# Genetic Diversity, Variability and Correlation Studies in Sesame (*Sesamum indicum* L.)

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Thirty genotypes of sesame were evaluated for seven quantitative characters to assess the genetic diversity, variability and correlation. The genotypes were grouped into seven clusters. Cluster I had largest number of genotypes. Fruiting stem length accounted for 26.6% of total diversity. The extent of variability was high in all the traits studied. The PCV and GCV values were higher for number of capsules and seed yield per plant. Heritability and genetic advance were higher for plant height, fruiting stem length, number of capsules, number of seeds per capsule, 1000 seed weight and seed yield per plant and it indicates that these characters are under the control of additive gene action and selection for these traits will be effective. The association of seed yield was found to be positive and significant with plant height, fruiting stem length, number of capsules, number of seeds per capsule and 1000 seed weight.

**Key Words: Sesame, *Sesamum indicum*, Diversity, Correlation**

## Introduction

Crop improvement depends on the magnitude of genetic variability and the extent of transmission of traits in successive generations. Yield, being a complex polygenic trait is highly influenced by the environmental factors. Therefore, it is essential to partition the variability into its heritable and non-heritable components which will enhance the precision of selection. Beside the quantum of variability, the information on the nature of association between yield and its components helps in simultaneous selection for many characters associated with yield improvement. Present study was aimed (1) to study the diversity among 30 sesame genotypes collected from different parts of the country (2) to assess the quantum of variability and (3) to examine the association between yield and its components in the available germplasm.

## Materials and Methods

Based on the seed coat texture, 30 genotypes comprising smooth and rough seed coat each numbering 15 genotypes representing diverse geographical regions of the country were selected for this study. All the genotypes were raised in randomized block design with three replications at the Regional Research Station, Vriddhachalam during Kharif 2000. The details of pedigree and origin of the cultures/varieties involved in this study are given in Table 1. Each genotype was raised in five rows of 5 metre length spaced 30 cm apart maintaining 30 cm between plants within row. Data were recorded on five plants chosen at random per replication for seven economic traits and mean of 15 plants over three replication was used for analysis. The $D^2$ values corresponding to all possible pairs of genotypes were calculated to determine group constellations. The genetic diversity was assessed using Mahalanobis $D^2$ technique and the genotypes grouped on the basis of minimum generalized distance using the Tocher's method as suggested by Rao (1952). The genetic parameters *viz.*, PCV, GCV, heritability and genetic advance were computed following the standard procedures. Genotypic and phenotypic correlation coefficients are calculated using the method proposed by Johnson *et al.* (1955).

## Results and Discussion

### *(i) Genetic Diversity*

Analysis of variance revealed highly significant difference among the genotypes for all the seven characters studied, indicating thereby the existence of genetic variability. On the basis of diversity, 30 genotypes have been grouped into seven clusters (Table 2). Cluster I, being the largest, possess 20 genotypes; while, cluster II consists of three genotypes. Only two genotypes are present in each of cluster III and V, whereas cluster IV, VI and VII had only one genotype each. The clustering pattern revealed that geographical diversity was not related to genetic diversity. Similar observations were recorded by Dikshit and Swain (2000), Ganesh and Thangavelu (1995), Mahapatra *et al.* (1993), Manivannan and Nadarajan (1996), Manivannan and Ganesan (2000), Gupta *et al.* (2001) and Patil and Sherief (1994).

The largest cluster I was comprised of 20 genotypes of which nine were from Tamil Nadu, five from Haryana, two from Kerala, one each from Karnataka, Andhra Pradesh, Maharashtra and Israel. Such grouping of genotypes from different locations may be attributed to free flow/exchange of breeding material from one place

**Table 1. Details of pedigree and origin of the cultures/varieties.**

| S.No. | Name of the culture/variety | Type of genotype | Pedigree | Origin |
|---|---|---|---|---|
| 1 | Si 1721 | Local | Not known | Andhra Pradesh |
| 2 | Si 1671 | Local | Not known | Israel |
| 3 | S 0651 | Local | Not known | Tamil Nadu |
| 4 | SVPR 1 | Improved variety | Selection from westernghat white | Tamil Nadu |
| 5 | Si 320 | Local | Not known | Haryana |
| 6 | Si 9087 | Local | Not known | Haryana |
| 7 | Si 97 | Local | Not known | Haryana |
| 8 | Si 1576 | Local | Not known | Haryana |
| 9 | Si 1618 | Local | Not known | Haryana |
| 10 | S 0626-NL-4 | Local | Not known | Karnataka |
| 11 | Si 102 | Local | Not known | Kerala |
| 12 | TC 328 | Local | Not known | Gurdaspur |
| 13 | TMV 6 | Improved variety | Selection from Andhra Local | Tamil Nadu |
| 14 | TMV 4 | Improved variety | Pureline selection from Sattur Local | Tamil Nadu |
| 15 | Si 0613 | Local | Not known | Tamil Nadu |
| 16 | TMV 3 | Improved variety | Derivative of South Arcot local X Malabar variety | Tamil Nadu |
| 17 | S 0530 | Local | Not known | Tamil Nadu |
| 18 | VS 9104 | Improved culture | TMV 3 X VS 345 | Tamil Nadu |
| 19 | Si 0480 | Local | Not known | Tamil Nadu |
| 20 | Si 53102 | Local | Not known | Kerala |
| 21 | Si 1711 | Local | Not known | Andhra Pradesh |
| 22 | Si 3012 | Local | Not known | Not known |
| 23 | Si 917 | Local | Not known | Not known |
| 24 | AUS 9105 | Improved culture | Not known | Tamil Nadu |
| 25 | TNAU 72 | Improved culture | Not known | Tamil Nadu |
| 26 | Si 3214 | Local | Not known | Assam |
| 27 | RT 46 | Improved variety | T 12 X Pb.Til.No.1 | Mandore |
| 28 | Si 1160 | Local | Not known | Tamil Nadu |
| 29 | CO 1 | Improved variety | (TMV 3 X Si 1878) X Si 1878 | Tamil Nadu |
| 30 | VRI SV 1 (VS 117) | Improved variety | Pureline selection from Thirukkattupalli Local | Tamil Nadu |

**Table 2. Distribution of sesame genotypes into different clusters**

| Cluster | Number of genotypes | Genotypes |
|---|---|---|
| I | 20 | Si 1721, Si 1671, S 0651, SVPR 1, Si 320, Si 9087, Si 97, Si 1576, Si 1618, Si 0626-NL-4, Si 102, TC 328, TMV 6, TMV 4, Si 0613, TMV 3, S 0530, VS 9104, Si 0480, Si 53102 |
| II | 3 | Si 1711, Si 3012, Si 917 |
| III | 2 | AUS 9105, TNAU 72 |
| IV | 1 | Si 3214 |
| V | 2 | RT 46, Si 1160 |
| VI | 1 | CO 1 |
| VII | 1 | VS 117 |

to another (Verma and Mehta, 1976; Jain *et al.*, 1981) and/or to the unidirectional selection practiced by breeders of different locations (Singh and Bains, 1968).

The intra and inter cluster values among the seven clusters are presented in Table 3. The intra cluster generalized distance was maximum for cluster II (32.72) and minimum for cluster IV, VI and VII (0.00). The highest inter cluster distance (508.17) was recorded between cluster I and VII, while the cluster II and III were the least divergent (42.26).

Cluster mean values for all the characters are depicted in Table 4. The difference between cluster means were substantially high for all the characters except for number of seeds per capsule. In general, cluster VI had high mean values for plant height, fruiting stem length, 1000 seed weight and seed yield per plant. Cluster III had high mean values for number of branches and number of capsules. Number of seeds per capsule recorded higher mean values in cluster VII.

### *Contribution of Characters to Diversity*

The ranking technique was adopted to rank the characters in the order of contribution to total genetic diversity (Murthy *et al.*, 1965). Contribution of individual characters to the diversity (Table 5) revealed that fruiting stem length contributed maximum diversity (26.60%) followed by plant height (17.24%), seed yield per plant (15.63%),

**Table 3. Intra cluster (in bold) and inter cluster distance for seven characters in sesame**

| Clusters | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| **I** | **20.47** | 47.12 | 121.42 | 277.27 | 182.19 | 445.39 | 508.17 |
| **II** | | **32.72** | 42.26 | 144.63 | 111.27 | 348.65 | 435.06 |
| **III** | | | **11.98** | 56.57 | 94.62 | 242.62 | 377.98 |
| **IV** | | | | **0.00** | 54.29 | 178.64 | 242.54 |
| **V** | | | | | **17.16** | 163.28 | 217.49 |
| **VI** | | | | | | **0.00** | 205.43 |
| **VII** | | | | | | | **0.00** |

**Table 4. Character means in different clusters of sesame genotypes**

| Clusters | Plant height | Number of branches | Fruiting stem length | Number of capsules | Number of seeds per capsule | 1000 seed weight | Seed yield per plant |
|---|---|---|---|---|---|---|---|
| **I** | 67.39 | 3.62 | 43.50 | 34.13 | 47.34 | 3.58 | 4.51 |
| **II** | 70.14 | 3.17 | 35.94 | 27.09 | 41.76 | 2.98 | 2.12 |
| **III** | 94.23 | **4.80** | 54.2 | **51.20** | 41.55 | 3.25 | 5.80 |
| **IV** | 53.93 | 2.20 | 39.86 | 18.13 | 47.46 | 3.37 | 1.90 |
| **V** | 67.09 | 4.19 | 41.73 | 41.92 | 49.44 | 2.94 | 3.14 |
| **VI** | **96.33** | 3.86 | **59.73** | 46.00 | 49.93 | **4.33** | **7.68** |
| **VII** | 52.00 | 3.06 | 34.26 | 21.73 | **64.40** | 2.09 | 4.52 |

number of seeds per capsule (13.79%), number of capsules per plant (11.26%), 1000 seed weight (10.34%) and number of branches per plant (5.05%). In contrast to the present findings, Manivannan and Nadarajan (1996) and Manivannan and Ganesan (2000) reported higher contribution of plant height followed by number of branches per plant.

Cluster means for seven characters indicated that the genotype in cluster VI had highest height, fruiting stem length, 1000 seed weight and seed yield per plant; whereas, genotypes of cluster III recorded maximum number of branches and number of capsules per plant. Therefore, hybridization between the genotypes of these two clusters, will lead to accumulation of favourable genes in a single variety. In view of this, it is suggested that for varietal development, the crosses between the genotypes of divergent clusters should be made rather than between the genotypes of those clusters which have the minimum diversity.

### *(ii) Variability and Correlation*

Analysis of variance showed that genotypic difference were significant for all the characters studied, indicating the presence of considerable amount of genetic variability in the material selected for the study (Table 6). In general, PCV was higher than GCV for all the characters studied which indicates the variation observed in the genotype is not only due to genotype but also due to the influence of environment. The GCV was high for number of capsules and seed yield per plant. Govindarasu *et al.* (1990), Chandrasekhara and Ramana Reddy (1993), Sverup John and Gopinathan Nair (1993), Singh *et al.* (1997), Sadhakshari *et al.* (1992 & 1995), and Backiyarani *et al.* (1997) also reported high GCV for these traits. The characters like plant height, number of branches per plant, fruiting stem length, number of seeds per capsule and 1000 seed weight in that order registered moderate GCV. Similar observations were obtained by Chandra Sekhara and Ramana Reddy (1993), Sadhakshari *et al.* (1992 and 1995) and Backiyarani *et al.* (1997). Thus, it is evident from these observations that, all the said characters are amenable for improvement through simple selection.

Burton (1952) suggested that GCV together with heritability estimate gives the best picture of the extent of advance to be expected by selection. High heritability was observed for plant height, fruiting stem length, number of capsules per plant, number of seeds per capsule, 1000 seed weight and seed yield per plant. A similar trend was also reported by Mishra *et al.* (1995), Chandrasekara and Ramana Reddy (1993), Backiyarani *et al.* (1997), Shanmugavalli and Vanniarajan (1998), Shadakshari (1992 & 1995), Sverup John and Gopinathan Nair (1993), Govindarasu *et al.* (1990) and Umesh Kumar Reddy and Stephen Dorairaj (1990). Heritability shows the effectiveness of phenotypic performance for a character. High heritability along with high genetic advance render the selection more effective (Johnson *et al.*, 1955). The genetic advance as per cent of mean was found to be high for plant height, fruiting stem length, number of capsules, number of seeds per capsule, 1000 seed weight and seed yield per plant. This is in consonance with the findings of Umesh Kumar Reddy and Stephen Dorairaj

**Table 5. Contribution of individual traits in the divergence among 30 genotypes of sesame**

| S.No. | Character | Contribution (%) |
|---|---|---|
| 1 | Plant height | 17.24 |
| 2 | Number of branches per plant | 5.05 |
| 3 | Fruiting stem length | 26.66 |
| 4 | Number of capsules per plant | 11.26 |
| 5 | Number of seeds per capsule | 13.79 |
| 6 | 1000 seed weight | 10.34 |
| 7 | Seed yield per plant | 15.63 |

(1990), Govindarasu *et al.* (1990), Sverup John and Gopinathan Nair (1993), Shadakshari *et al.* (1992 & 1995), Shanmugavalli and Vanniyarajan (1998), Backiyarani *et al.* (1997), Chandrasekhara and Ramana Reddy (1993) and Mishra *et al.* (1995).

If the heritability of a particular trait is mainly due to non-additive gene action, the genetic advance will be low, whereas if the heritability was due to additive gene effects it would be associated with high genetic advance. High heritability accompanied with high genetic advance observed for plant height, fruiting stem length, number of capsules, number of seeds per capsule, 1000 seed weight and seed yield per plant indicates that these characters are under the control of additive gene effects and selection for these traits will be effective. Low heritability along with low genetic advance was observed for number of branches indicates the influence of environment upon this trait and selection would be ineffective in such instances. Kandaswami *et al.* (1990) reported low heritability and low genetic advance for number of branches. Contrary to the present findings, Jayalakshmi *et al.* (1998) observed high heritability and genetic advance for primary branches. In general, a character with high genotypic variance and high heritability value coupled with a greater genetic gain would be responsive to selection in the positive direction.

Study of simple correlation indicated that plant height, fruiting stem length, number of capsules per plant, number of seeds per capsule and 1000 seed weight had significant phenotypic and genotypic correlation with seed yield per plant (Table 7). However the relationship between seed yield per plant with number of branches is significant in phenotypic correlation only. Vanisri *et al.* (1994) reported positive association of seed yield with number of capsules and 1000 seed weight. Rai *et al.* (1997) registered positive association of seed yield with number of capsules per plant and number of seeds per capsule. Singh *et al.* (1997) and Mishra *et al.* (1995) observed strong association among productive capsules and seed yield per plant. Shadakshari *et al.* (1992) noticed significant but strong association between seed yield per plant with total number of capsules per plant, plant height, total number of branches and 1000 seed weight. Backiyarani *et al.* (1998) reported positive and significant association of seed yield with number of capsules.

Variability studies clearly revealed that characters *viz.*, plant height, fruiting stem length, number of capsules, number of seeds per capsule, 1000 seed weight and seed yield per plant recorded high heritability coupled with high genetic advance, which indicates the involvement of additive gene action in the inheritance of these traits. The association of seed yield was found to be positive and significant with plant height, fruiting stem length, number of capsules, number of seeds per capsule and 1000 seed weight. Hence, selection of these yield components will simultaneously improve the seed yield.

From the foregoing results, it may be concluded that, the characters *viz.*, plant height, fruiting stem length, number of capsules, number of seeds per capsule and 1000 seed weight showed strong correlation with seed yield per plant. Hence, when selection is imposed upon these traits, seed yield can be improved ultimately. Crossing genotypes in the VI and III cluster may generate more variable segregants and it may be possible to fix a genotype with higher seed yield in the early generation itself, as most of the characters are under the control of additive gene action.

**Table 6. Mean, genotypic and phenotypic coefficient variation and heritability for seven characters in sesame**

| Characters | Mean ±SE | Genotypic coefficient of variation | Phenotypic coefficient of variation | Heritability (broad sense) | Genetic advance | Genetic advance as per cent of mean |
|---|---|---|---|---|---|---|
| Plant height | 70.05±4.18 | 15.88 | 17.48 | 82.49 | 20.81 | 29.71 |
| Number of branches | 4.01±3.00 | 14.94 | 92.81 | 2.59 | 0.199 | 4.95 |
| Fruiting stem length | 43.44±3.57 | 17.29 | 20.02 | 74.63 | 13.37 | 30.77 |
| Number of capsules | 35.14±6.01 | 29.10 | 35.86 | 65.83 | 17.09 | 48.63 |
| Number of seeds per capsule | 47.96±4.17 | 14.41 | 7.92 | 64.59 | 11.44 | 23.85 |
| 1000 seed weight | 3.43±0.22 | 12.69 | 15.09 | 75.46 | 21.97 | 64.81 |
| Seed yield per plant | 4.40±0.86 | 37.19 | 44.35 | 70.31 | 2.82 | 64.09 |

**Table 7. Correlation (r) coefficient between different characters in sesame**

| Characters | | Plant height | Number of branches | Fruiting stem length | Number of capsules | Number of seeds per capsule | 1000 seed weight | Seed yield per plant |
|---|---|---|---|---|---|---|---|---|
| Plant height | rP | 1.000 | 0.5045** | 0.7581** | 0.7859** | -0.0565 | 0.2887** | 0.6359** |
| | rG | | 0.1073 | 0.7544** | 0.7388** | -0.0423 | 0.1855** | 0.6100** |
| Number of branches | rP | | 1.000 | 0.4911** | 0.1040 | 0.3328** | -0.2378** | 0.1899** |
| | rG | | | 0.1624** | 0.3016** | -0.0427 | 0.0208 | 0.1057 |
| Fruiting stem length | rP | | | 1.000 | 0.7468** | -0.0456 | 0.4793** | 0.6697** |
| | rG | | | | 0.6899** | -0.0855 | 0.3238** | 0.6161** |
| Number of capsules | rP | | | | 1.000 | 0.2052** | 0.1884** | 0.7890** |
| | rG | | | | | 0.1531* | 0.1546* | 0.7876** |
| Number of seeds per capsule | rP | | | | | 1.000 | -0.1872** | 0.5136** |
| | rG | | | | | | -0.1759** | 0.4264** |
| 1000 seed weight | rP | | | | | | 1.000 | 0.3905** |
| | rG | | | | | | | 0.2483** |
| Seed yield per plant | rP | | | | | | | 1.000 |
| | rG | | | | | | | |

rP, rG – Phenotypic and genotypic correlation coefficient; *, ** significant at 5% and 1% level respectively

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