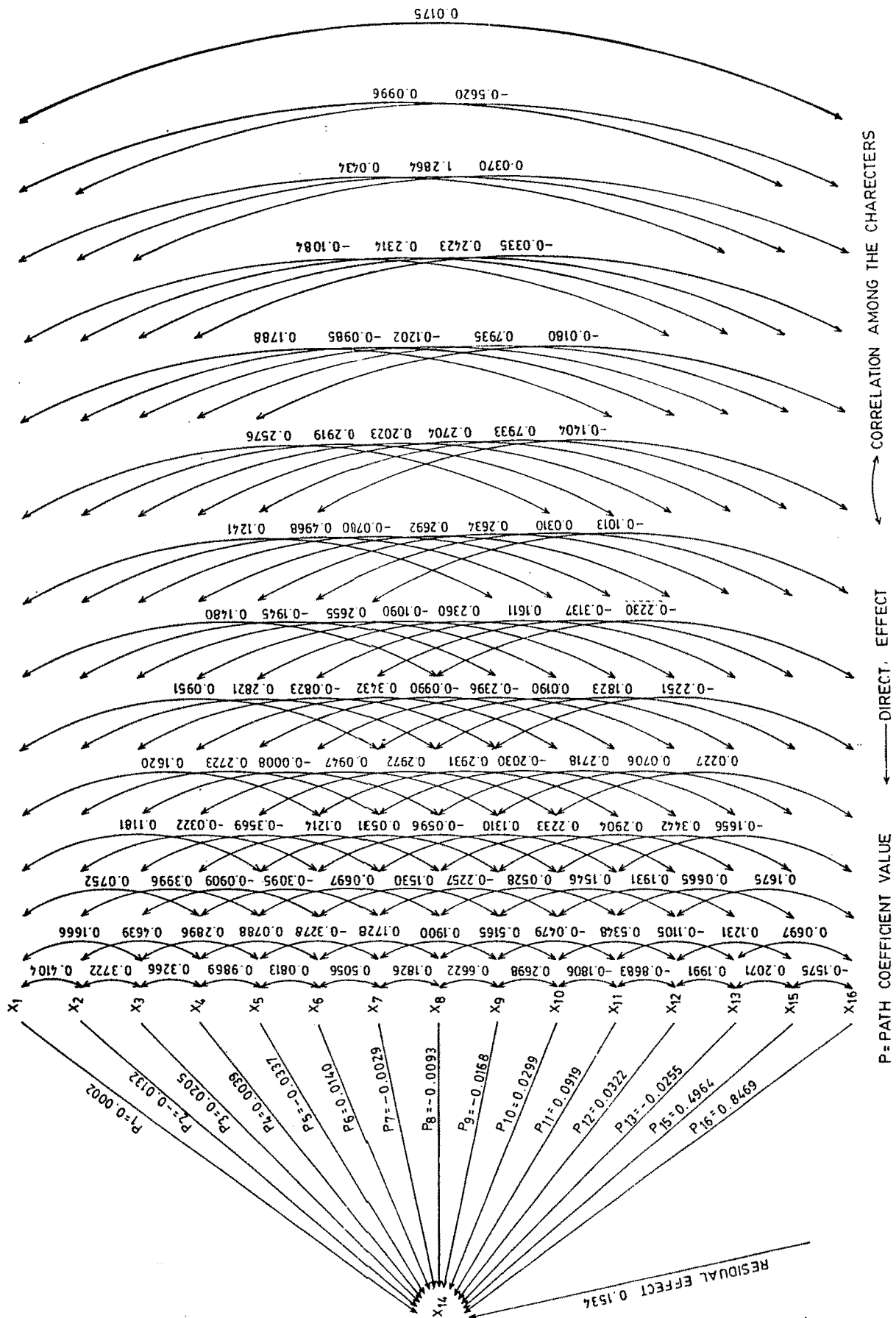


FIG.9 PATH DIAGRAM SHOWING COEFFICIENT OF FACTORS INFLUENCING THE YIELD IN SESAME-S II

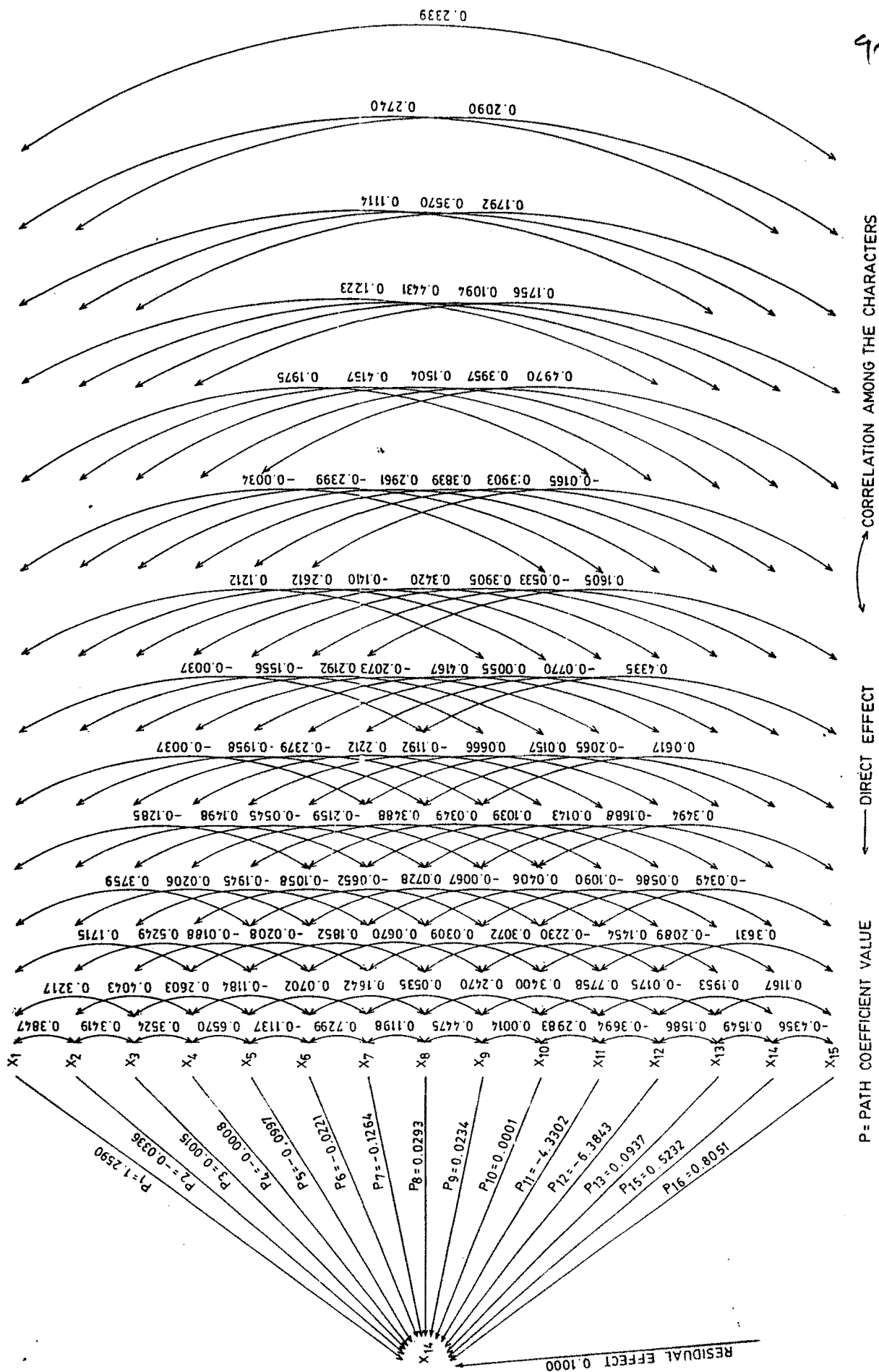


FIG.10 PATH DIAGRAM SHOWING COEFFICIENT OF FACTORS INFLUENCING THE YIELD IN SESAME-S II.

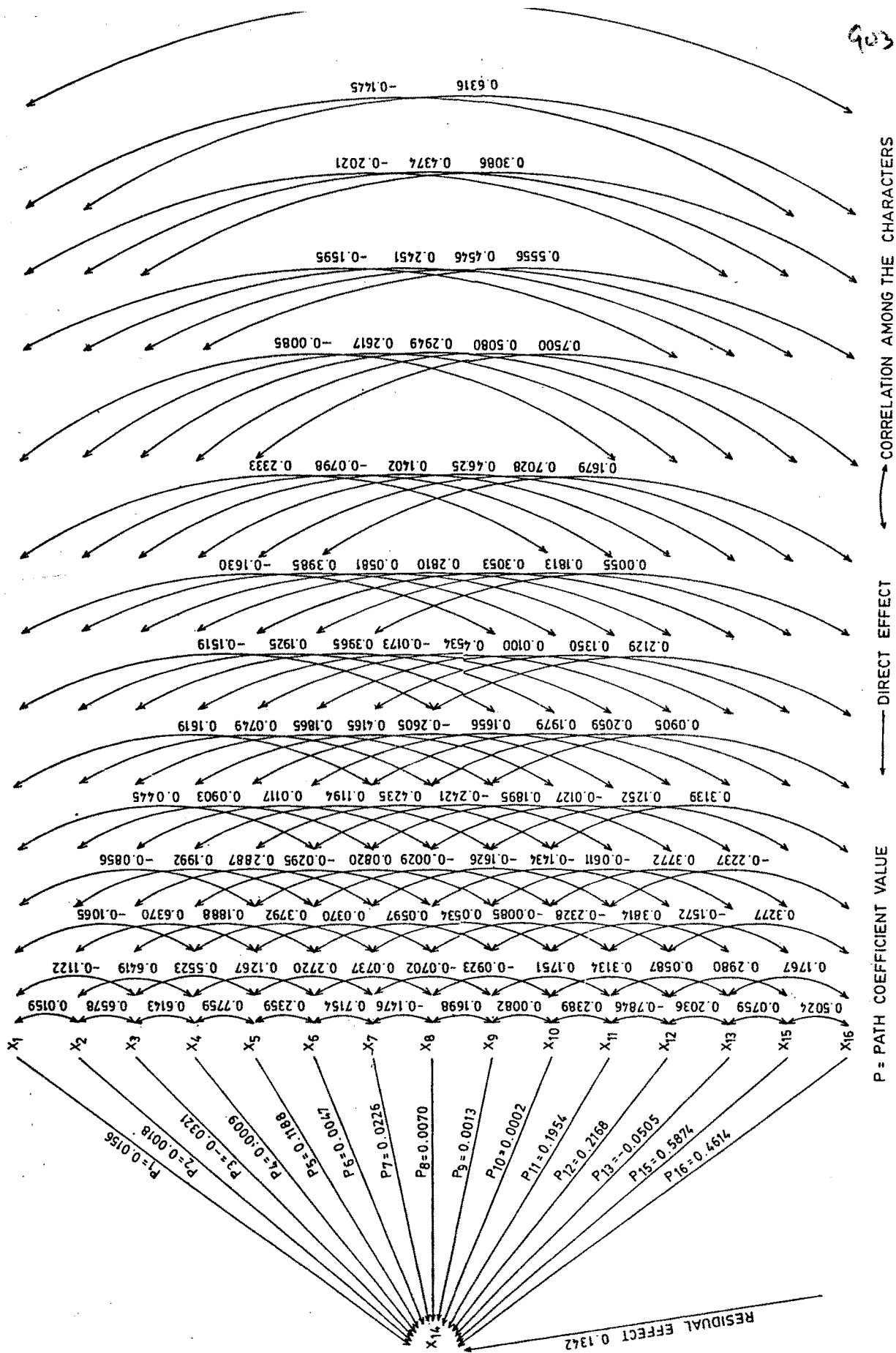


FIG.11 PATH DIAGRAM SHOWING COEFFICIENT OF FACTORS INFLUENCING THE YIELD IN SESAME-POOLED

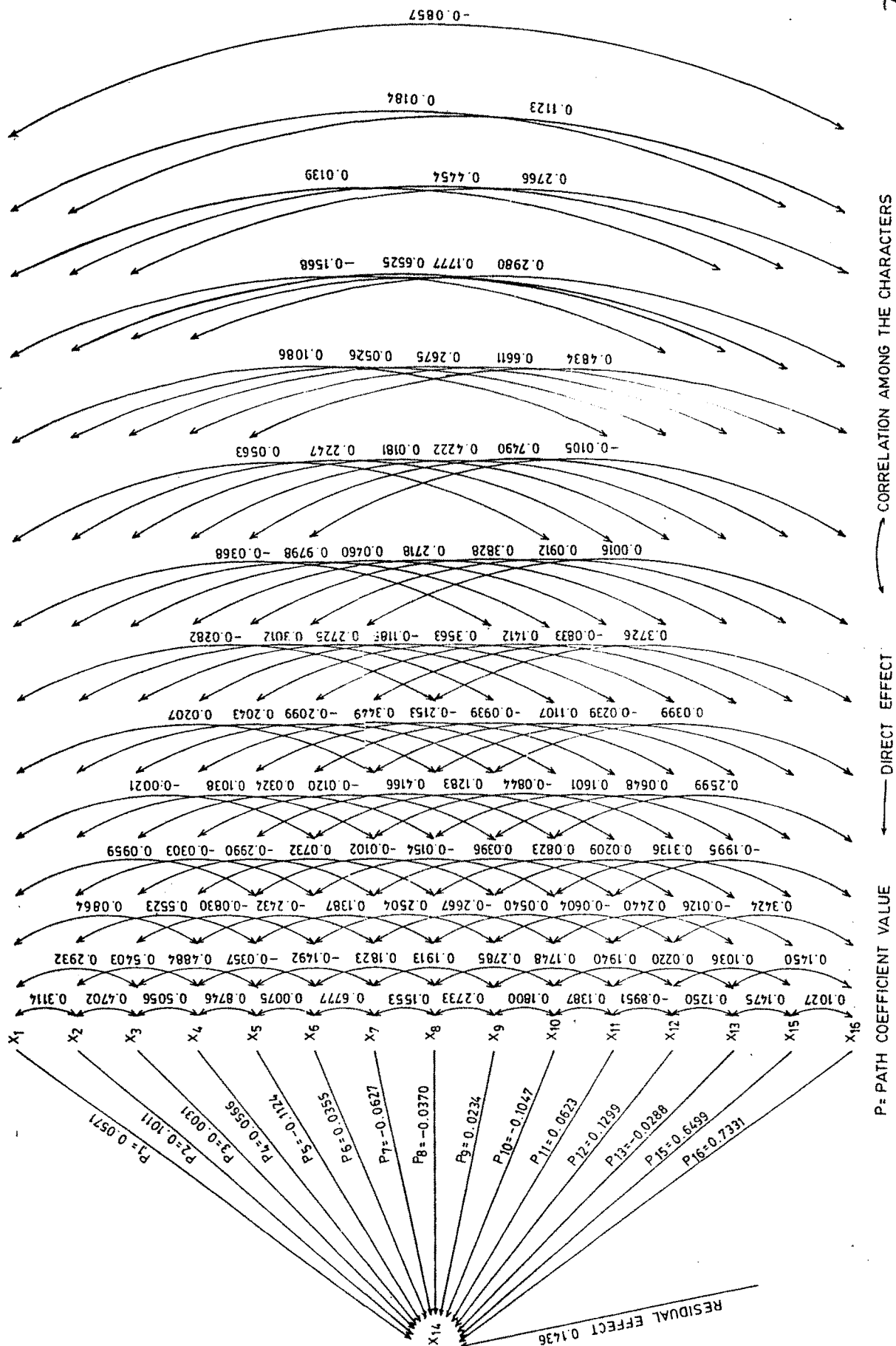


FIG.12. ANALYSIS OF VARIANCE FOR POOLED DATA OVER SEASONS.

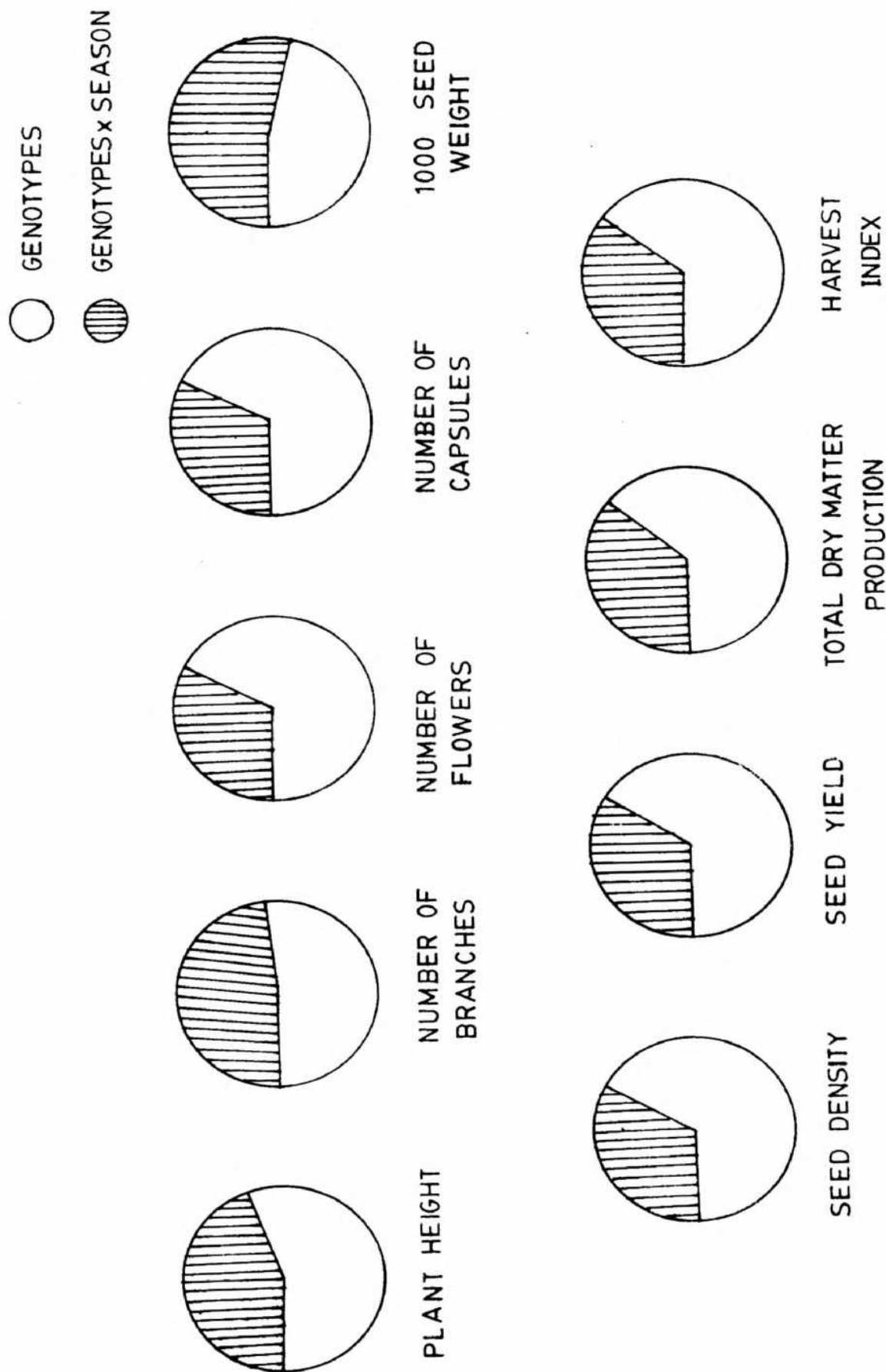


FIG.13. DIFFERENTIAL RESPONSIVENESS OF GENOTYPES WITH HIGH MEAN -
HEIGHT OF THE PLANT AT MATURITY (cm).

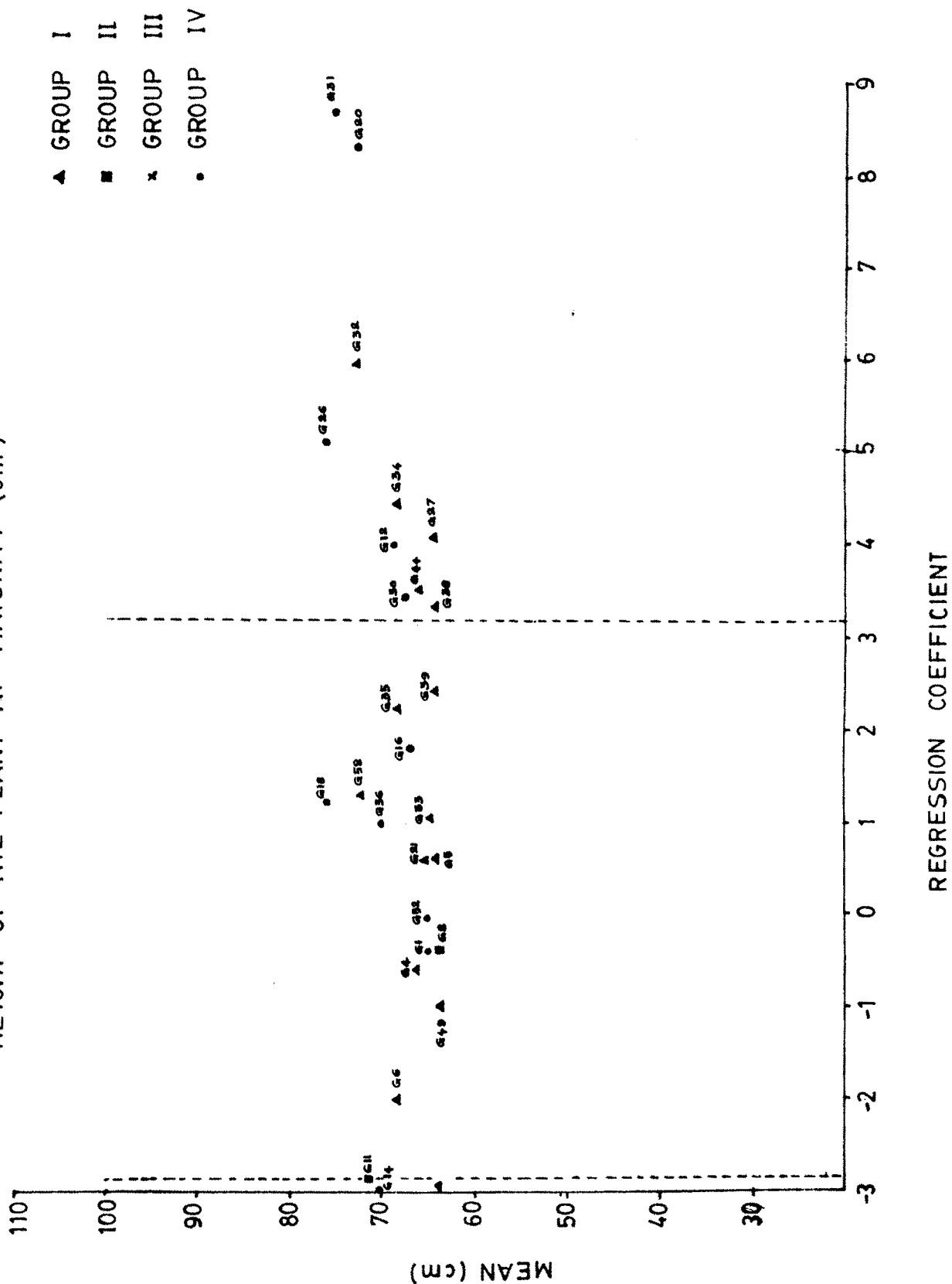


FIG.14. DIFFERENTIAL RESPONSIVENESS OF GENOTYPES WITH HIGH MEAN -
NUMBER OF BRANCHES

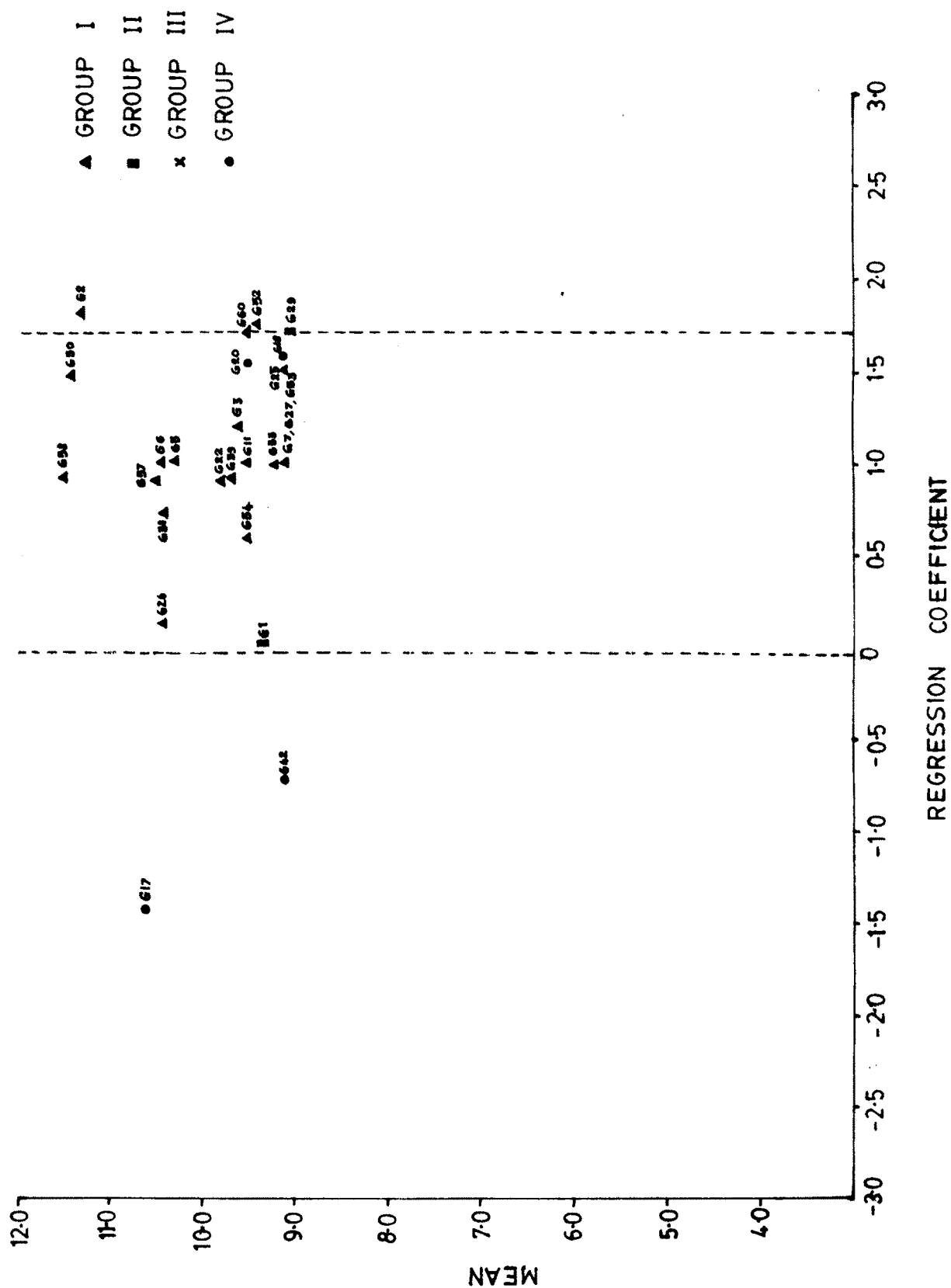


FIG.15. DIFFERENTIAL RESPONSIVENESS OF GENOTYPES WITH HIGH MEAN -
NUMBER OF FLOWERS

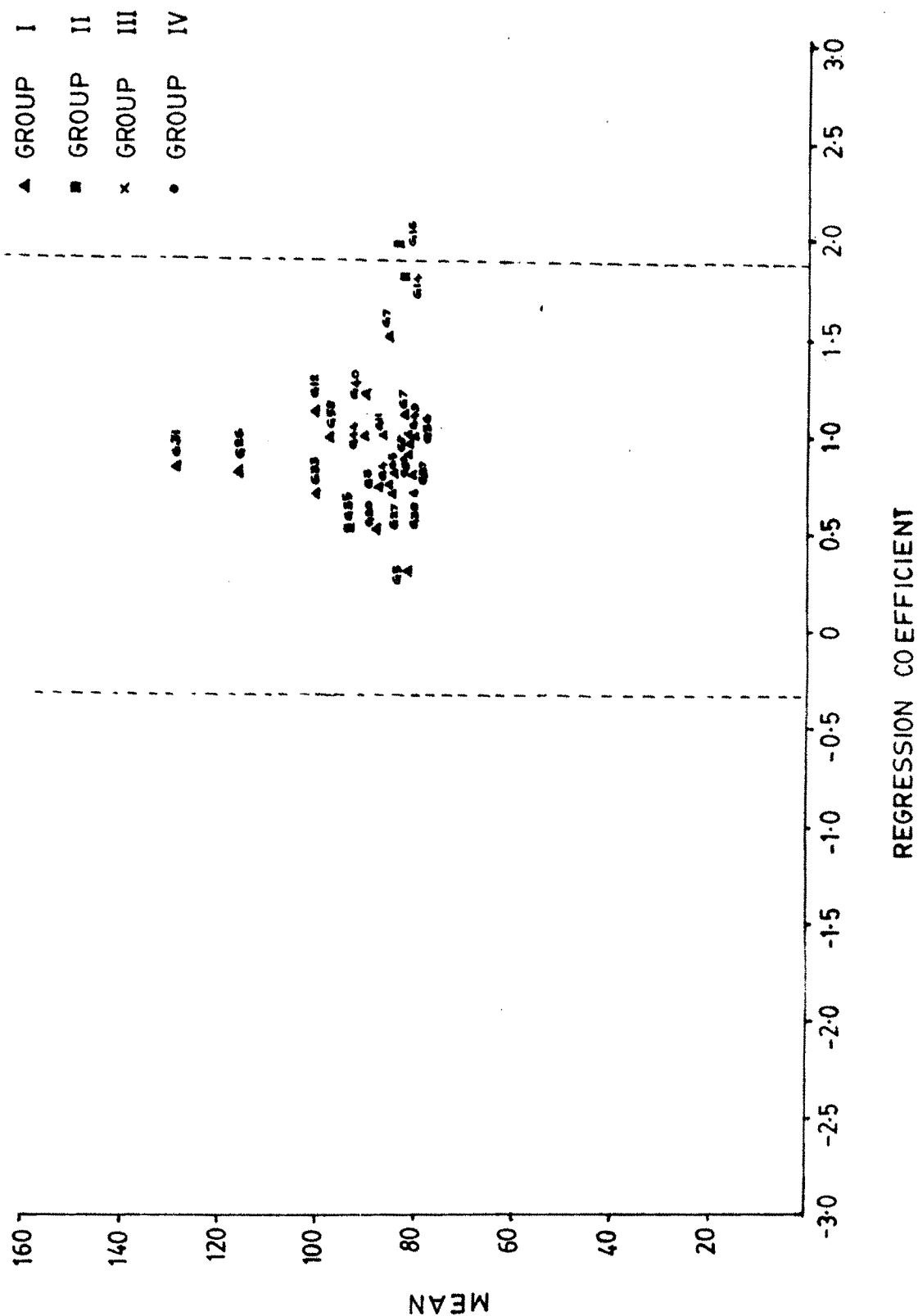
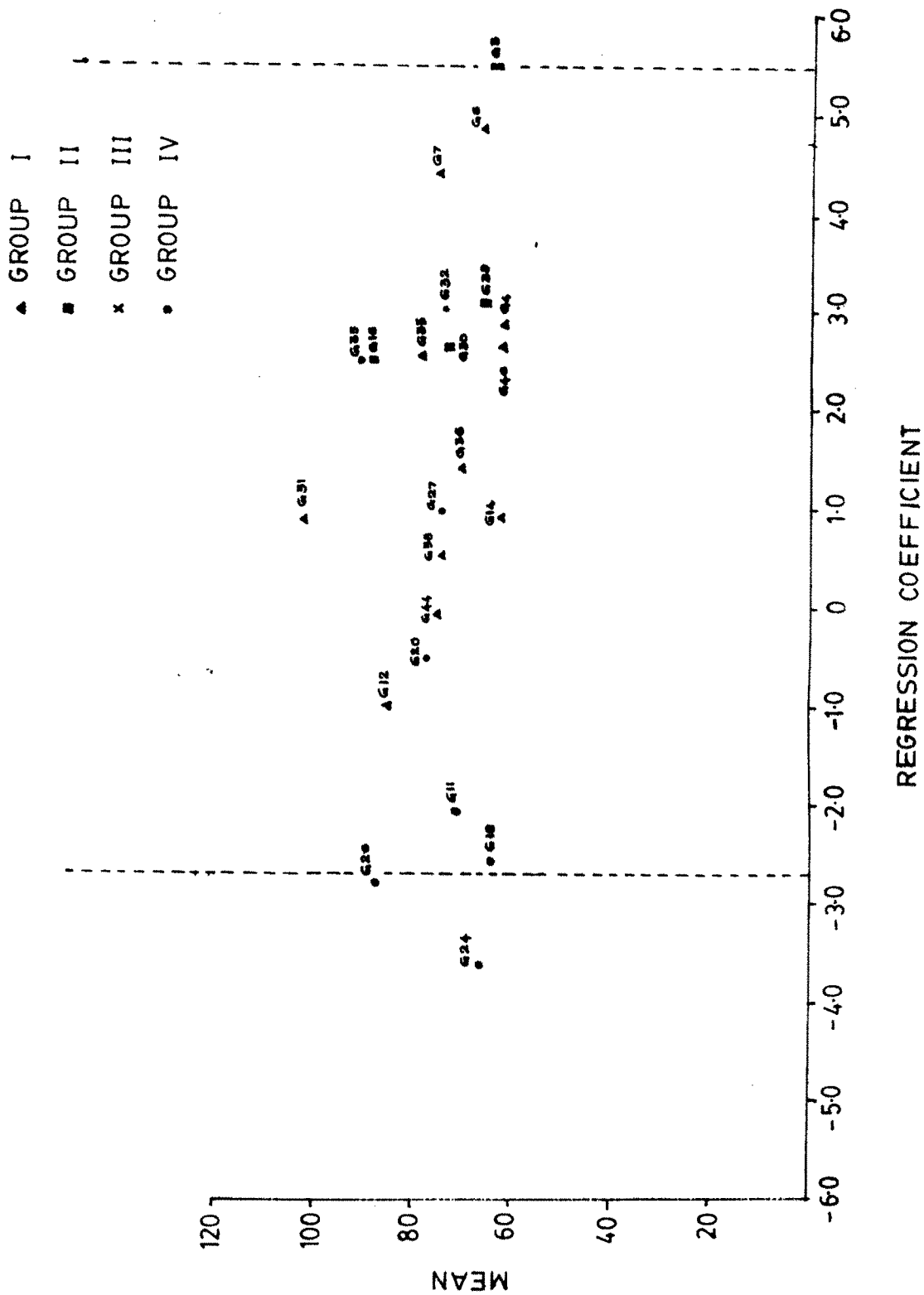


FIG.16. DIFFERENTIAL RESPONSIVENESS OF GENOTYPES WITH HIGH MEAN -
NUMBER OF CAPSULES.



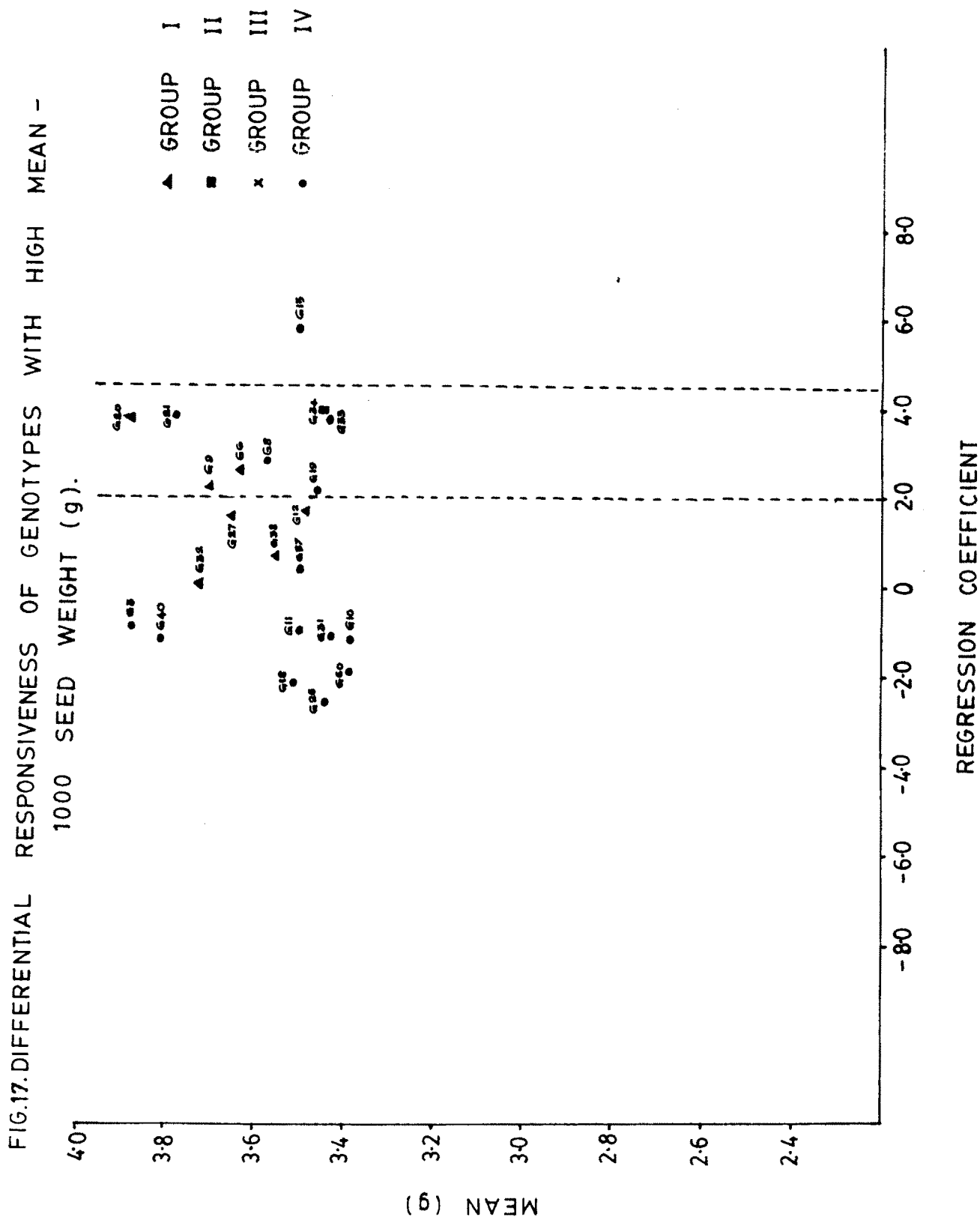


FIG.18. DIFFERENTIAL RESPONSIVENESS OF GENOTYPES WITH HIGH MEAN -
SEED DENSITY (g/ml).

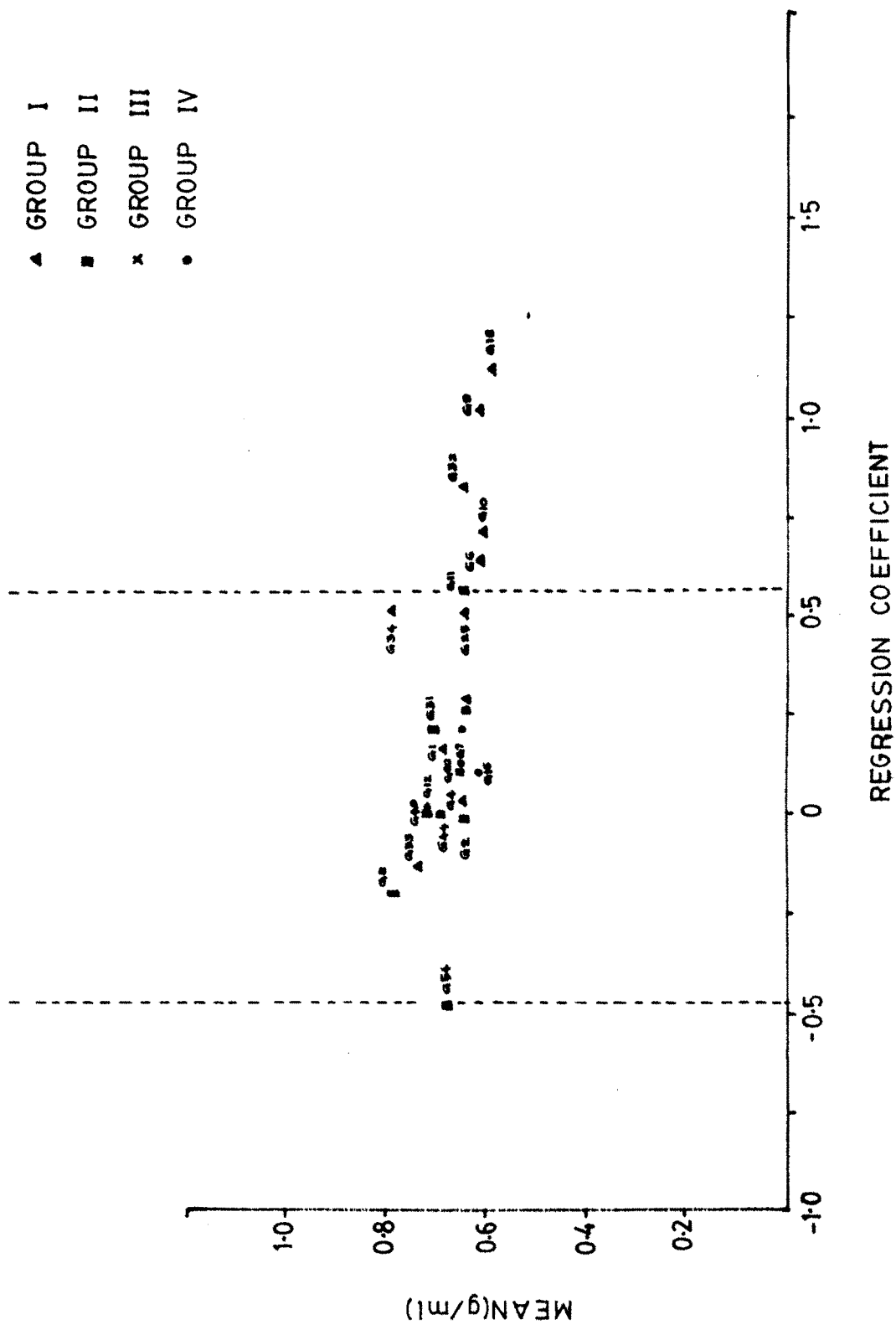


FIG.19. DIFFERENTIAL RESPONSIVENESS OF GENOTYPES WITH HIGH MEAN SEED YIELD (g).

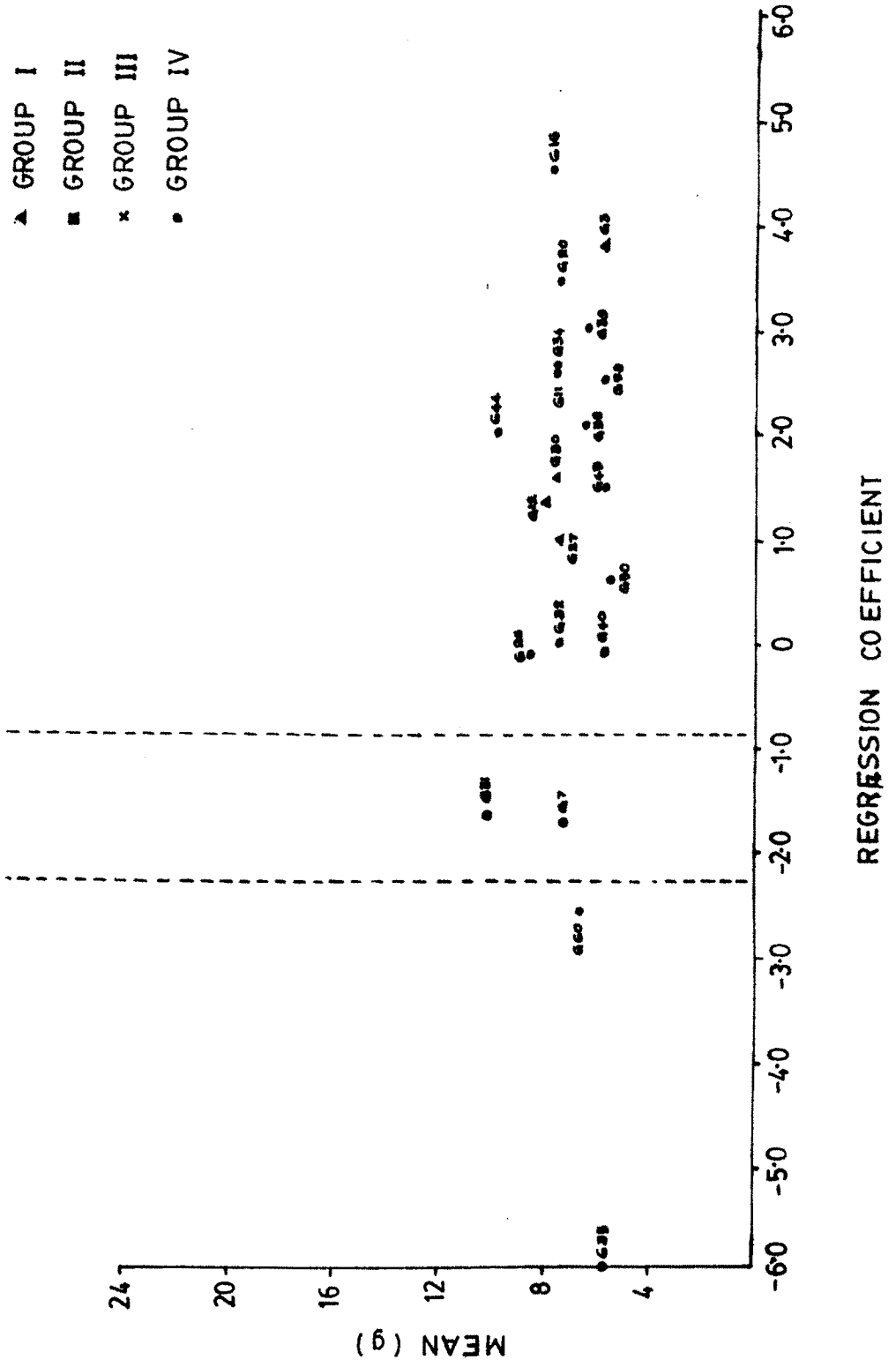


FIG.20. DIFFERENTIAL RESPONSIVENESS OF GENOTYPES WITH HIGH MEAN -
TOTAL DRY MATTER PRODUCTION (g).

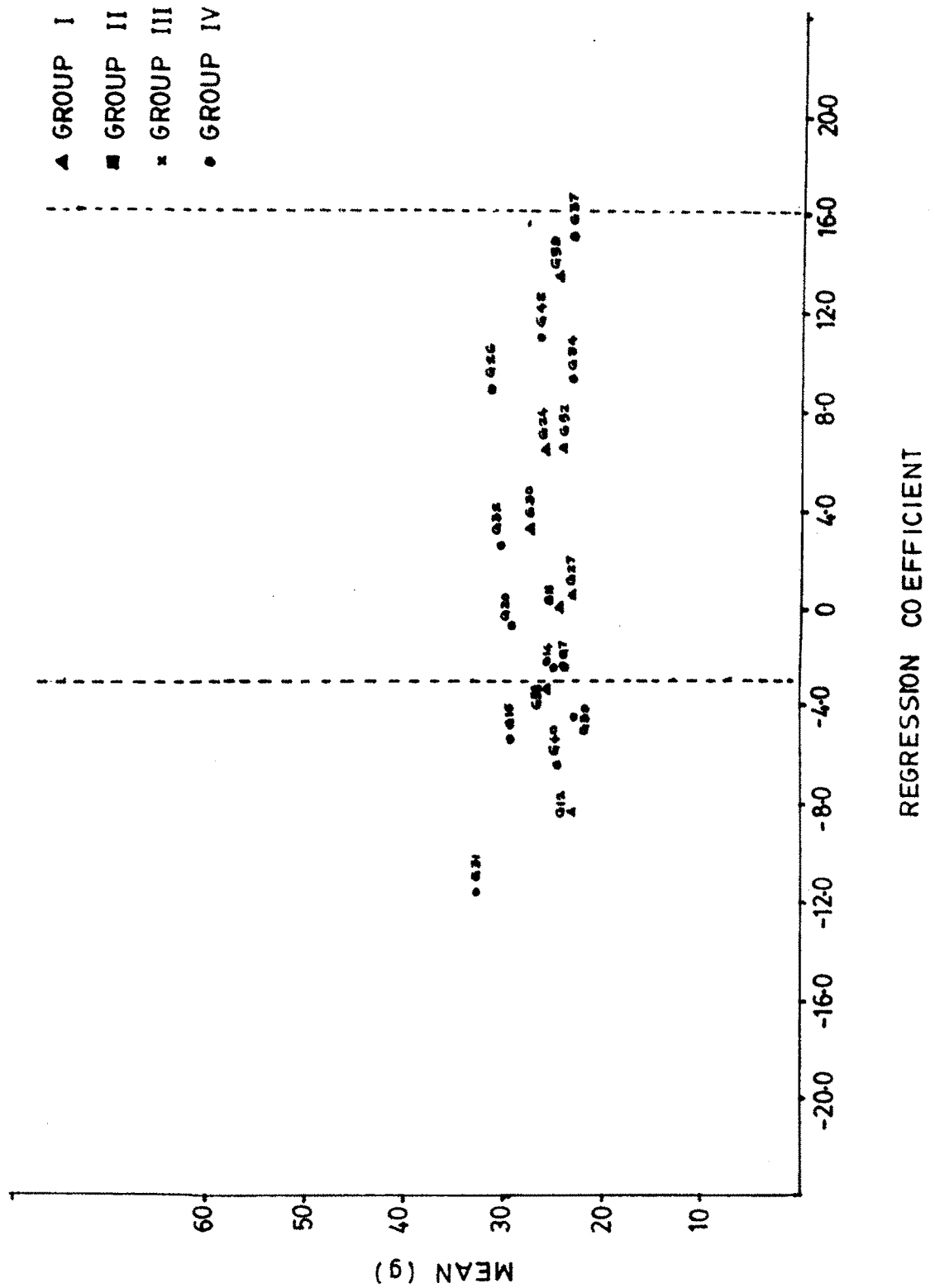


FIG. 21. DIFFERENTIAL RESPONSIVENESS OF GENOTYPES WITH HIGH MEAN -
HARVEST INDEX (%)

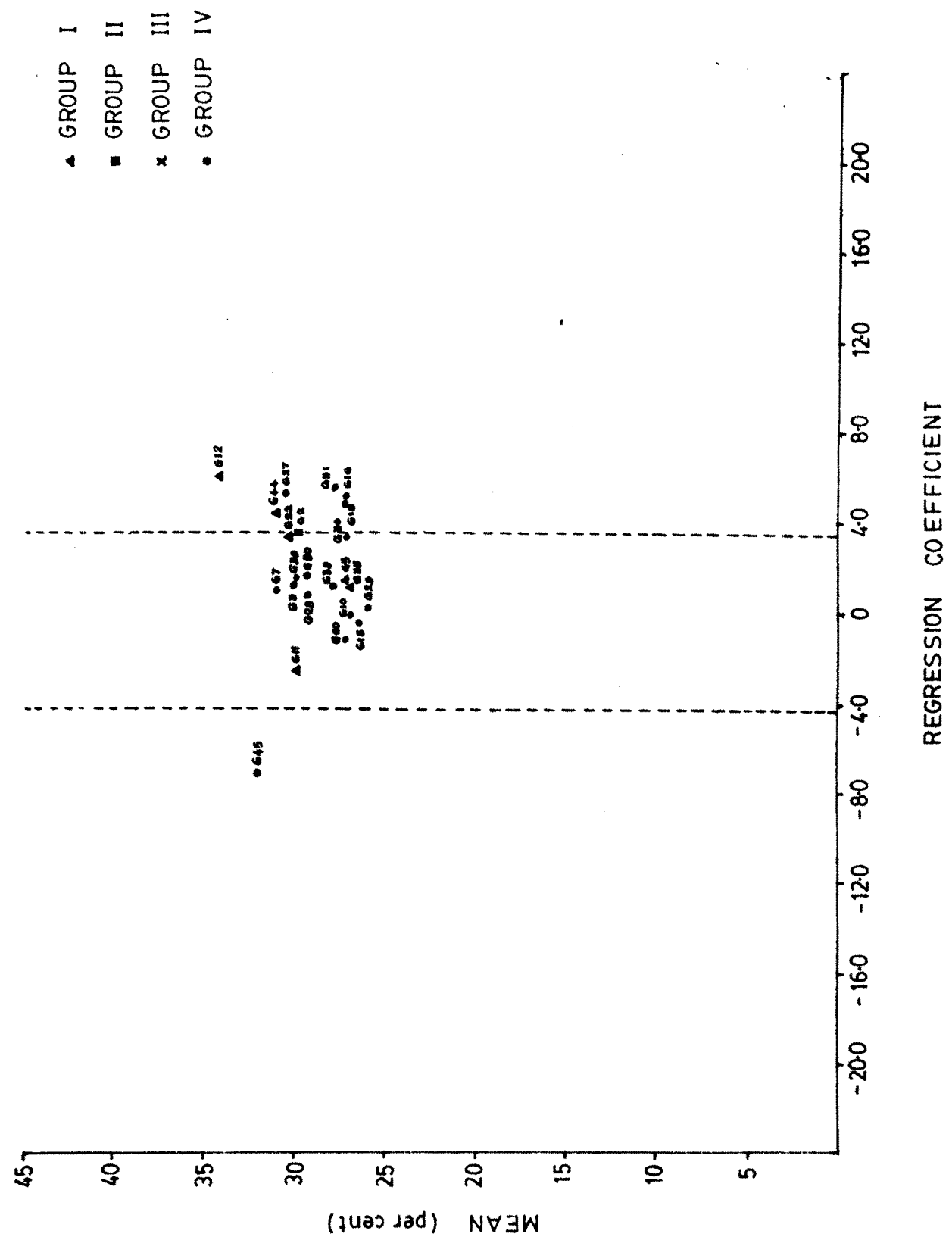
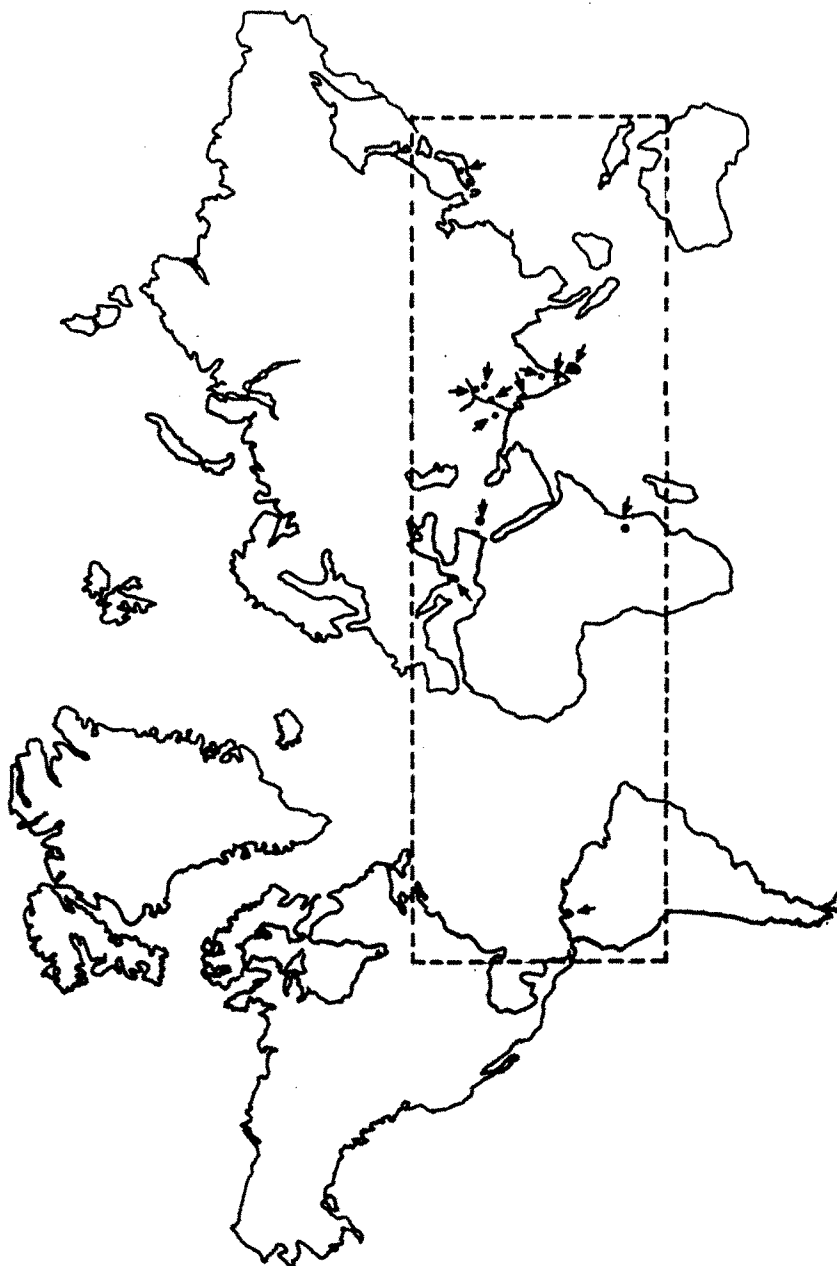


FIG. 22 GEOGRAPHICAL DISTRIBUTION OF SESAME GENOTYPES



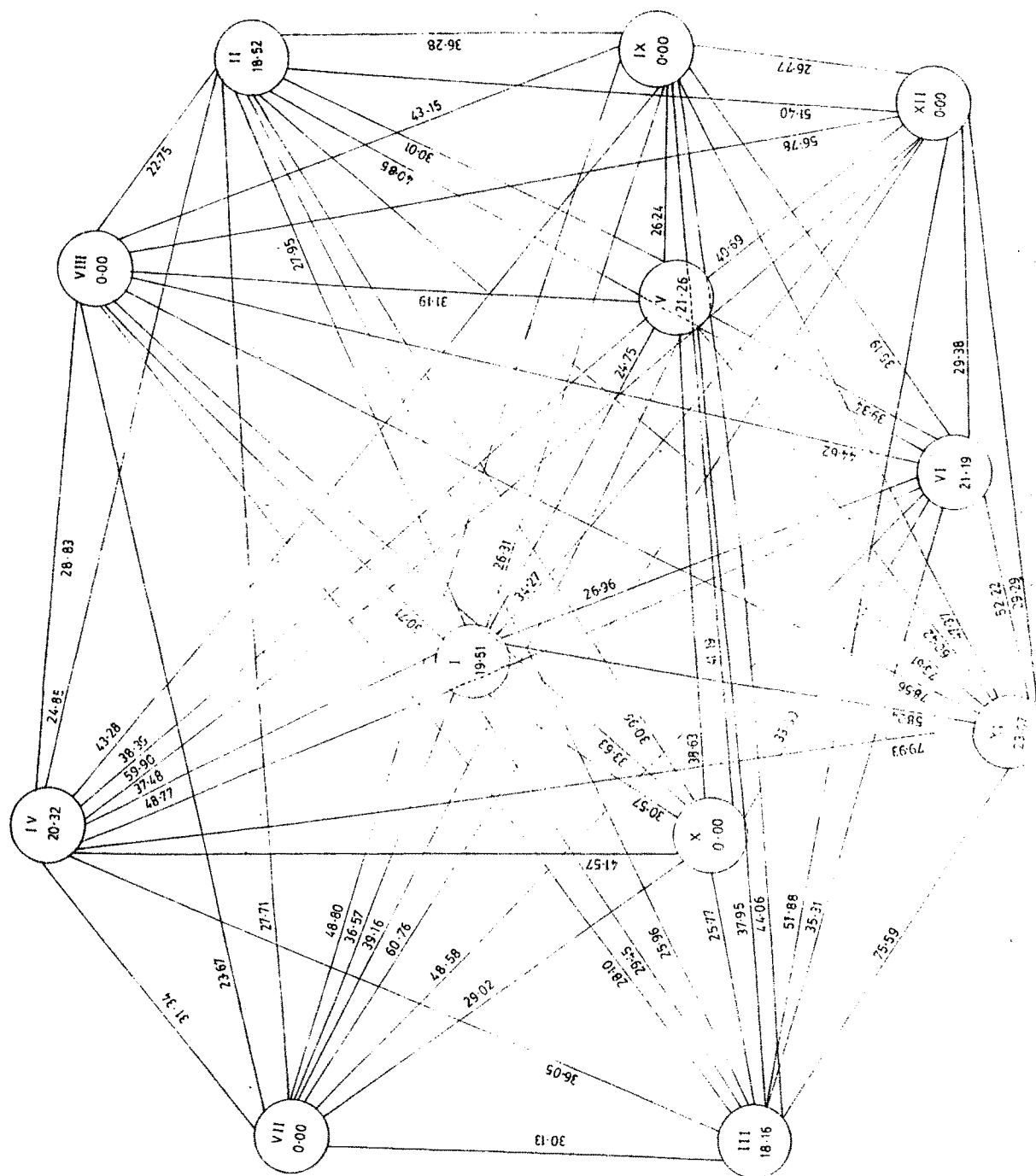


FIG.24. SPATIAL DISTRIBUTION OF CLUSTERS IN SESAME (NOT TO SCALE) -SII

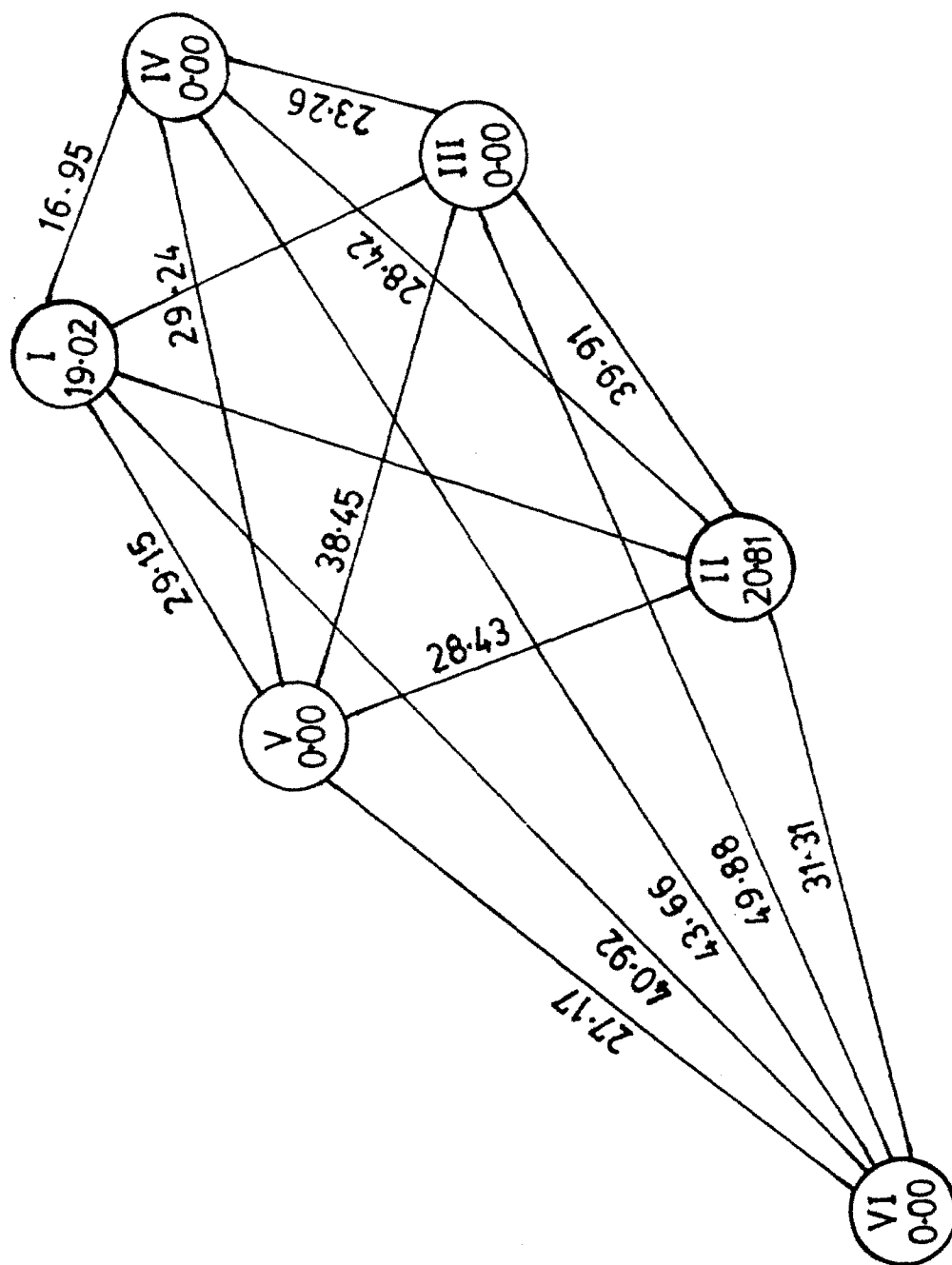


FIG.25.SPATIAL DISTRIBUTION OF CLUSTERS IN SESAME (NOT TO SCALE) - S III

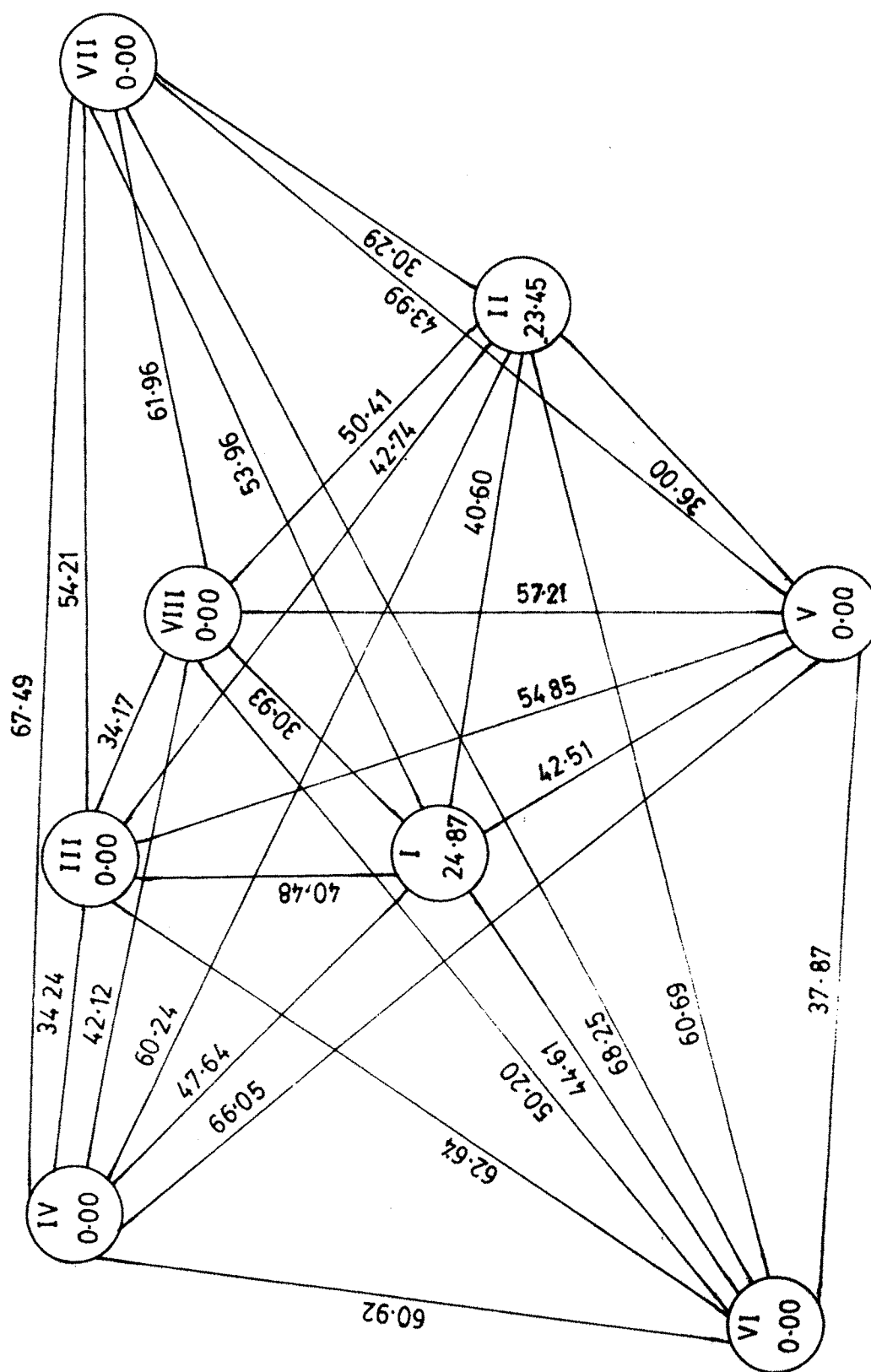


FIG.26.SPATIAL DISTRIBUTION OF CLUSTERS IN SESAME (NOT TO SCALE) -
POOLED ANALYSIS.

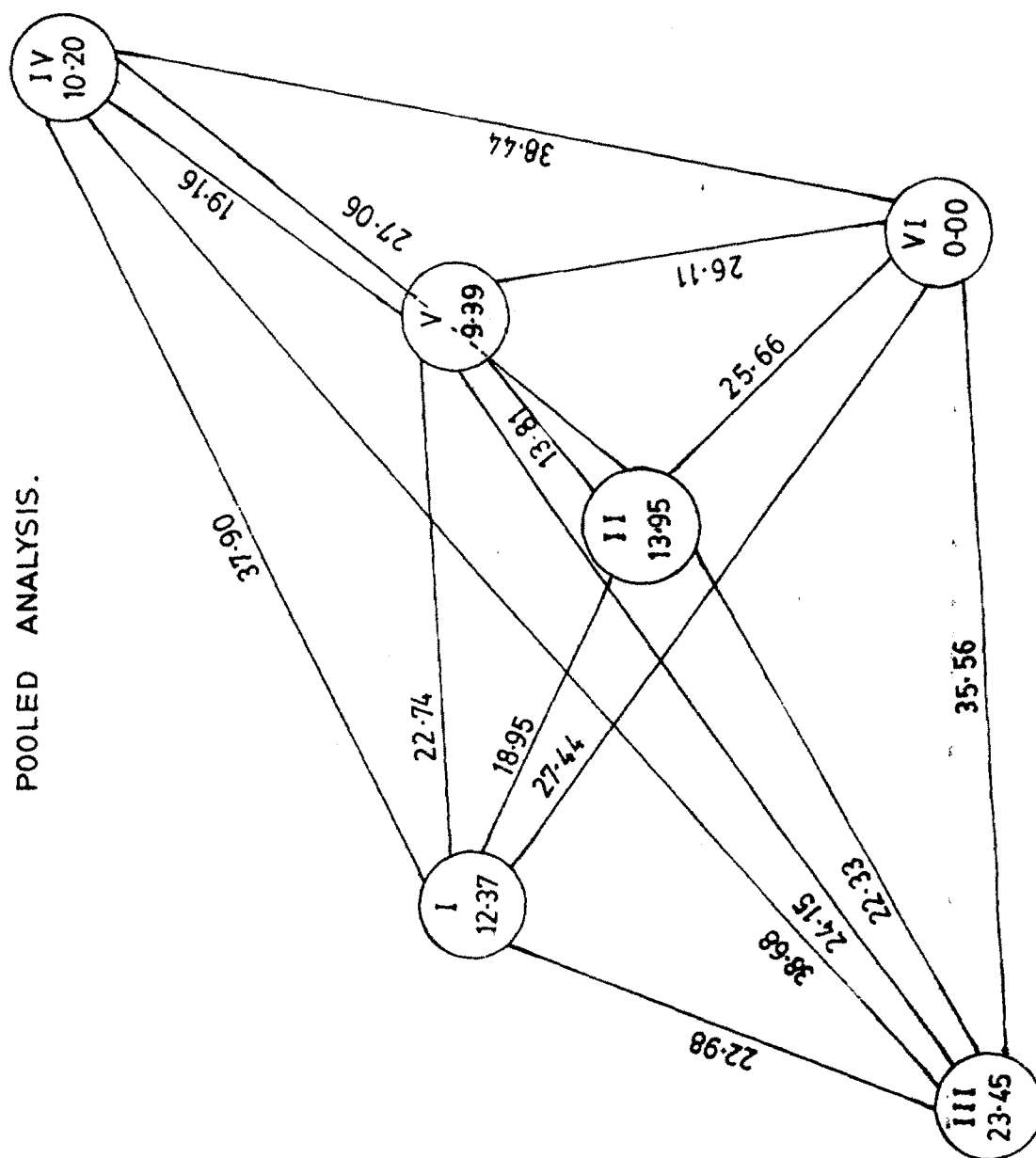


FIG.27. PROPORTIONAL CONTRIBUTION BY LINES, TESTERS AND LINE $\times$ TESTER INTERACTION TO THE TOTAL VARIANCE - S_1

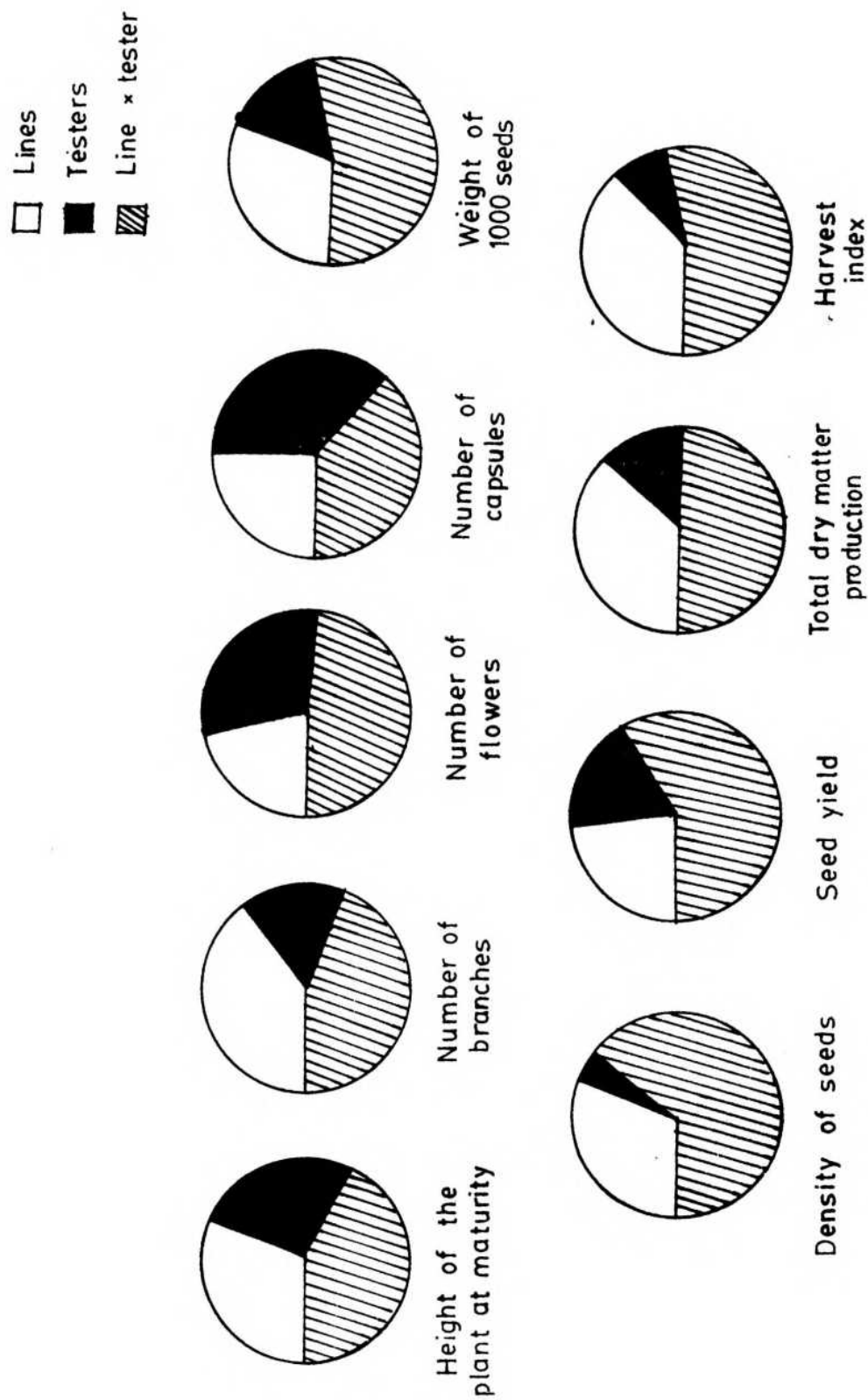


FIG.28.PROPORTIONAL PERCENTAGE CONTRIBUTION BY LINES, TESTERS AND LINE $\times$ TESTER INTERACTION TO THE TOTAL VARIANCE - S_2 .

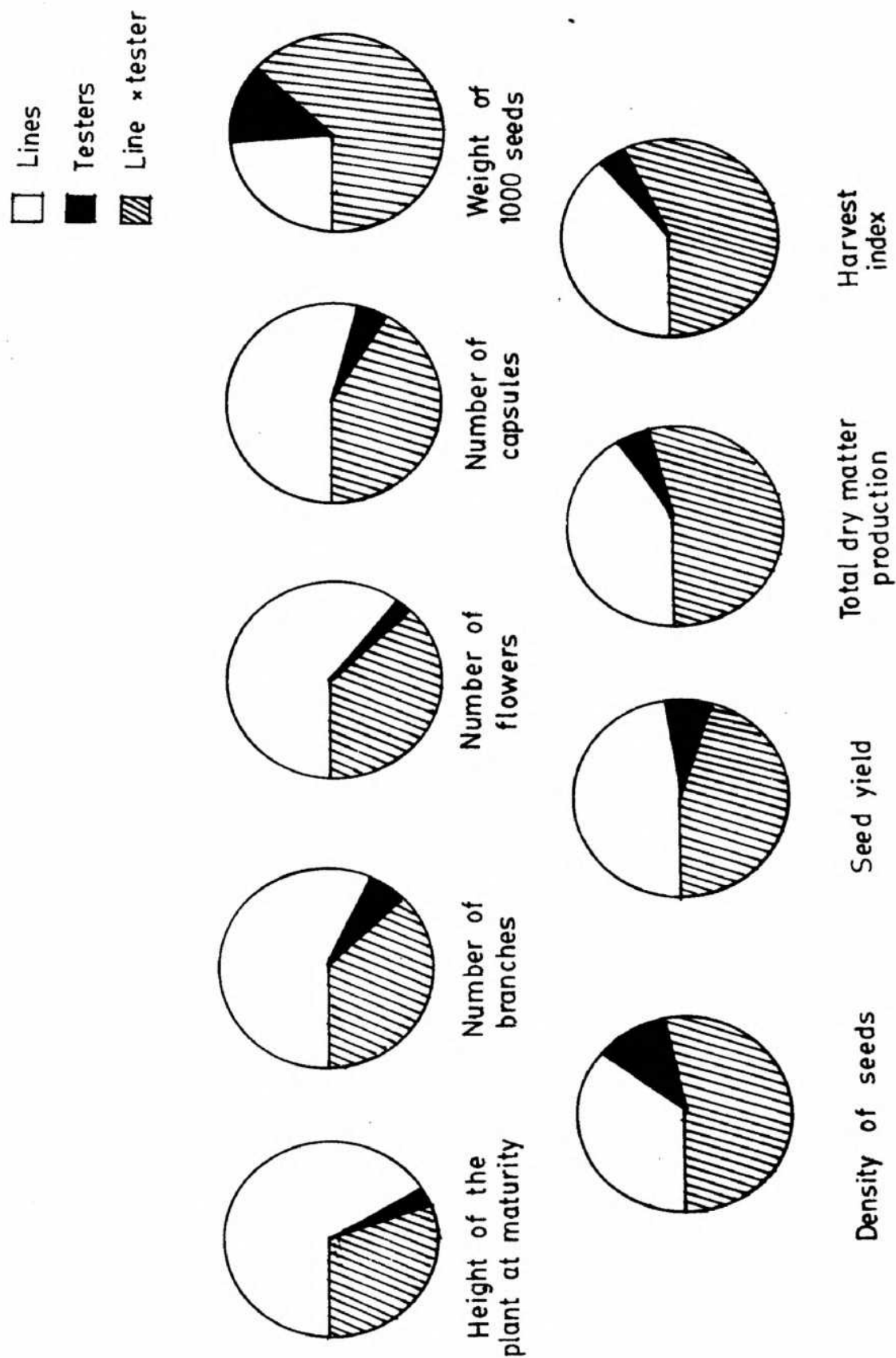


FIG.29. PROPORTIONAL PERCENTAGE CONTRIBUTION BY LINES, TESTERS AND LINE $\times$ TESTER INTERACTION TO THE TOTAL VARIANCE - POOLED ANALYSIS.

Lines
 Testers
 Line $\times$ tester

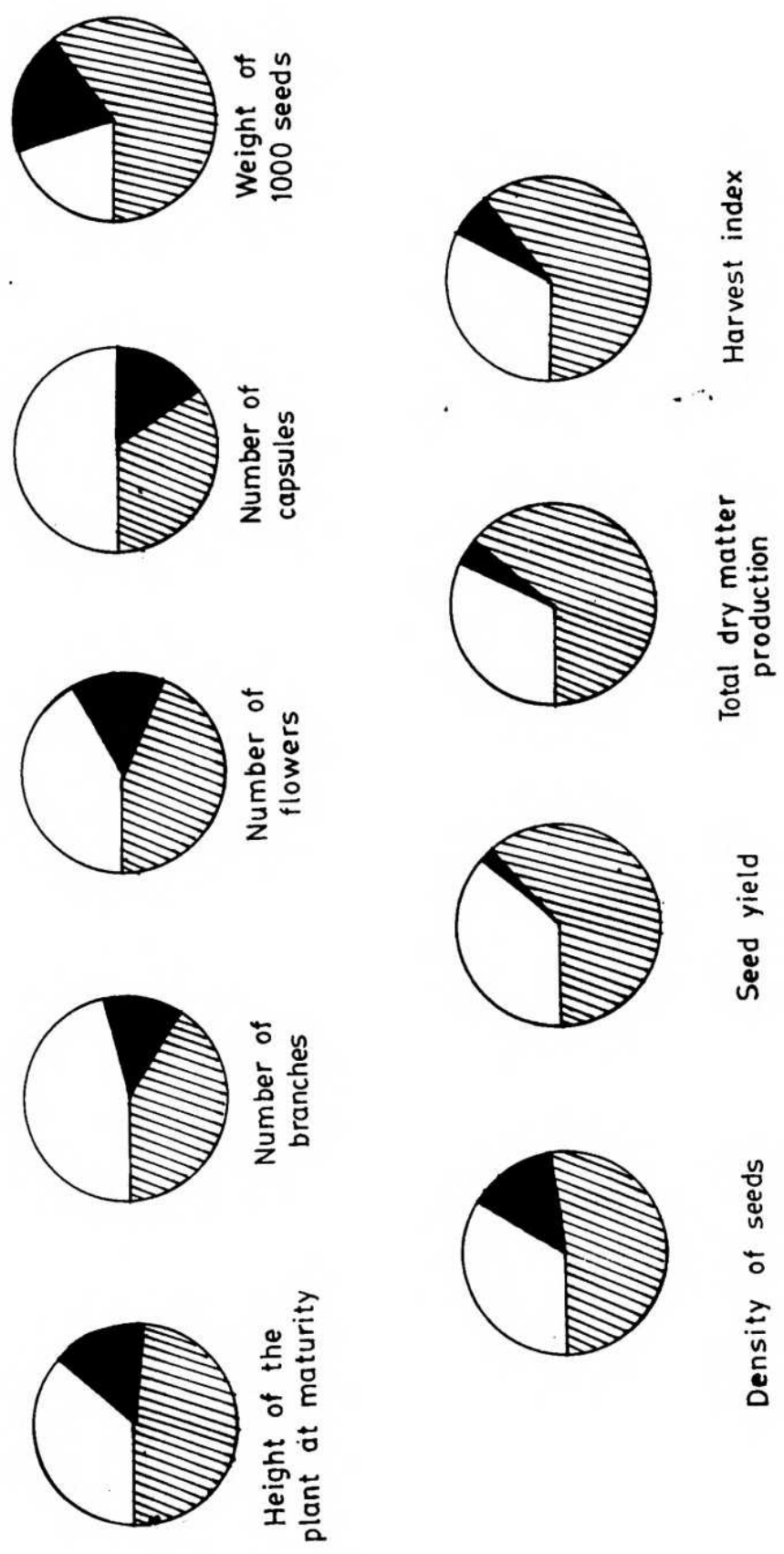


FIG. 30. RATIO OF GCA AND SCA VARIANCE

GCA Variance - S_1
 GCA Variance - S_2
 SCA Variance

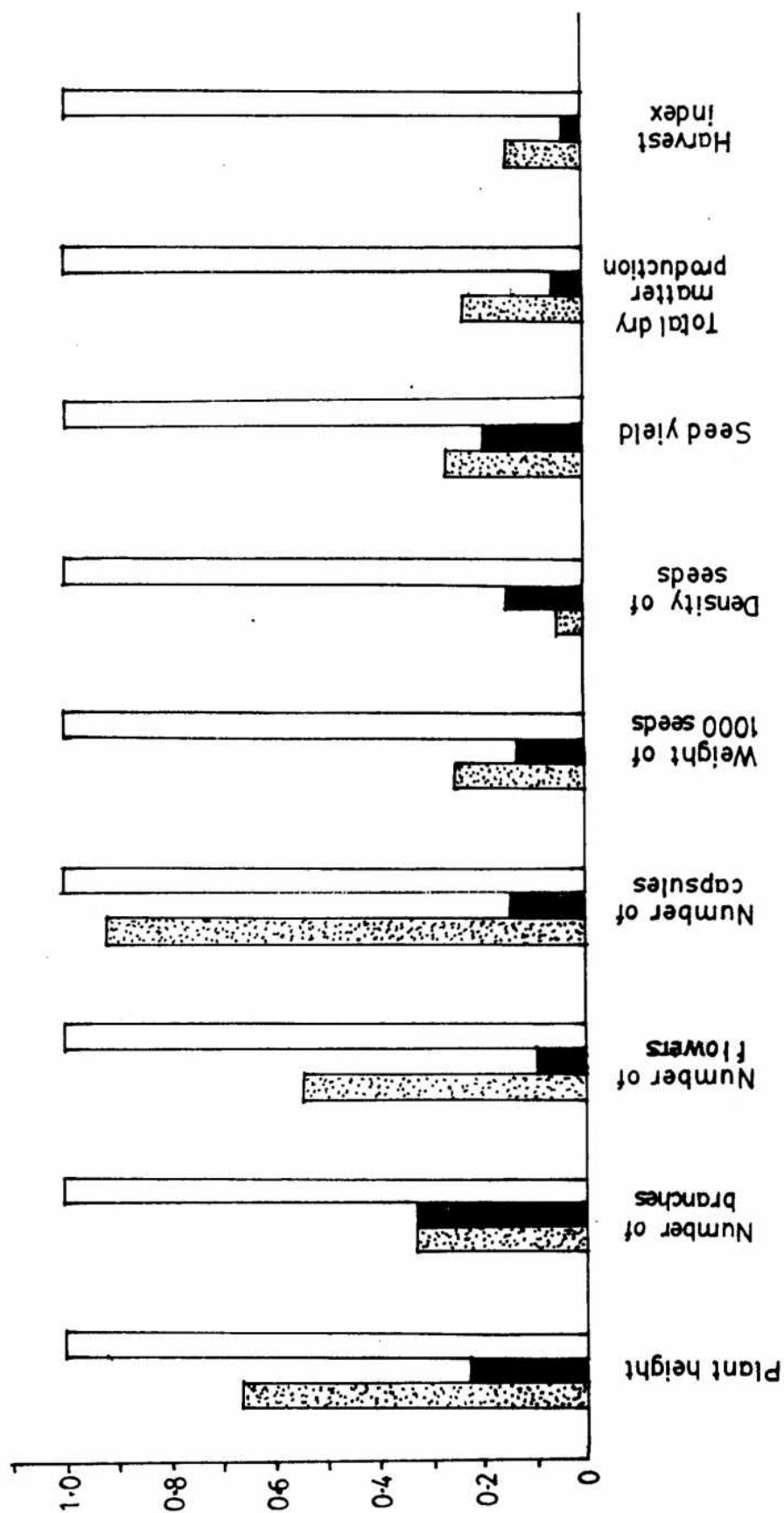
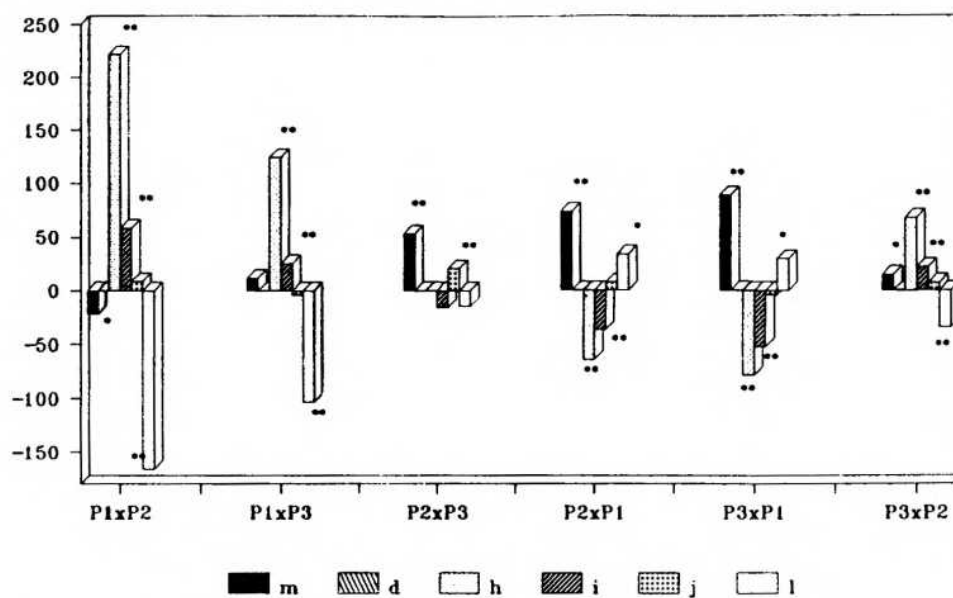


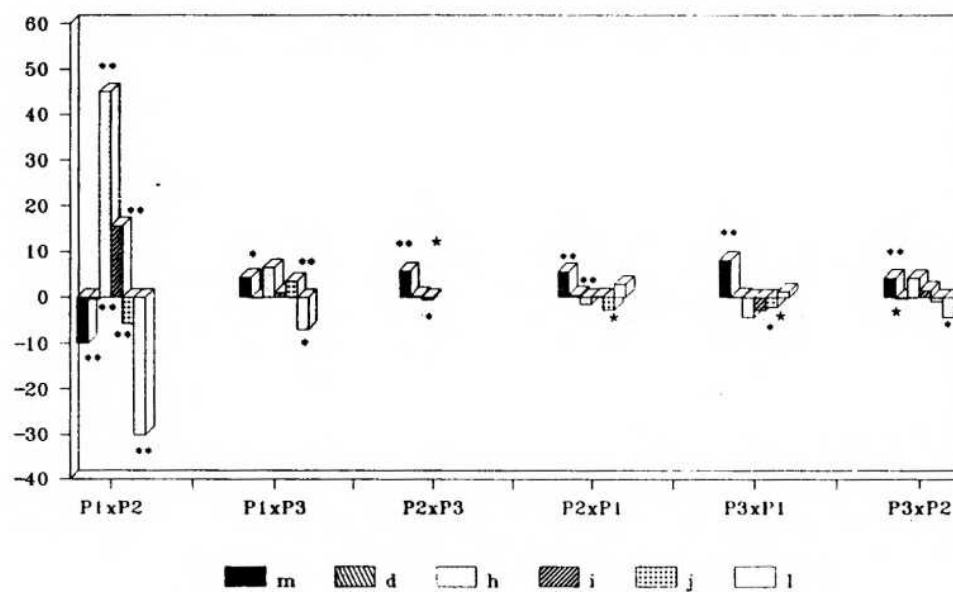
Fig.31 Genetic effects for height of the plant at maturity (cm)

924



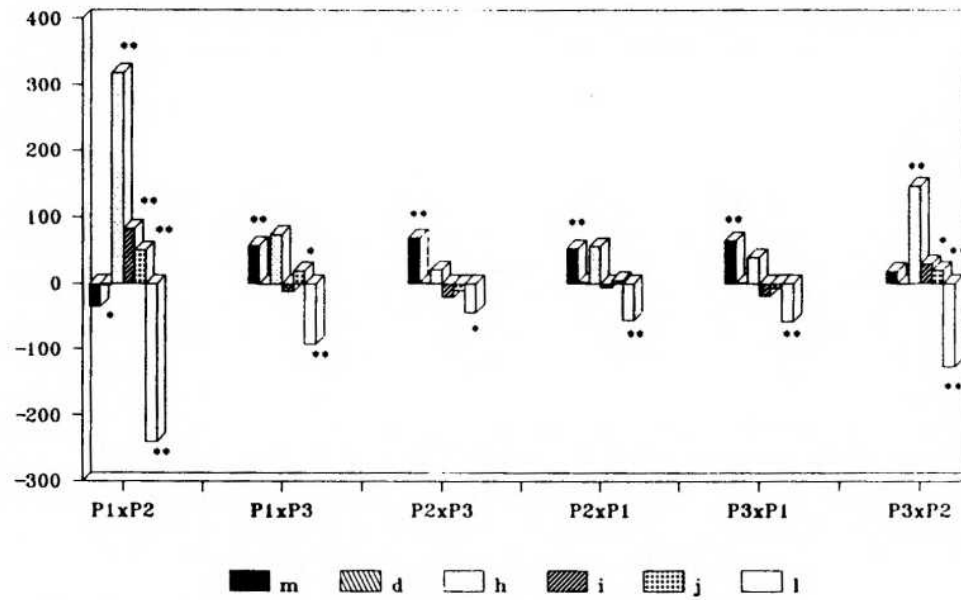
* Significant at P=5% level
 ** Significant at p=1% level

Fig.32 Genetic effects for number of branches



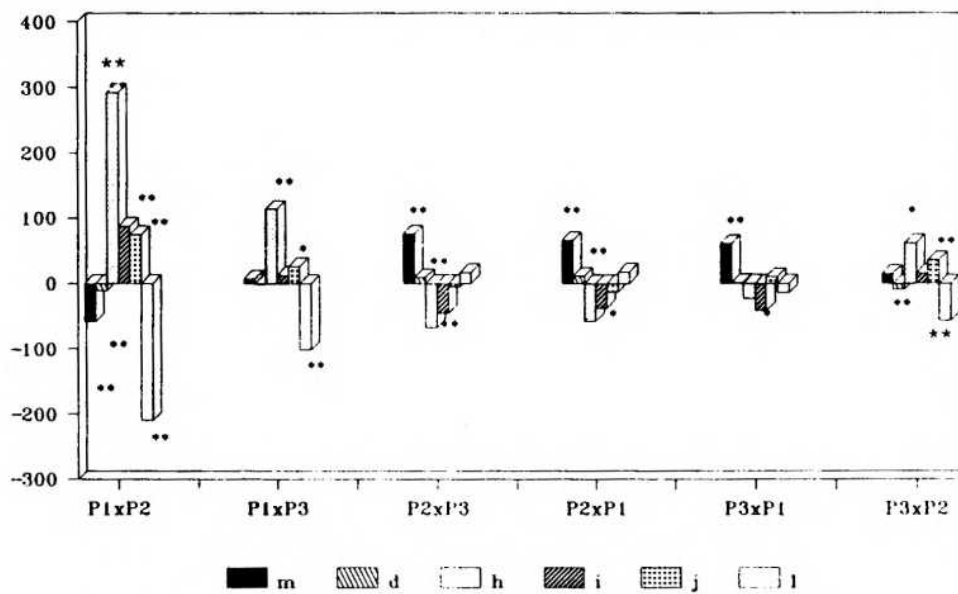
* Significant at P=5% level
 ** Significant at p=1% level

Fig.33 Genetic effects for number of flowers



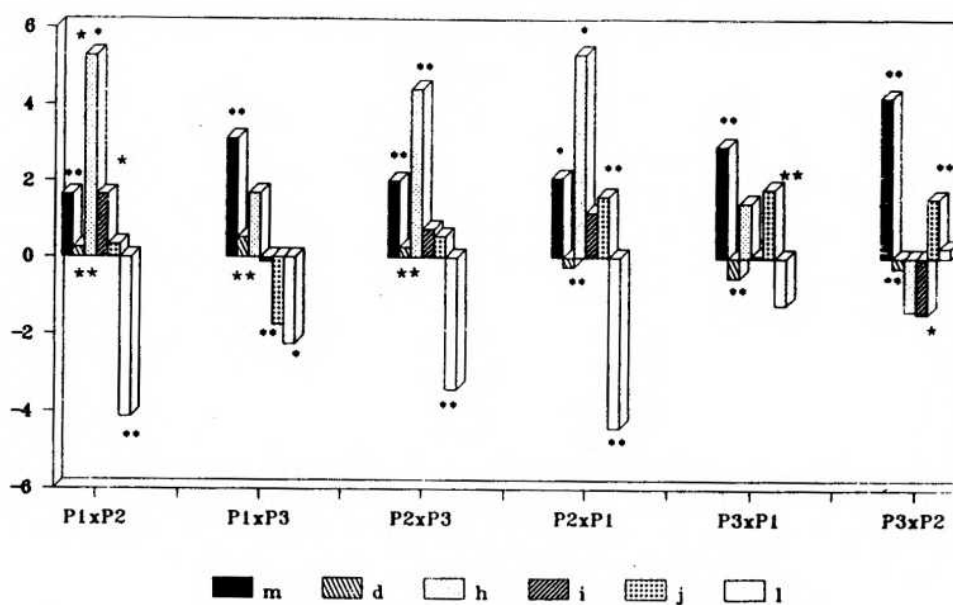
* Significant at P=5% level
 ** Significant at p=1% level

Fig.34 Genetic effects for number of capsules



* Significant at P=5% level
 ** Significant at p=1% level

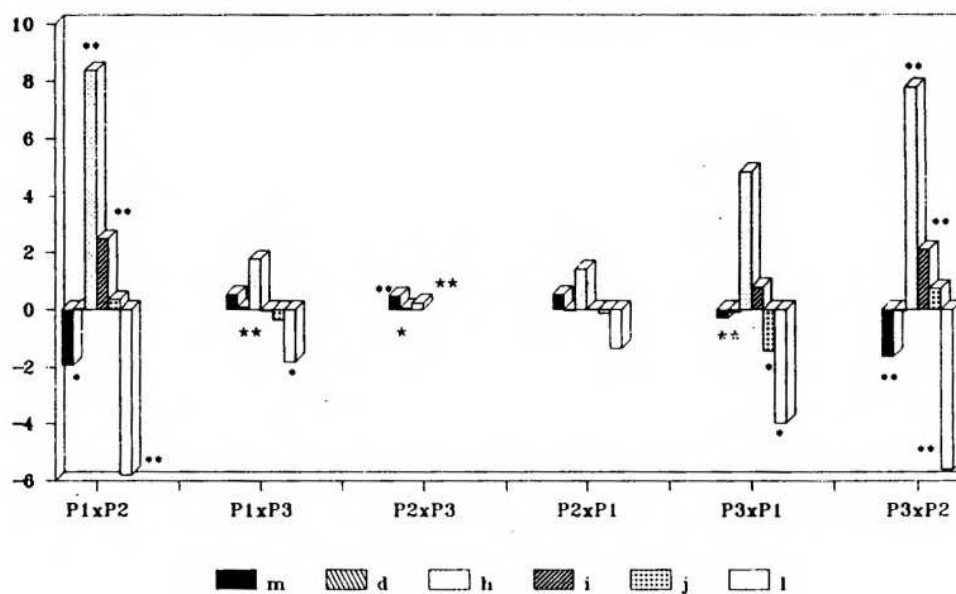
Fig. 35 Genetic effects for weight of
1000 seeds (g)



* Significant at P=5% level

** Significant at p=1% level

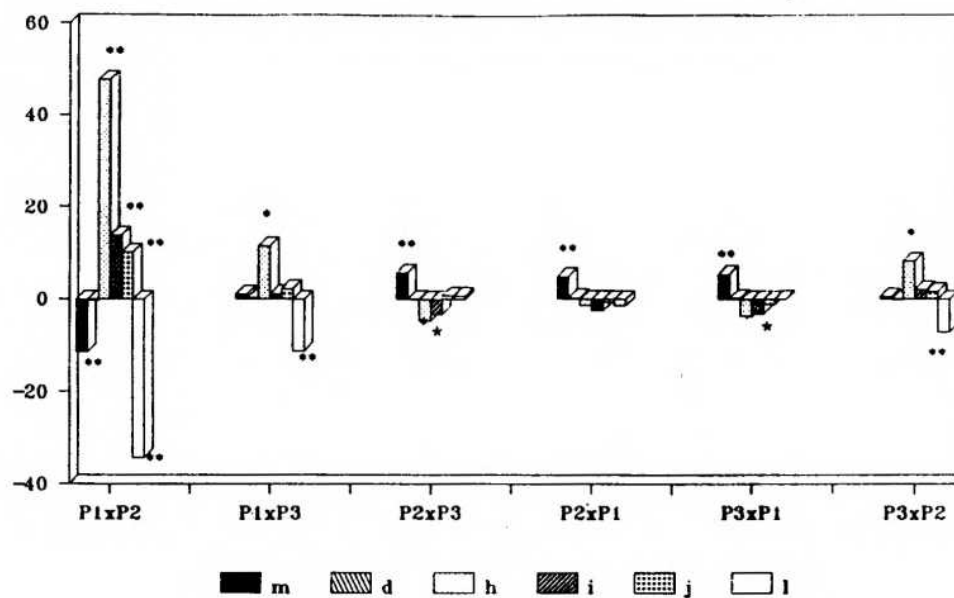
Fig. 36 Genetic effects for density of
seeds (g/ml)



* Significant at P=5% level

** Significant at p=1% level

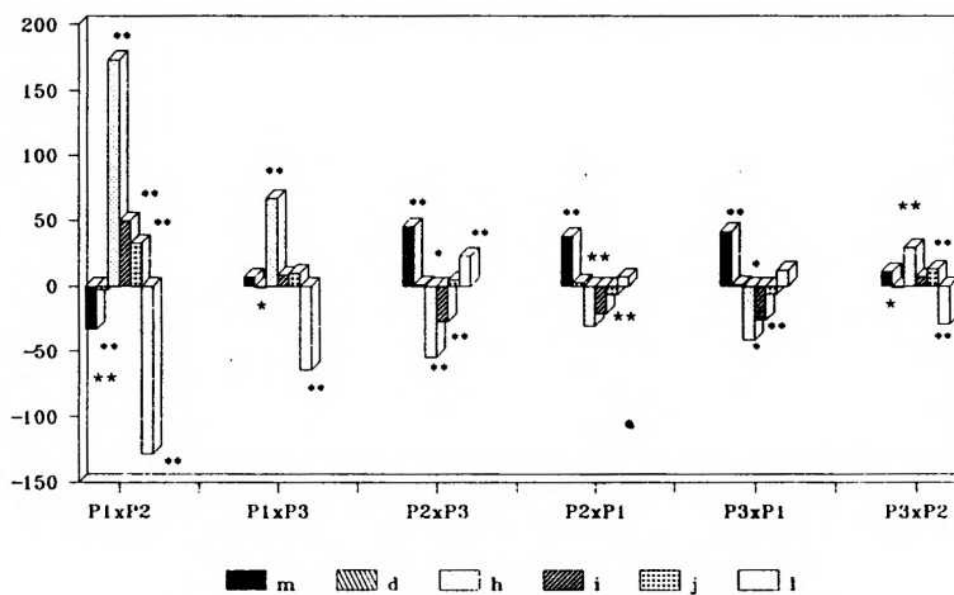
Fig. 37. Genetic effects for
seed yield (g)



* Significant at P=5% level

** Significant at p=1% level

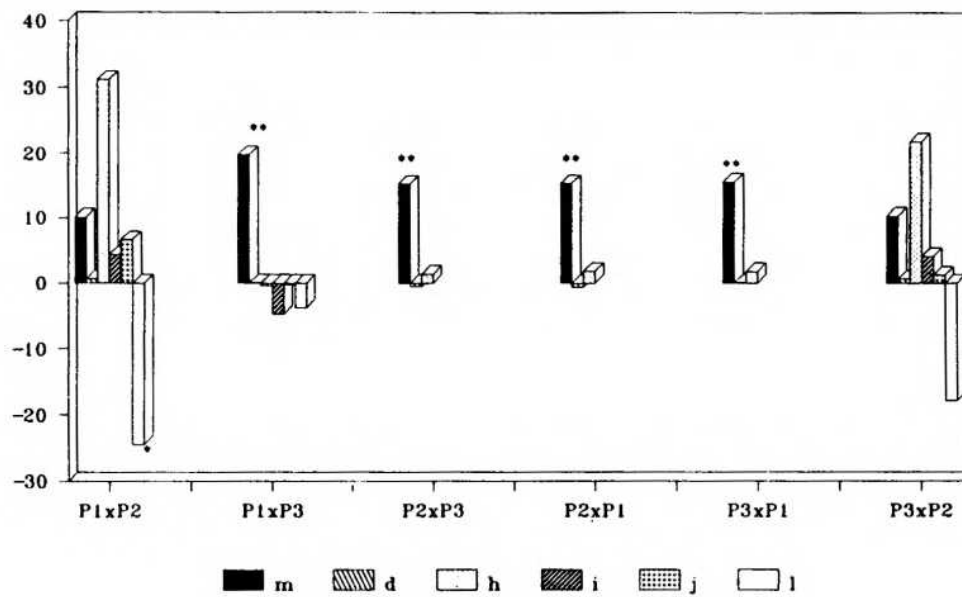
Fig.38. Genetic effects for total
dry matter production (g)



* Significant at P=5% level

** Significant at p=1% level

Fig. 39. Genetic effects for
harvest index (%)



* Significant at P=5% level

** Significant at p=1% level

Fig. 40 Breeding techniques adopted, identified traits and genotypes for future breeding programs

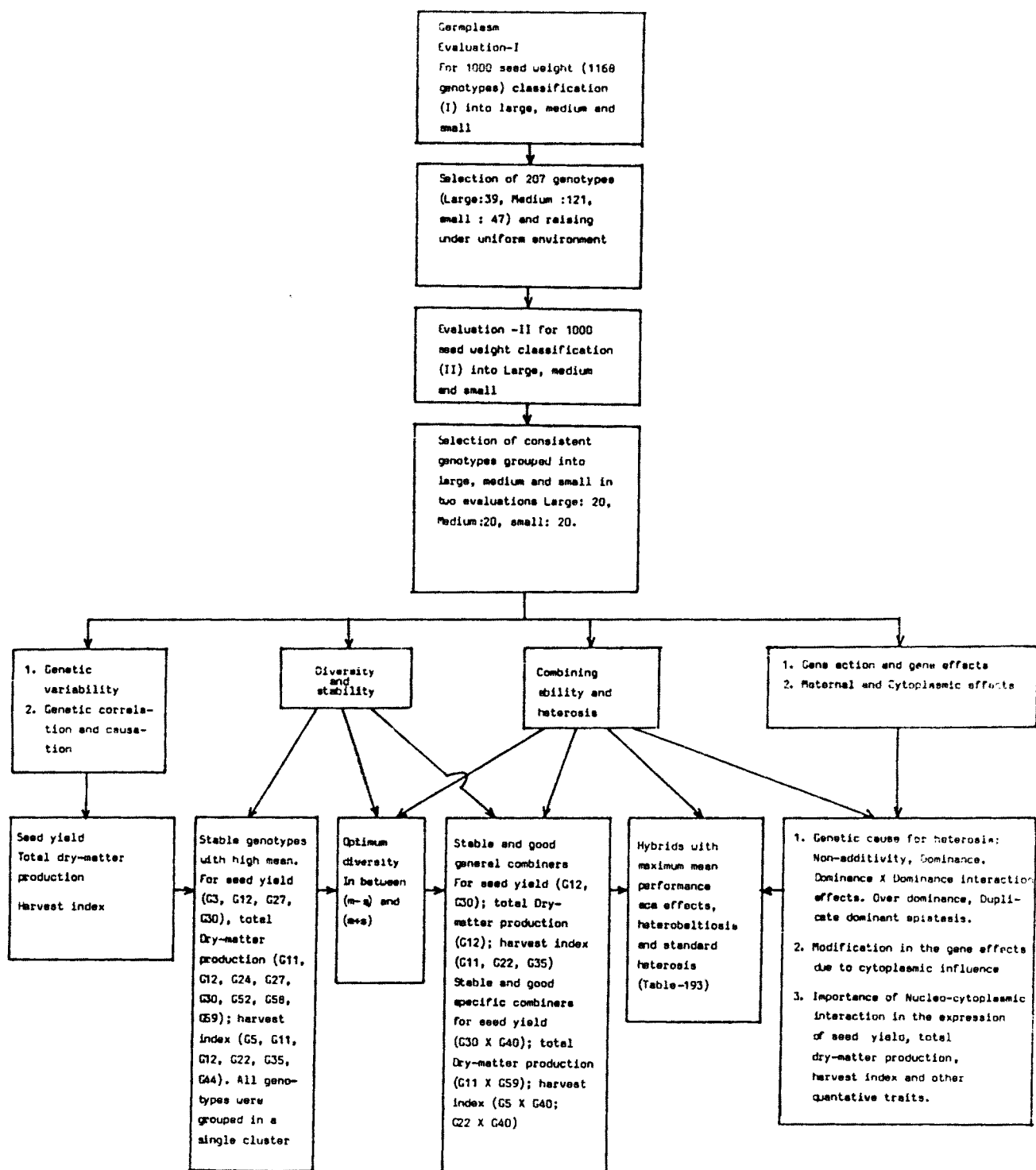
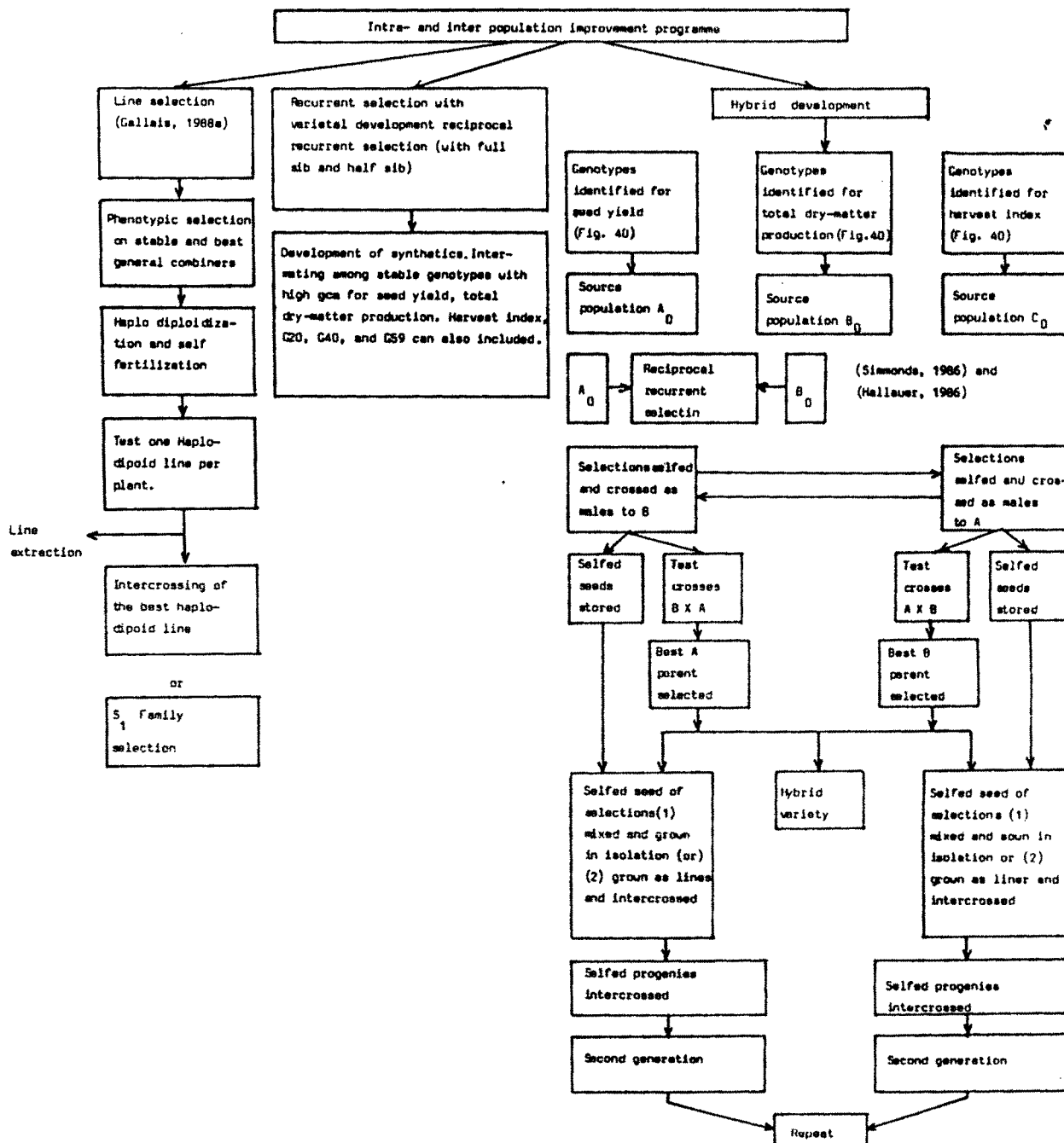


Fig. 41 Suggested future breeding programs



* The improved line may be crossed with C₀ similarly, if necessary.

APPENDICES

Table 1. Genotypes evaluated for 1000 seed weight and seed size grouping (First evaluation)

<u>S.No.</u>	<u>Genotypes</u>	<u>1000 seed weight (g)</u>	<u>S.No.</u>	<u>Genotypes</u>	<u>1000 Seed weight (g)</u>
1.	SMALL:				
	Less than mean - 1 SD (2.53g)				
1.	A - 6 - 13	2.20	31.	*IS.299	2.00
2.	AT.8	2.40	32.	IS - 482	2.38
3.	*AT - 9	2.20	33.	IS - 712	2.50
4.	B1(s) 100049	2.20	34.	JGL x 127	2.50
5.	BS - 5 - 18 - 6(a)	2.50	35.	JLT - 2	2.10
6.	BS - 5 - 18 - 6(G)	2.50	36.	JLT - 9	2.10
7.	C - 7	2.50	37.	JLT - 63 - 177	2.26
8.	C - 10	2.20	38.	LS - 62 - 10	2.34
9.	*C - 16	1.90	39.	Margo - 3	2.42
10.	Callona	2.30	40.	NAL-78-221/31.1	2.10
11.	*CIANNOO(27-1)	2.20	41.	NAL - 78 - 221-31-1-1	2.20
12.	CIANO 27/1	2.04	42.	NAL-78-221-31-2	2.24
13.	CIANO 27/3	2.50	43.	NAL-78-221-31-4	2.32
14.	CIANO 27/7	2.22	44.	NAL-78-304-43-4	2.40
15.	CIANO - 038/2	2.25	45.	NAL-78-304/43.5	2.20
16.	*CO 1	2.44	46.	NAL-78-304-43-18	2.24
17.	Corde Bore GA/18	2.16	47.	NAL-78-304-43-19	2.10
18.	DPI - 1484	2.30	48.	NAL-78-1624/1.1	2.30
19.	*EC. 137935	2.20	49.	NAL-79-111/4-3	2.36
20.	ES - 90	2.40	50.	NAL-79-111-4-5	2.42
21.	GANNO - 33 - 6	2.20	51.	NAL-79-111-4-10	2.50
22.	GANNO - 33 - 10	2.30	52.	NAL-79-111-4-11	2.40
23.	GANNO - 33 - 12	2.40	53.	NAL-79-111-4-12	2.38
24.	Gujarat T11 - 1	2.50	54.	*NAL-79-111-4-20	1.55
25.	Gujarat- 38	2.43	55.	NAL.79-111-79-5	2.50
26.	H.78.179 - 1	2.10	56.	NO.582	2.28
27.	*HT.6	2.30	57.	*NS-78-221-32-1	2.05
28.	INSI 16/1	2.40	58.	NS-78-221-32-2	2.14
29.	*IS - 102	2.06	59.	OLT-3	2.50
30.	*IS. 232	2.00	60.	OLT-7	2.50

61.	OLT - 19	2.42	91.	* S.0325	2.36
62.	OLT - 36	2.50	92.	* S.0328	2.32
63.	OLT - 41	2.44	93.	S.0330	2.32
64.	OLT - 43	2.35	94.	S.0331	2.05
65.	OTS - 1	2.40	95.	S.0368/1	2.50
66.	OTS - 2	2.20	96.	S.0373	2.40
67.	Popn. 1-2	2.50	97.	S.0377	2.40
68.	Pudukkottai - 6	2.46	98.	S.0379	2.20
69.	Pudukkottai - 16	2.38	99.	S.0396	2.48
70.	Pudukkottai - 23	2.42	100.	S.0405	1.90
71.	Pudukkottai - 27	2.24	101.	S.0413	2.50
72.	R - 2 - 352	2.50	102.	S.0414	2.50
73.	Rauss - 17 - 4	2.30	103.	S.0448	2.40
74.	RJS - 4	2.40	104.	S.0462	2.40
75.	RJS -5	2.47	105.	S.0463	2.42
76.	RSE-3	2.38	106.	S.0529	2.40
77.	RT - 4	2.50	107.	* S.0551	2.02
78.	RT - 44 IET	2.40	108.	* S.0554	2.14
79.	RT. 55	1.30	109.	S.0584	2.50
80.	S.0175	2.24	110.	S.0586	2.50
81.	S.0193	2.44	111.	S.0588	2.36
82.	S.0197	2.50	112.	S.0601	2.50
83.	S.0201	2.23	113.	S.0613	2.30
84.	S.0209	2.40	114.	S.0615	2.10
85.	*S.0210	1.80	115.	S.0618	2.30
86.	S.0216	2.42	116.	S.0625	2.50
87.	S.0217	2.50	117.	* S.00646	2.30
88.	S.0220	2.35	118.	S.00666	2.00
89.	S.0289	2.46	119.	S.0008	2.50
90.	*S.0321	2.30	120.	S.00095	2.45

121.	S.H.50	2.30	151.	VS.91	2.50
122.	S1.877	2.13	152.	YORRI - 77	2.00
123.	S1.957	2.10	153.	YORRI - 77 - 2	2.10
124.	S1.976	2.34	154.	51.276	2.44
125.	S1.983	2.48	155.	51.281	2.40
126.	S1.1050	2.45	156.	51.287	2.50
127.	S1.1166	2.49	157.	51.289	2.50
128.	S1.1167	2.47	158.	52.595	2.40
129.	S1.1240	2.50	159.	59.815	2.40
130.	S1.1720	2.47	160.	78.226	2.40
131.	S1.1841	2.28	161.	78.762	2.16
132.	S1.2123	2.35	162.	170 - 3 - A/5	1.60
133.	S1.2526	2.47	163.	250 A	2.40
134.	S1.2584	2.26	164.	470 - 3 - B - 1	2.20
135.	S1.2785	2.50	165.	470 - 3 - Bo - 3	2.40
136.	S1.3117	2.40	166.	470 - 3 - Bo - 4	2.50
137.	S1.3224	2.50	167.	470 - 3-Bo - 6	2.26
138.	S1.3279	2.30	168.	646 (A)	2.50
139.	Suwcon.9	2.50	169.	664 - 3 - Bo - 4	2.40
140.	Suwcon - 10	2.23	170.	664 - 3 - Bo - 5	2.10
141.	Suwcon - 16	2.08	171.	*672 - 3 -130 - 12	1.40
142.	Suwcon - 50	2.33	172.	722 - 300/2	2.13
143.	TC - 45	2.30	173.	724.3 - 130 - 4	2.50
144.	TC - 167	2.36	174.	724.300/2	2.10
145.	TC - 328	2.45	175.	724 - 390/1	2.40
146.	*TMV.6	2.50	176.	791 / 1-2	2.50
147.	TNAU - 12	2.40	177.	840 (A)	2.10
148.	Villupuram	2.40	178.	873 (A)	2.30
149.	VS - 48	2.50	179.	1210 (A)	2.10
150.	VS - 80	2.34	180.	7648	2.50

II. MEDIUM

In between mean + 1 SD (2.53 to 3.21 g)

1.	AT - 1	3.10	31.	Chagula Local - 5	2.80
2.	AT - 4	2.60	32.	Chagula Local - 6	3.00
3.	AT - 5	2.90	33.	CIANO 27/2	3.02
4.	AT - 7	3.10	34.	CIANO 27/4	2.60
5.	AT - 11	2.70	35.	CIANO 27/5	3.00
6.	AT - 12	2.98	36.	CIANO 27/6	2.70
7.	AT - 13	3.00	37.	CIANO 27/8	3.18
8.	AT - 14	3.10	38.	CIANO 27/8A	2.80
9.	AT - 16 IET	2.60	39.	CIANO 33/2	2.90
10.	B - 27	2.70	40.	CIANO 33/13	2.80
11.	B - 45	2.80	41.	Corde Bore G/1	2.60
12.	B - 67	2.80	42.	Corde Bore G/4	2.62
13.	B - 98	2.70	43.	Corde Bore G/5-1	2.82
14.	B - 406	2.70	44.	Corde Bore G/8	2.54
15.	Bangalore Local - 1	2.92	45.	Corde Bore G/11	2.70
16.	Bangalore Local - 2	3.20	46.	Corde Bore G/11-B	2.60
17.	Bharan Local	2.80	47.	Corde Bore G/12	2.72
18.	Bon of Japan - 1	2.60	48.	Corde Bore G/GA	3.08
19.	Bon of Japan - 2	3.00	49.	Corde bore G/15	2.60
20.	* B1(S) 100043	2.90	50.	Corde Bore GA/1	2.90
21.	BS - 5 - 18	2.94	51.	Corde Bore G0/18	2.70
22.	BS - 5 - 18 - 6	3.12	52.	CST - 721	2.80
23.	BS - 6 - 1	3.10	53.	CST - 781	2.80
24.	BS - 6 - 1 - 1	3.20	54.	CST - 781 A	2.80
25.	BS - 49	3.02	55.	CST - 782	2.70
26.	BS - 281 - 4	3.20	56.	CST - 782 A	2.70
27.	BS - 301 - 2	2.60	57.	CST - 782 B	2.60
28.	C - 6	3.20	58.	CST-782 C	2.67
29.	Chagula Local - 2	3.02	59.	CST - 783	3.00
30.	Chagula Local - 3	2.90	60.	D7 - 11 - 1 x TC -289	3.00

61.	D-7-11-1 x TC-289/2	3.00	91.	GANNO 33-5	2.70
62.	Dhandrar Local	2.90	92.	GANNO 33-7	2.60
63.	DPI - 1443	2.80	93.	GANNO 33-9	2.80
64.	E.8	2.90	94.	Gouri	2.64
65.	E.8-11-8	3.00	95.	Gulproga Local - 2	2.90
66.	EC.1328-28	2.96	96.	Hancam	3.00
67.	EC.137933	3.14	97.	HT.24	3.10
68.	EC.137933(A)	2.90	98.	IC.24981	3.10
69.	EC.137934	2.82	99.	INSI - 15/2-1	2.80
70.	EC.137935(A)	2.58	100.	INSI - 15/3	2.80
71.	EC.137936	3.00	101.	INSI- 15/4	2.60
72.	EC.137936 A	3.06	102.	INSI - 15/5	3.00
73.	EC.137937	2.56	103.	INSI-15/6	2.90
74.	EC.137937 A	2.90	104.	IS.31	2.70
75.	EC.137938	3.06	105.	IS.61	2.60
76.	EC.137938 A	2.62	106.	IS.76	3.20
77.	ES.19	2.76	107.	IS.210	2.97
78.	ES.43.659	3.00	108.	* IS.212	2.85
79.	ES.75	2.89	109.	IS.222	2.90
80.	ES.240	3.10	110.	IS.233	3.14
81.	ES.246	2.70	111.	IS.234	2.57
82.	ES.262	3.00	112.	IS.269	2.80
83.	ES.267	2.60	113.	IS.279	2.92
84.	ES.305	3.20	114.	IS.290	3.20
85.	ES.382	2.80	115.	IS.294	2.95
86.	ES.384	2.66	116.	IS.317	3.06
87.	ES.414	3.20	117.	IS.319	3.10
88.	G/2	3.10	118.	IS.333	2.90
89.	*G51266	2.80	119.	IS.334	3.00
90.	GANNO 33-4	2.80	120.	IS.341	2.60

121.	IS.342	2.80	151.	JT - 66 - 135	2.70
122.	IS.382	2.90	152.	K.2	2.90
123.	IS.388	2.80	153.	Kayamkulam	2.90
124.	IS.391	2.90	154.	KIS - 345	3.00
125.	IS.395	3.00	155.	KIS - 356	3.10
126.	IS.400	2.80	156.	KIS-357	3.20
127.	IS.401	3.00	157.	KRR.2	2.90
128.	IS.403	2.90	158.	Kurinja Padl S.00659	2.95
129.	IS.407	3.14	159.	Local - 1	3.10
130.	IS.409	2.88	160.	M -32	3.15
131.	IS.410	3.20	161.	Margo - 2	2.83
132.	IS.423	2.70	162.	Margo - 4	3.10
133.	IS.503	3.16	163.	Margo - 5	2.80
134.	IS.522	3.20	164.	* Margo - 7	2.90
135.	IS.523	3.16	165.	Margo - 8	3.00
136.	IS.572	3.15	166.	Margo - 10	3.02
137.	IS.655	3.00	167.	MT - 67 - 76	3.20
138.	IS.689	3.00	168.	N-66 - 173	3.00
139.	IS.693	3.04	169.	N-74-24	2.92
140.	IS.699	2.90	170.	N-139	2.80
141.	IS.709	3.10	171.	* N-369-50	2.90
142.	IS.739	3.20	172.	NAL - 78 - 164/5	2.90
143.	IS.842	2.60	173.	NAL-78-221-31-3	2.80
144.	JGL x 96	2.90	174.	NAL-78-221-31-8	2.54
145.	JGL x 136	2.90	175.	NAL-78-221-32-4	2.70
146.	JLSC - 8	2.70	176.	NAL-78-221-32-7	2.60
147.	JLT - 3	2.90	177.	NAL-78-221-311/9	2.90
148.	* JLT - 7	2.90	178.	NAL-78-304-43-2	2.60
149.	JT - 7	3.02	179.	NAL-78-304-43-10	3.00
150.	JT - 66 - 18	3.14	180.	NAL-78-304-43-13	2.82

181.	NAL-78-304-43-14	3.00	211.	OLT - 31	2.62
182.	NAL-79-111/4-1	2.60	212.	OLT-39	2.95
183.	NAL-79-111-4-7	2.60	213.	OLT - 44	2.62
184.	NAL-79-111-4-9	2.70	214.	OMT - 3	3.02
185.	NAL-79-111-4-14	2.80	215.	OTS - 3	2.55
186.	NAL-79-111-4-15	2.80	216.	OTS - 4	2.90
187.	NAL-79-111-4-18	2.90	217.	Palladam-3	3.02
188.	NAL-79-111-4-19	2.82	218.	Popn. 2-3-5	2.60
189.	NAL-79-111-5-1	2.60	219.	*Pudukkottai- 8	2.90
190.	NAL-79-111-79-1	2.70	220.	Pudukkottai - 19	2.60
191.	NAL-79-111-79-2	2.56	221.	Pudukkottai - 30	3.06
192.	NAL-79-111-79-3	3.08	222.	Pudukkottai - 31	2.70
193.	NAL-79-111-79-4	2.70	223.	Raichur Local - 1	2.94
194.	NAL-79-111-79-6	2.70	224.	RCR-2	3.00
195.	NO.2	2.70	225.	RCR-4	3.10
196.	NO.4	3.10	226.	RJS.30	2.56
197.	NO.6	2.98	227.	RJS.33	2.81
198.	NO.14+1	3.10	228.	RJS.34	2.60
199.	NO.25	3.00	229.	RJS.43	3.10
200.	NO.32	2.97	230.	RJS.52	3.00
201.	NO.128	2.60	231.	RJS.77/1	3.10
202.	NO.9525	2.70	232.	RJS.165	3.06
203.	NS-78-221-32-3	2.62	233.	RSE-1	2.90
204.	OLT - 5	2.90	234.	RSE.2	2.60
205.	OLT - 9	2.80	235.	RS.ME-1	3.00
206.	OLT-11	3.02	236.	RS.ME.2	2.92
207.	OLT-17	2.82	237.	S.011/4	3.10
208.	OLT-17(A)	3.10	238.	S.49	3.10
209.	OLT-18	2.70	239.	S.0130	2.96
210.	OLT-30	2.80	240.	S.0140	2.80

241.	S.0164	3.21	271.	S.0227	2.56
242.	S.0165	2.90	272.	S.0233	2.62
243.	S.0166	3.08	273.	S.0238	2.90
244.	S.0169	2.60	274.	S.0244	2.65
245.	S.0170	2.58	275.	S.0251	3.00
246.	S.0171	2.70	276.	S.0258	3.06
247.	S.0172	3.12	277.	S.0260	3.21
248.	S.0173	3.00	278.	S.0261	2.95
249.	S.0174	3.00	279.	S.0263	2.90
250.	S.0176	2.83	280.	S.0270	3.20
251.	S.0177	2.98	281.	S.0271	2.95
252.	S.0179	3.10	282.	S.0272	3.15
253.	S.0180	3.10	283.	S.0273	2.78
254.	S.0181	2.81	284.	S.0280	2.74
256.	S.0182	3.00	285.	S.0282	3.00
256.	S.0183	2.98	286.	S.0284	2.90
257.	S.0184	2.70	287.	S.0292	2.86
258.	S.0187	2.80	288.	S.0297	2.78
259.	S.0188	2.70	289.	S.0298	3.16
260.	S.0191	2.90	290.	S.0307	3.05
261.	S.0195	3.02	291.	S.0315	2.84
262.	S.0196	3.02	292.	S.0316	2.60
263.	S.0200	2.56	293.	S.0317	3.14
264.	S.0203	3.01	294.	S.0318	2.90
265.	S.0205	3.00	295.	S.0322	3.00
266.	S.0206	3.16	296.	S.0324	2.96
267.	S.0207	2.56	297.	*S.0327	2.86
268.	S.0219	3.15	298.	S.0329	2.70
269.	S.0224	2.55	299.	S.0335	2.90
270.	S.0226	2.99	300.	S.0332	3.10

301.	S.0337	2.70	331.	S.0403	2.98
302.	S.0338	2.96	332.	S.0404	2.88
303.	S.0340	3.16	333.	S.0406	2.55
304.	S.0341	2.90	334.	S.0407	2.70
305.	S.0342	2.60	335.	S.0408	3.04
306.	S.0344	2.78	336.	S.0409	3.00
307.	S.0347	2.74	337.	S.0410	2.60
308.	S.0348	2.92	338.	S.0411	2.70
309.	S.0351	3.10	339.	S.0416	2.90
310.	S.0352	3.00	340.	S.0429	2.66
311.	S.0362	2.80	341.	* S.0431	2.85
312.	S.0364	2.60	342.	S.0432	3.20
313.	S.0374	2.80	343.	S.0437	3.02
314.	S.0375	2.80	344.	S.0438	2.64
315.	S.0376	2.60	345.	S.0439	2.78
316.	S.0378	3.02	346.	S.0440/1	3.10
317.	S.0380	2.90	347.	S.0441	2.60
318.	S.0381	3.14	348.	S.0443	3.10
319.	S.0383	2.80	349.	S.0444	3.02
320.	S.0384	2.60	350.	S.0445	2.52
321.	S.0388	2.70	351.	S.0446	3.10
322.	S.0389	3.14	352.	S.0449	3.14
323.	S.0390	2.78	353.	S.0450	2.98
324.	S.0391	3.08	354.	S.0451	2.80
325.	S.0392	2.60	355.	S.0452	2.62
326.	S.0393	2.68	356.	S.0453	3.04
327.	S.0395	3.20	357.	S.0454	2.80
328.	S.0397	2.70	358.	S.0455	3.12
329.	S.0400	3.04	359.	S.0456	2.70
330.	S.0401	2.56	360.	S.0460	2.62

361.	S.0464	2.90	391.	S.0534	2.90
362.	S.0465	3.04	392.	S.0535	2.70
363.	S.0467/3	2.80	393.	S.0536	2.80
364.	S.0468/2	2.58	394.	S.0537	2.60
365.	S.0469	2.80	395.	S.0538	2.80
366.	S.0470	2.60	396.	S.0539	2.60
367.	S.0472	2.90	397.	S.0540	3.00
368.	S.0474	2.70	398.	S.0541	2.60
369.	S.0475	3.10	399.	S.0542	2.92
370.	S.0477	2.70	400.	S.0543	2.98
371.	S.0479	3.00	401.	S.0544	2.76
372.	S.0481	2.70	402.	S.0545	2.82
373.	S.0490	3.20	403.	S.0546	2.84
374.	S.0496	3.00	404.	S.0547	2.84
375.	S.0501	2.90	405.	S.0548	2.95
376.	S.0506	2.70	406.	S.0549	2.60
377.	S.0508	2.60	407.	S.0550	2.80
378.	S.0509	3.00	408.	S.0552	2.82
379.	S.0511	2.70	409.	S.0553	2.64
380.	S.0512	3.20	410.	S.0574	3.04
381.	S.0513	2.60	411.	S.0575	3.00
382.	S.0514	3.03	412.	S.0585	2.70
383.	*S.0516	2.85	413.	S.0587	3.00
384.	S.0517	3.20	414.	S.0589	2.80
385.	S.0519	3.00	415.	S.0598	2.60
386.	S.0520	2.80	416.	S.0600	2.70
387.	S.0523	2.70	417.	*S.0604	2.90
388.	S.0530	2.60	418.	S.0606	2.60
389.	S.0531	2.80	419.	*S.0607	2.90
390.	S.0533	3.20	420.	S.0610	3.00

421.	S.0611	3.00	451.	S.00641	2.60
422.	S.0612	2.70	452.	S.00642	2.70
423.	S.0616	3.00	453.	S.00643	2.62
424.	S.0617	2.80	454.	S.00644	2.64
425.	S.0630	2.80	455.	S.00645	2.54
426.	S.0632	3.00	456.	S.00647	2.80
427.	*S.0639	2.60	457.	S.00648	3.02
428.	S.0671	3.20	458.	S.00649	2.80
429.	S.0766	2.70	459.	S.00650	2.70
430.	S.0784	2.90	460.	S.00651	2.72
431.	S1.3315/4	3.18	461.	S.00652	3.00
432.	S.7615	2.90	462.	S.00652 (A)	2.84
433.	S.7617	2.54	463.	S.00653	3.00
434.	S.7618	3.04	464.	S.00656	3.20
435.	S.7619	3.10	465.	S.00667	3.00
436.	S.7623	2.94	466.	S.00668	2.60
437.	S.7624	3.00	467.	S.0002/1	2.87
438.	S.7626	3.10	468.	S.00040	3.16
439.	S.7640	2.70	469.	S.00049	3.10
440.	S.11929	3.02	470.	S.00055	3.14
441.	S.0010	3.07	471.	S.00057	3.17
442.	S.0014/3	2.72	472.	S.00059	2.89
443.	S.0025	3.00	473.	S.00064	3.10
444.	S.00101	2.80	474.	SH. 97	2.70
445.	S.00635	2.62	475.	S1.11 (5)	3.08
446.	S.00636	2.82	476.	S1.44	2.82
447.	S.00637	2.92	477.	S1.47	2.60
448.	S.00638	2.80	478.	S1.48	2.81
449.	S.00639	2.88	479.	S1.52	2.66
450.	S.00640	2.70	480.	S1. 56	2.64

GUL

481.	\$1.57	2.91	511.	\$1.784	2.88
482.	\$1.58	3.17	512.	\$1.789	3.06
483.	\$1.59	3.00	513.	\$1.853	3.17
484.	\$1.65	2.78	514.	\$1.855	2.94
485.	\$1.66	3.08	515.	\$1.858	2.82
486.	\$1.68	2.83	516.	\$1.864	2.81
487.	\$1.71	3.05	517.	\$1.865	2.56
488.	\$1.72	2.65	518.	\$1.866	3.02
489.	\$1.73	3.19	519.	\$1.867	3.07
490.	\$1.75	2.72	520.	\$1.868	2.94
491.	\$1.76	2.84	521.	\$1.871	2.73
492.	\$1.242	3.15	522.	\$1.872	3.16
493.	\$1.244	2.83	523.	\$1.882	3.08
494.	\$1.245	3.08	524.	\$1.885	3.15
495.	\$1.247	2.67	525.	\$1.889	3.06
496.	\$1.250	3.06	526.	\$1.898	3.05
497.	\$1.251	2.82	527.	\$1.902	3.17
498.	\$1.253	2.94	528.	\$1.909	2.92
499.	\$1.255	2.75	529.	\$1.911	3.09
500.	\$1.256	3.14	530.	\$1.917	2.84
501.	\$1.258	2.72	531.	\$1.918	2.65
502.	\$1.259	2.74	532.	\$1.919	2.70
503.	\$1.260	2.82	533.	\$1.921	2.81
504.	\$1.282	3.20	534.	\$1.923	2.79
505.	\$1.0335	2.94	535.	\$1.924	3.00
506.	\$1.0439	2.82	536.	\$1.925	3.14
507.	\$1.503	3.10	537.	\$1.926	3.06
508.	\$1.765	2.72	538.	\$1.928	2.95
509.	\$1.770	3.15	539.	\$1.931	3.04
510.	\$1.771	3.06	540.	\$1.935.	2.93

541.	S1.945	3.10	571.	S1.1058	3.00
542.	* S1.953	2.86	572.	S1.1059	2.54
543.	S1.963	3.20	573.	S1.1060	2.81
544.	S1.964	2.73	574.	S1.1061	3.08
545.	S1.967	2.99	575.	S1.1062	3.00
546.	S1.968	2.60	576.	S1.1063	3.19
547.	S1.972	2.74	577.	S1.1065	3.15
548.	S1.978	2.56	578.	S1.1066	2.67
549.	S1.981	2.56	579.	S1.1074	3.14
550.	S1.988	2.73	580.	S1.1107	3.00
551.	S1.990	2.56	581.	S1.1115	2.94
552.	S1.994	2.65	582.	S1.1116	3.01
553.	S1.1001	2.78	583.	S1.1125	3.16
554.	S1.1002	3.10	584.	S1.1139	3.15
555.	S1.1003	2.95	585.	S1.1141	2.94
556.	S1.1004	3.00	586.	S1.1144	2.96
557.	S1.1006	3.20	587.	S1.1146	3.17
558.	S1.1012	3.00	588.	S1.1151	3.12
559.	S1.1013	3.14	589.	S1.1153	3.01
560.	S1.1017	2.84	590.	S1.1156	3.10
561.	S1.1018	3.05	591.	S1.1161	3.15
562.	S1.1024	3.00	592.	S1.1162	2.75
563.	S1.1029	3.21	593.	S1.1163	3.15
564.	S1.1032	2.81	594.	S1.1165	3.10
565.	S1.1035	2.56	595.	S1.1169	2.63
566.	S1.1036	3.06	596.	S1.1170	2.56
567.	S1.1045	2.95	597.	S1.1171	2.93
568.	S1.1052	2.81	598.	S1.1172	2.90
569.	S1.1056	2.95	599.	S1.1173	3.20
570.	S1.1057	3.00	600.	S1.1225	2.96

601.	S1.1211	3.00	631.	S1.1672	3.20
602.	* S1.1249	2.86	632.	* S1.1702	2.90
603.	S1.1277	3.00	633.	S1.1711	3.00
604.	S1.1366	3.20	634.	S1.1712	2.79
605.	S1.1391	3.00	635.	S1.1713	3.20
606.	S1.1400 (A)	2.95	636.	S1.1719	3.10
607.	S1.1451	3.10	637.	S1.1721	3.01
608.	S1.1453	3.00	638.	S1.1722	3.00
609.	S1.1460	3.16	639.	S1.1723	2.98
610.	S1.1482	2.97	640.	S1.1724	3.00
611.	S1.1483	3.09	641.	S1.1727	3.00
612.	S1.1484	3.15	642.	S1.1729	3.15
613.	S1.1498	3.10	643.	S1.1730	3.13
614.	S1.1500	2.90	644.	S1.1740	3.00
615.	S1.1505	3.00	645.	* S1.1755	2.86
616.	S1.1508	3.16	646.	S1.1760	3.00
617.	S1.1509	3.00	647.	S1.1770	2.96
618.	S1.1513	3.21	648.	S1.1777	2.67
619.	S1.1543	2.74	649.	S1.1780	2.71
620.	S1.1560	3.10	650.	S1.1782	2.67
621.	S1.1577	3.10	651.	S1.1784	2.76
622.	S1.1582	3.01	652.	S1.1785	2.60
623.	S1.1585	3.20	653.	S1.1855	3.20
624.	S1.1588	2.80	654.	S1.1865	2.91
625.	S1.1601	2.54	655.	S1.1867/2	2.81
626.	S1.1608	2.67	656.	S1.1875	3.10
627.	S1.1611	3.00	657.	S1.1885	3.00
628.	S1.1665	2.80	658.	S1.1926	2.82
629.	S1.1667	3.00	659.	S1.1982	2.75
630.	S1.1671	3.10	660.	S1.2138	2.97

945

661.	S1.2167	2.57	691.	S1.3218	2.90
662.	S1.2175	2.76	692.	S1.3223	3.00
663.	S1.2176	2.79	693.	S1.3232	2.70
664.	S1.2179	2.84	694.	S1.3236	2.92
665.	S1.2188	2.70	695.	S1.3252	2.90
666.	S1.2225	2.95	696.	S1.3268	3.10
667.	S1.2439	3.06	697.	S1.3269	3.20
668.	S1.2572	3.04	698.	S1.3271	2.62
669.	S1.2573	3.21	699.	S1.3273	2.84
670.	S1.2575	3.00	700.	S1.3274	2.90
671.	S1.2580	3.17	701.	S1.3276	2.60
672.	S1.2582	3.20	702.	S1.3278	2.92
673.	S1.2636	3.06	703.	S1.3281	2.70
674.	* S1.2678	2.86	704.	S1.3282	2.60
675.	S1.2993	3.20	705.	S1.3286	2.80
676.	S1.3004	3.10	706.	S1.3287	3.10
677.	S1.3055	2.90	707.	S1.3291	2.84
678.	S1.3084	3.00	708.	S1.3296	2.90
679.	S1.3089	3.00	709.	S1.3299	3.01
680.	S1.3093	3.10	710.	S1.3315/5	3.00
681.	S1.3113	2.56	711.	S1.3315/10	3.14
682.	S1.3118	3.10	712.	S1.3318	3.16
683.	S1.3119	3.00	713.	SP-1184	2.72
684.	S1.3169	3.10	714.	SP-1185	2.70
685.	S1.3170	3.00	715.	Suwcon-5	2.60
686.	S1.3171	3.00	716.	Suwcon-5A	2.60
687.	* S1.3175	2.85	717.	Suwcon - 6	3.10
688.	S1.3178	2.58	718.	Suwcon - 7	2.54
689.	S1.3189	3.10	719.	Suwcon- 9 (a)	2.80
690.	S1.3216	2.70	720.	Suwcon-97	2.70

721.	T-1	3.00	751.	X 99-9-9-8	2.54
722.	T-10	2.90	752.	X-495-X7-3-1	2.90
723.	TC - 16	2.52	753.	X-791/1-1	2.60
724.	TC - 25	2.60	754.	YORRI 77-3	3.20
725.	TC - 30	2.80	755.	YORRI-77-4	2.70
726.	TC - 229	2.70	756.	YORRI-77-5	2.97
727.	Típus 1-8	3.04	757.	3/2 Kanda	3.20
728.	* TMV - 4	2.89	758.	0005/1	2.79
729.	TMV - 5	2.70	759.	0007/1	2.80
730.	T.4	2.74	760.	0007/11	2.90
731.	TNAU - 6	2.84	761.	0008/1	2.70
732.	TNAU-10	2.54	762.	16 IET	2.60
733.	TNAU - 11	3.02	763.	0036/3	3.14
734.	T.Prr 1-2	3.20	764.	51.262	2.94
735.	UT-43	2.73	765.	51.264	2.96
736.	Vinayak (m)	2.90	766.	51.265	2.80
737.	VS-2	2.82	767.	51.266	2.86
738.	VS - 16 CUL	2.90	768.	51.267	3.16
739.	VS - 27 IET	2.72	769.	51.268	2.86
740.	VS - 44	2.90	770.	51.269	2.94
741.	VS - 49	2.96	771.	51.270	2.92
742.	VS - 69	3.06	772.	51.271	3.10
743.	VS - 71	2.70	773.	51.273	3.14
744.	VS - 81	2.62	774.	51.274	2.72
745.	VS - 90	2.60	775.	51.275	3.04
746.	X 70 - 1 - 9	2.62	776.	51.277	2.72
747.	X 73 - 13	3.00	777.	51.278	2.94
748.	X 77 - 550	2.80	778.	51.279	2.98
749.	X 79 - 1-4	2.70	779.	51.280	2.66
750.	X 79- 1 - 5	2.70	780.	51.282	2.98

781.	51.286	3.08	811.	79.228	2.70
782.	6.51.288	2.80	812.	180.20N	3.20
783.	51.4271	2.78	813.	282 (A)	3.00
784.	54.055	3.00	814.	294 (A)	3.00
785.	54.056	3.12	815.	394 (A)	3.10
786.	55822/1	3.20	816.	470 - 3-80 - 2	2.60
787.	55.823	2.86	817.	470 - 3-Bon	3.10
788.	59.812	2.90	818.	637 A	2.80
789.	59.813	3.00	819.	653 (A)	2.90
790.	59.814	2.60	820.	672.3 - Bo-1	3.10
791.	59.816	2.83	821.	679-715	2.70
792.	59.817	2.80	822.	687 (A)	2.80
793.	59.818	3.02	823.	704 A	2.90
794.	78.15/1	3.04	824.	724 - Bon	2.60
795.	78.263	2.90	825.	724 - 3 - 130.2	2.60
796.	78.267	2.80	826.	740 (A)	3.10
797.	78.290	2.80	827.	751 (A)	2.70
798.	78.294	2.60	828.	791/1-3	2.70
799.	78.301	3.00	829.	862 (A)	3.20
800.	78.314	2.80	830.	866 (A)	2.70
801.	78.326	2.70	831.	1041 (A)	3.20
802.	78.327	3.10	832.	1104 (A)	2.70
803.	78.330	3.10	833.	1124 (A)	2.80
804.	78.390	3.12	834.	1151 (A)	2.60
805.	78.478	2.96	835.	1270 (A)	2.70
806.	78.486	3.12	836.	1289 (A)	2.90
807.	78.505	2.56	837.	1869-59-820	2.80
808.	78.595	2.62	838.	1869-59-825	2.90
809.	78.819	3.06	839.	1869-59-827	3.10
810.	79.3	2.70	840.	1875-59-826	2.70

840.	1877-59-828	2.90	16.	RJS.1	3.46
842.	1881-59-833	2.80	17.	RJS.40	3.24
843.	1980-R-50-29	2.80	18.	RJS.54	3.55
844.	1980-R-50-31	3.00	19.	RJS.71	3.61
845.	1980-R-52-12	3.04	20.	RJS.80	3.72
846.	1980-R-52-72	2.70	21.	RJS.81	3.36
847.	7614	3.20	22.	RJS.90	3.40
848.	7617	3.00	23.	RJS.144	3.36
849.	7619	2.80	24.	RJS.148	3.51
850.	7624	2.70	25.	RJS.218	3.60
851.	7626	2.80	26.	RS.1	3.60
852.	7640	2.96	27.	S.0126	3.60
853.	7770	3.00	28.	S.0167	3.56
III.	LARGE:		29.	S.0168	3.60
	Greater than mean + 1 SD (3.21 g)		30.	S.0186	3.30
1.	AT 2	3.30	31.	S.0189	3.23
2.	EC.1328-29	3.40	32.	S.0190	3.25
3.	EC.1328-30	3.70	33.	* S.0218	3.90
4.	ES.300	3.40	34.	S.0225	3.26
5.	ES.418	3.24	35.	S.0229	3.40
6.	IS.37(S)	3.30	36.	S.0265	3.26
7.	IS.231	3.36	37.	S.0269/1	3.31
8.	IS.237	3.32	38.	S.0274	3.26
9.	IS.252	3.26	39.	S.0278	3.31
10.	IS.292/4	3.61	40.	S.0281	3.44
11.	* IS.298	3.46	41.	S.0288	3.50
12.	IS.316	3.36	42.	S.0294	3.44
13.	IS.424	3.65	43.	S.0296	3.36
14.	IS.514	3.36	44.	S.0311	3.32
15.	IS.526	3.30	45.	S.0312	3.24

46.	S.0314	3.51	77.	S1.0476	3.30
47.	S.0361	3.50	78.	S1.1025	3.24
48.	S.0424	3.40	79.	S1.1027	3.29
49.	S.0447	3.70	80.	* S1.1033	3.85
50.	S.0459	3.24	81.	S1.1041	3.30
51.	S.0471	3.40	82.	S1.1072	3.44
52.	*S.0476	3.40	83.	* S1.1075	3.95
53.	S.0482	3.28	84.	* S1.1088	3.75
54.	S.0515	3.40	85.	S1.1121	3.70
55.	S.7648	3.27	86.	S1.1143	3.36
56.	S.00634	3.40	87.	S1.1145	3.24
57.	S.00018	3.56	88.	* S1.1147	3.74
58.	* S.00027	3.80	89.	S1.1149	3.35
59.	* S.00028	4.23	90.	* S1.1150	3.74
60.	* S.00033	3.81	91.	S1.1154	3.86
61.	S.00056	3.45	92.	S1.1157	3.27
62.	S.00060	3.30	93.	S1.1158	3.29
63.	S1.1	3.45	94.	S1.1159	3.24
64.	S1.42	3.54	95.	* S1.1160	3.74
65.	S1.43	3.64	96.	* S1.1209	3.44
66.	S1.53	3.24	97.	* S1.1210	3.92
67.	S1.261	3.28	98.	S1.1248	3.30
68.	S1.772	3.29	99.	S1.1251	3.23
69.	S1.870	3.26	100.	S1.1252	3.27
70.	S1.895	3.26	101.	S1.1274	3.34
71.	S1.897	3.32	102.	S1.1275	3.26
72.	* S1.930	3.55	103.	* S1.1278	3.32
73.	S1.933	3.26	104.	S1.1281	3.50
74.	S1.946	3.31	105.	S1.1370 (A)	3.53
75.	S1.952	3.30	106.	S1.1496	3.34
76.	S1.977	3.54	107.	S1.1541	3.31

108.	S1.1542	3.56		
109.	S1.1580	3.28		
110.	S1.1589	3.72		
111.	S1.1610	3.35	Total genotypes	: 1168
112.	* S1.1669	3.60	Mean	; 2.87 g
113.	* S1.1703	3.45	Range	: 1.30 to 4.23 g
114.	S1.1718	3.36		
115.	S1.1769	3.46	SD	: 0.34
116.	S1.1776	3.25	Mean + ISD	: 3.21
117.	S1.1976	3.24	Mean - ISD	: 2.53
118.	S1.2237	3.57		
119.	S1.2247	3.30	Small (Less than mean - ISD)	: 180
120.	S1.2287	3.30	Medium (In between mean <u>+</u> ISD)	: 853
121.	* S1.2293	3.80	Larger (Greater than mean + ISD)	: 135
122.	S1.2528	3.50		
123.	S1.2586	3.51		
124.	S1.2594	3.30		
125.	S1.2641	3.56		
126.	S1.2671	3.30		
127.	S1.2766	3.24		
128.	S1.3315/11	3.22		
129.	Sp.1162	3.40		
130.	* TMV - 3	3.22		
131.	TNAU 2	3.60		
132.	59.819	3.60		
133.	78.268	3.40		
134.	78-831	3.40		
135.	1066 A	3.30		

* Selected for the main study.

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APPENDIX - 2

Table 2. Genotypes evaluated for 1000 seed weight and seed size grouping (Second evaluation)

<u>S.No.</u>	<u>Genotypes</u>	<u>1000 seed weight (g)</u>	<u>S.No.</u>	<u>Genotype</u>	<u>1000 seed weight (g)</u>
I. SMALL			31.	S.00055	2.52
Less than mean - ISD (2.57g)			32.	S.00059	2.42
1.	*AT.9	2.51	33.	*S.00646	2.49
2.	*C.16	2.27	34.	Sl.1149	2.44
3.	*Ct.annoo 27/1	2.38	35.	Sl.1500	2.50
4.	*Co.1	2.47	36.	Sl.3296	2.48
5.	EC.132.830	2.44	37.	T.4	2.44
6.	EC.137.933(a)	2.46	38.	TC.45	2.51
7.	*EC.137.935	2.46	39.	TMV.5	2.46
8.	*HT.6	2.45	40.	*TMV.6	2.48
9.	*IS.102	2.44	41.	TNAU.2	2.46
10.	*IS.232	2.43	42.	TNAU.6	2.40
11.	*IS.299	2.26	43.	Vinayak	2.41
12.	NAL.78.162.4/1	2.41	44.	VS.16	2.56
13.	NAL79.111.4.18	2.46	45.	0007/11	2.37
14.	*NAL.79.111.4.20	2.18	46.	664.3.130.5	2.45
15.	No.582	2.40	47.	* 672.3.130.12	2.14
16.	*NS.78.221.32.1	2.37	II. MEDIUM		
17.	OTS.2	2.45	Inbetween mean + ISD (2.57 to 3.19g)		
18.	RJS.1	2.49	1.	AT.2	3.05
19.	RJS.148	2.46	2.	AT.5	3.06
20.	RJS.218	2.52	3.	* B.I.(S) 100043	2.91
21.	S.0191	2.23	4.	C.10	2.90
22.	*S.0210	2.51	5.	Chagla Local	2.96
23.	*S.0321	2.39	6.	CIANO 27-7	2.69
24.	*S.0325	2.50	7.	Corde bore G/14	2.78
25.	*S.0328	2.51	8.	Corde Bore GA/18	2.65
26.	S.0331	2.46	9.	DPI.1484	2.91
27.	S.0404	2.40	10.	E.8	2.80
28.	*S.0551	2.46	11.	EC.100.049	2.84
29.	*S.0554	2.46	12.	EC.132.829	2.86
30.	S.0784	2.37	13.	EC.137.937 (A)	2.84

14.	*G.51.266	2.88	45.	RJS.81	2.91
15.	G.51.268	2.85	46.	RJS.144	2.70
16.	Gannoo.33-10	2.82	47.	RSE.1	3.01
17.	H.78.179.1	2.85	48.	S.0165	2.59
18.	*IS.212	3.10	49.	S.0168	2.70
19.	IS.222	2.95	50.	S.0175	2.78
20.	IS.316	2.92	51.	S.0201	2.99
21.	IS.313	2.75	52.	S.9220	3.01
22.	IS.391	2.98	53.	S.0263	3.02
23.	IS.403	2.64	54.	S.0284	3.06
24.	IS.409	2.85	55.	S.0294	2.86
25.	JGL x 136	3.04	56.	S.0318	3.08
26.	JLT.2	2.91	57.	*S.0327	3.11
27.	*JLT-7	3.08	58.	S.0335	2.86
28.	K.2	2.86	59.	S.0380	2.70
29.	KRR.2	2.92	60.	*S.0431	2.84
30.	*Margo.7	2.92	61.	S.0464	3.06
31.	*N.369.50	2.90	62.	*S.0516	2.92
32.	NAL.78.221/31.2	2.81	63.	S.0534	3.02
33.	NAL.78.221.311.1	2.87	64.	*S.0604	2.86
34.	NAL.78.221.311/9	2.73	65.	*S.0607	2.90
35.	NAL.78.304.43.5	2.78	66.	S.0612	2.80
36.	NAL.78.304.43.19	3.12	67.	*S.0639	2.87
37.	NAL.79.111/4-3	2.95	68.	S.0002/1	2.91
38.	NS.78.221.32.2	3.11	69.	S.00056	3.10
39.	OLT.5	2.84	70.	S1.42	2.87
40.	OLT.43	3.05	71.	S1.43	3.08
41.	OTS.4	3.09	72.	S1.897	3.02
42.	*Pudukkottai.8	2.90	73.	S1.946	3.13
43.	RJS.71	3.05	74.	*S1.953	2.88
44.	RJS.80	3.13	75.	S1.976	2.91

76.	S1.977	3.04	106.	S1.0424	2.82
77.	S1.1016	3.15	107.	S1.0472	2.92
78.	S1.1041	2.99	108.	S1.0447	2.78
79.	S1.1121	3.00	109.	S1.0515	2.97
80.	S1.1143	3.12	110.	S1.00060	2.85
81.	S1.1172	2.79	111.	T.10	3.11
82.	* S1.1249	2.78	112.	* TMV.4	2.88
83.	S1.1274	2.82	113.	TNAU.11	2.99
84.	S1.1289	2.79	114.	VS.44	3.00
85.	S1.1370(A)	2.88	115.	X.495-X.7-3-1	2.81
86.	S1.1496	2.82	116.	Yorri 77-2	2.94
87.	S1.1542	2.92	117.	0005/1	2.89
88.	S1.1589	3.04	118.	0036/3	2.69
89.	S1.1610	3.04	119.	78.263	2.91
90.	* S1.1702	2.92	120.	558.23	2.80
91.	* S1.1755	2.67	121.	724.300/2	2.82
92.	S1.1769	2.86			
93.	S1.2237	3.11	III. LARGE:		
94.	S1.2247	2.98	Greater than mean + 1SD (3.19g)		
95.	S1.2528	2.89	1.	CIANO 33/2	3.23
96.	S1.2584	2.89	2.	Gannoo 27/5	3.22
97.	S1.2586	2.98	3.	Gannoo 33-6	3.29
98.	* S1.2678	2.92	4.	INSI-15-6	3.22
99.	* S1.3175	2.83	5.	* IS .298	3.26
100.	S1.3218	2.71	6.	IS.382	3.24
101.	S1.3274	3.02	7.	Kayankulam-1	3.23
102.	S1.3279	2.96	8.	Rauss 17.4	3.33
103.	S1.0167	3.03	9.	* S.0218	3.45
104.	S1.0168	2.89	10.	S.0281	3.36
105.	S1.0238	2.66	11.	S.0288	3.28

12.	S.0330	3.23	28.	* S1.1210	3.47
13.	S.0501	3.24	29.	S1.1248	3.27
14.	S.00018	3.24	30.	* S1.1278	3.22
15.	* S.00027	3.49	31.	* S1.1669	3.40
16.	* S.00028	3.37	32.	* S1.1703	3.21
17.	* S.00033	3.46	33.	S1.1718	3.31
18.	* Sd.930	3.22	34.	* S1.2893	3.58
19.	S1.957	3.28	35.	S1.2841	3.31
20.	* S1.1033	3.24	36.	* S .0476	3.30
21.	* S1.1075	3.51	37.	* TMV.3	3.29
22.	* S1.1088	3.31	38.	78.762	3.35
23.	* S1.1147	3.59	39.	1877-59-828	3.36
24.	* S1.1150	3.28			
25.	S1.1154	3.23			
26.	* S1.1160	3.32			
27.	* S1.1209	3.28			

Total genotypes : 207

Mean : 2.88 g

Range : 2.14 to 3.59 g

SD : 0.31

Mean + ISD : 3.19

Mean - ISD : 2.57

Small (Less than mean - ISD) : 47

Medium (Inbetween mean + ISD) : 121

Large (Greater than mean + ISD) : 39

* Selected for the main study