



# Genetic Variability and Association among Yield and Yield Related Traits of Sesame (*Sesamum indicum* L.) Genotype

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## Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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## ABSTRACT

A field experiment was carried out with 42 genotypes of sesame (*Sesamum indicum* L.) at the Niger Research Station, Navsari Agricultural University, Vanarasi, Ta. Vansda. The study was performed to evaluate the genetic variability, characters association, path analysis and genetic diversity based on yield and yield related traits. The highest genotypic coefficient of variation was observed for seed yield per plant followed by capsules per cluster and harvest index. High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for the traits viz., capsule width, capsules per cluster, leaf area, harvest index and seed yield per plant indicating that these characters are under the control of additive gene effect. The seed yield per plant was found to be significant and positively correlated with days to maturity, capsule length, capsule width, capsules per cluster, 1000 seed weight and harvest index at

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genotypic and phenotypic levels. The maximum direct effects as well as appreciable indirect influences were exerted by harvest index, capsule width, capsule length and 1000 seed weight.  $D^2$  analysis indicated wider genetic diversity among the forty-two genotypes which were grouped in ten clusters indicating there is no formed relationship between geographical diversity and genetic diversity. Cluster III and X showed the maximum inter cluster distance of 16.51. Hence, the genotypes belonging to the X, IX and VIII cluster could be used in hybridization program for obtaining a wide spectrum of variability among the segregants. Among different eleven traits studied, leaf area followed by capsules per cluster, harvest index, capsule width, seed yield per plant and capsule length contributed maximum towards the total genetic divergence. Results of mean cluster analysis showed that cluster X recorded highest cluster mean for four important yield attributing characters and cluster IX for two important characters. Genotypes from these cluster may produce progenies with high genetic variation.

**Keywords:** Genetic variability; heritability; genetic advance; path analysis; cluster; genetic divergence;  $D^2$  technique; *Sesamum indicum* L.

## 1. INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the most important ancient cultivated oilseeds crop grown in Asia and Africa. It belongs to Pedaliaceae family having chromosome number ( $2n=26$ ) and is an annual and oilseed crop. Sesame oil is characterized for its stability and quality hence it is regarded as “Queen of the Oil seed”. The crop is highly tolerant to drought, grows well in most of the well-drained soils and various agro climatic regions, and is well adapted to different rotations. Sesame is self-pollinated crop with the cross pollination 4 to 5% and cross pollination may occur through insect activity and environmental condition. Due to the stability of its healthy oil, easiness of extraction and resistance to drought, sesame was popular in the ancient world, Sesame is considered as a nutritious oil seed crop being rich source of protein (18–25%), carbohydrate (13.5%), minerals and poly unsaturated fatty acid [1]. Variation is a prerequisite to start a breeding programme in any crop. Genetic variability is necessary for continued genetic improvement of crop species. Biometrical technique to evaluate the genetic variability and extent of heritability of economic character serve as useful tool in evaluating the segregating population. Variation and selection are two basic essentiality of genetic improvement in any crop. Yield is the resultant product of various morphological, physiological and biological components which is determined by growth and development processes [2] and more particularly by yield related traits which are greatly influenced by both genetic and environmental factors [3]. If information on genetic variability is available then the selection based on yield component traits is advantageous. Phenotypic and genotypic

correlation coefficient and yield components and their contribution in path analysis provide information on their relative importance in determining the yield [4].

Genetic diversity is a fundamental element in plant breeding which provide the information about genetic relatedness among elite breeding material [5]. Genetic diversity among landrace will help in the selection and breeding of high yielding, good quality cultivars that will increase production [6]. But limited study on genetic diversity has been done in sesame. Some genetic parameters like phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability and genetic gain help to evaluate genetic diversity of experimental materials. Assessment of genetic diversity using agro-morphological and molecular markers is one of the effective methods for diversity analysis in sesame that can be used in future breeding program and also significant to improve sesame varieties. Diversity analyses based only on morphological characters are prone to environmental bias due to biotic influences and also complex genetic structure of different morphological traits [7].

## 2. MATERIALS AND METHODS

The experiment was conducted to evaluate forty-two genotypes under irrigated condition, in Randomized Block Design with three replications at Research Farm of Niger Research Station, Navsari Agricultural University, Vanarasi, Ta. Vansda, Dist. Navsari, Gujarat. The seeds were sown at 60 cm between rows and 15cm between plants in the row. Total area of experimental unit was 24.5 m<sup>2</sup>. The genotypes were randomly assigned to the plots in every replication. The

experiment was laid out with one row of 2.10 m length of each genotype surrounded by one guard rows to avoid damage and border effects. All recommended practices were followed and timely plant protection measures were taken timely to avoid damage through insect-pests and diseases. The data were recorded on five randomly selected plants from each genotype on different characters viz. days to 50% flowering, days to maturity, plant height (cm), capsule length (cm), capsule width (cm), capsules per cluster, leaf area (cm<sup>2</sup>), 1000 seed weight (g), oil content (%), harvest index (%) and seed yield per plant (g). The phenotypic and genotypic coefficient of variability was computed as per Burton and De vane (1953). Heritability (h<sup>2</sup>) in broadsense and genetic advance percent of mean was calculated for each character according to the method suggested by Johnson (1955). Correlation coefficients for yield and yield components were evaluated using the formula suggested by Panse and Sukhatme (1987).

### 3. RESULTS AND DISCUSSION

The experimental result showed that a wide range of variation by virtue of exhibiting highly significant genotypic differences for nine out of eleven traits studied viz., days to 50% flowering, plant height, capsule length, capsule width, capsules per cluster, leaf area, 1000 seed weight, harvest index and seed yield per plant while remaining two traits i.e. days to maturity and oil content showed significant difference (Table-1). This suggests that the presence of substantial variation in the inherent genetic potential of the genotypes studied depicting the possibility of selecting high yielding sesame genotypes. Similar results in related to sesame for most of the characters were also reported by Valarmathi [8], Raghuwanshi [9], Sarwarand Haq [10], Gawali [11], Parameshwarappa (2009) for days to 50% flowering, plant height, capsule

length, 1000 seed weight and seed yield per plant; Sumathi and muralidharan [12], Gidey et al. [13], Bharathi et al. [14], Abate and Mekbib [15] and Iqbal et al. [16].

The estimates of GCV and PCV indicated that the values of PCV were higher than GCV for most of the traits due partly to interaction of the genotypes with the environment or other environmental factors influencing the expression of these characters (Table-2). The highest value of GCV and PCV was observed for some of the traits like capsules per cluster, harvest index and seed yield per plant. High magnitude of GCV indicated the presence of wide variation for the characters under study to allow further improvement by selection of the individual trait. High estimates of GCV in sesame have been also reported for seed yield per plant by Valarmathi [8], Mandal et al. [17], Gayathri [18] and Gidey [19].

High estimates of heritability coupled with high genetic advance expressed as percentage of mean (Table-2) were observed for the traits viz., capsule width, capsules per cluster, leaf area, harvest index and seed yield per plant indicating that these characters are under the control of additive gene effect. Therefore, further improvement in these traits using pure line selection would be worthwhile. Similar result reported by Reddy et al. [20], Krishnaiah et al. [21]; for harvest index by Mohanty [22].

The correlation coefficients between seed yield per plant and yield component characters and among themselves were estimated at genotypic and phenotypic levels and are presented in Table-3 as Genotypic (r<sub>g</sub>) and phenotypic (r<sub>p</sub>) correlations coefficient are described under this table. In general, the values of genotypic

**Table 1. Analysis of variance for different character sin sesame**

Source of Variation	d.f.	MSS					
		DFF	DM	PH	CL	CW	CC
Replications	2	3.431	12.077	33.599	0.002	0.012	0.023
Genotypes	41	13.295**	37.643*	140.027**	0.159**	0.106**	4.778**
Error	82	4.347	23.315	49.248	0.036	0.009	0.249

Source of Variation	d.f.	MSS				
		LA	SW	OC	HI	SYP
Replications	2	3.970	0.016	0.320	0.502	0.909
Genotypes	41	102.905**	0.227**	9.218*	82.141**	6.154**
Error	82	5.289	0.043	5.457	4.957	0.429

\*, \*\* Significant at 0.05 and 0.01 probability level respectively,  
DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsules per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

**Table 2. Range, mean, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advances percent of mean for different characters of sesame**

Sr. No	Traits	Mean	GCV(%)	PCV(%)	h <sup>2</sup> (%)	GA	GAM
1	DFF	39.45	4.38	6.86	40.69	2.27	5.75
2	DM	94.58	2.31	5.60	17.00	1.86	1.96
3	PH	104.47	5.27	8.54	38.06	6.99	6.69
4	CL	3.00	6.76	9.23	53.69	0.31	10.20
5	CW	1.10	16.26	18.42	77.95	0.33	29.57
6	CC	5.03	24.42	26.36	85.82	2.34	46.61
7	LA	45.21	12.62	13.60	86.02	10.90	24.11
8	SW	3.21	7.72	10.07	58.80	0.39	12.20
9	OC	39.88	2.81	6.50	18.69	1.00	2.50
10	HI	21.90	23.17	25.30	83.85	9.57	43.70
11	SYP	5.07	27.24	30.14	81.65	2.57	50.70

DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsules per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

correlations coefficient were higher than their corresponding phenotypic correlations coefficient. This indicated that there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environment. In the present study, seed yield per plant was found to be highly significantly and positively correlated with capsule length, capsule width, 1000 seed weight and harvest index at genotypic and phenotypic levels. Positive and significant correlation between traits can be the result of strong coupling linkage between genes or the characters may be the result of pleiotropic genes that control these characters in the same direction (Kearsey and Pooni, 1996).

The positive genotypic association has been reported between seed yield per plant and capsule length by Parmeswarappa et al. (2009), Rao et al. [23], Abhijatha et al. [24], Patil and Lokesha [25]; for seed yield per plant and 1000 seed weight by Bhuvan and Sharma [26], Yol et al. [27], Fazal et al. [28], Imran and dash (2018); for seed yield per plant and harvest index by Gidey et al. [19], Bamrotiya et al. [29] and Patil and Lokesha [25], respectively. The present results on correlation coefficients revealed that, days to maturity, capsule length, capsule width, capsules per cluster, 1000 seed weight and harvest index were the most important attributes and may contribute considerably towards higher seed yield per plant. The inter relationship among yield components would help in increasing the yield levels and therefore, more emphasis should be given to these components while selecting better types in sesame improvement programmes.

Path coefficient analysis was carried out with the objective of partitioning the genotypic correlation

of yield component with seed yield into direct and indirect effects for eleven variables. The seed yield was regarded as resultant variable while the other traits as causal variable. The estimates of direct and indirect effects of various traits along with their genotypic correlations with yield are presented in Table-4. Path coefficient analysis revealed that days to 50% flowering, days to maturity, capsule length, capsule width, 1000 seed weight and harvest index exerted positive direct effects on seed yield per plant. In the present study, the residual effect at genotypic level was 0.2732 indicating, that all of the traits included in the study explained moderate percentage of variation in seed yield per plant (72.68%), while other factors not included in the study would explain 27.32%. These characters also exhibited highly significant and positive associations with seed yield per plant and hence, they may be considered as the most important yield contributing characters and due emphasis should be placed on these components while selecting for high yielding types in sesame.

The Mahalanobis's D<sup>2</sup> statistics was computed for all possible pair of populations under investigation. Forty-two genotypes of sesame were grouped into ten clusters on the basis of relative magnitude of D<sup>2</sup> values following Tocher's method [30]. Cluster I was the largest cluster having twenty one genotypes. The second largest cluster II had nine while cluster III had five genotypes, respectively where as cluster IV, V, VI, VII, VIII, IX and X were mono genotypic. Thus, the present results indicated that geographical distribution and genetic divergence did not follow the same pattern. Therefore, it can be concluded

**Table 3. Genotypic( $r_g$ ) and Phenotypic( $r_p$ ) correlation coefficients for yield and yield attributing traits in sesame genotypes**

Characters		DFF	DM	PH	CL	CW	CC	LA	SW	OC	HI	SYP
DFF	$r_g$	<b>1.000</b>										
	$r_p$	<b>1.000</b>										
DM	$r_g$	0.416**	<b>1.000</b>									
	$r_p$	0.130 <sup>NS</sup>	<b>1.000</b>									
PH	$r_g$	-0.446**	-0.017 <sup>NS</sup>	<b>1.000</b>								
	$r_p$	-0.166 <sup>NS</sup>	-0.075 <sup>NS</sup>	<b>1.000</b>								
CL	$r_g$	-0.259**	0.025 <sup>NS</sup>	0.043 <sup>NS</sup>	<b>1.000</b>							
	$r_p$	-0.175 <sup>NS</sup>	-0.025 <sup>NS</sup>	0.161 <sup>NS</sup>	<b>1.000</b>							
CW	$r_g$	-0.206*	-0.045 <sup>NS</sup>	0.119 <sup>NS</sup>	0.1079**	<b>1.000</b>						
	$r_p$	-0.113 <sup>NS</sup>	-0.011 <sup>NS</sup>	-0.014 <sup>NS</sup>	0.689**	<b>1.000</b>						
CC	$r_g$	0.122 <sup>NS</sup>	-0.030 <sup>NS</sup>	-0.232**	0.099 <sup>NS</sup>	0.242**	<b>1.000</b>					
	$r_p$	0.132 <sup>NS</sup>	-0.014 <sup>NS</sup>	-0.149 <sup>NS</sup>	0.039 <sup>NS</sup>	0.205*	<b>1.000</b>					
LA	$r_g$	0.012 <sup>NS</sup>	0.298**	0.244**	0.127 <sup>NS</sup>	0.047 <sup>NS</sup>	-0.264**	<b>1.000</b>				
	$r_p$	-0.021 <sup>NS</sup>	0.095 <sup>NS</sup>	0.070 <sup>NS</sup>	0.036 <sup>NS</sup>	0.050 <sup>NS</sup>	-0.201*	<b>1.000</b>				
SW	$r_g$	-0.272**	-0.406**	0.066 <sup>NS</sup>	0.862**	0.825**	0.260**	-0.069 <sup>NS</sup>	<b>1.000</b>			
	$r_p$	-0.131 <sup>NS</sup>	-0.133 <sup>NS</sup>	0.042 <sup>NS</sup>	0.535**	0.575**	0.159 <sup>NS</sup>	-0.079 <sup>NS</sup>	<b>1.000</b>			
OC	$r_g$	0.475**	-0.398**	-0.119 <sup>NS</sup>	-1.144**	-1.146**	-0.528**	0.074 <sup>NS</sup>	-0.984**	<b>1.000</b>		
	$r_p$	0.059 <sup>NS</sup>	-0.098 <sup>NS</sup>	-0.040 <sup>NS</sup>	-0.407**	-0.454**	-0.205*	0.082 <sup>NS</sup>	-0.405**	<b>1.000</b>		
HI	$r_g$	-0.427**	0.186*	0.215*	0.273**	0.293**	0.134 <sup>NS</sup>	-0.009 <sup>NS</sup>	0.320**	-0.747**	<b>1.000</b>	
	$r_p$	-0.246**	0.033 <sup>NS</sup>	0.125 <sup>NS</sup>	0.206*	0.248*	0.096 <sup>NS</sup>	-0.023 <sup>NS</sup>	0.202*	-0.321**	<b>1.000</b>	
SYP	$r_g$	-0.148 <sup>NS</sup>	0.235**	0.135 <sup>NS</sup>	0.848**	0.807**	0.243**	-0.083 <sup>NS</sup>	0.719**	-1.182**	0.592**	<b>1.000</b>
	$r_p$	-0.083 <sup>NS</sup>	0.197*	0.069 <sup>NS</sup>	0.557**	0.619**	0.197*	-0.070 <sup>NS</sup>	0.515**	-0.525**	0.472**	<b>1.000</b>

\*, \*\* Significant at 0.05 and 0.01 probability level respectively, DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsules per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

**Table 4. Genotypic path coefficient showing direct and indirect effects for yield and yield attributing traits in sesame genotype**

Characters	DF	DM	PH	CL	CW	CC	LA	SW	OC	HI	SYP(r)
DF	<b>0.0592</b>	0.1798	-0.0401	-0.0045	-0.0358	-0.0080	-0.0026	-0.1566	-0.0529	-0.0861	-0.1476
DM	0.0246	<b>0.4324</b>	-0.0015	0.0004	-0.0078	0.0020	-0.0635	-0.2335	0.0443	0.0374	0.2348
PH	-0.0264	-0.0074	<b>0.0900</b>	0.0007	0.0207	0.0152	-0.0520	0.0377	0.0132	0.0434	0.1351
CL	-0.0153	0.0109	0.0038	<b>0.0173</b>	0.1874	-0.0065	-0.0271	0.4954	0.1272	0.0552	0.8483
CW	-0.0122	-0.0193	0.0107	0.0187	<b>0.1737</b>	-0.0159	-0.0101	0.4744	0.1275	0.0591	0.8066
CC	0.0073	-0.0130	-0.0208	0.0017	0.0420	<b>-0.0656</b>	0.0563	0.1494	0.0587	0.0270	0.2430
LA	0.0007	0.1289	0.0220	0.0022	0.0082	0.0174	<b>-0.2129</b>	-0.0394	-0.0082	-0.0018	-0.0829
SW	-0.0161	-0.1757	0.0059	0.0149	0.1434	-0.0171	0.0146	<b>0.5747</b>	0.1095	0.0646	0.7187
OC	0.0282	-0.1722	-0.0107	-0.0198	-0.1991	0.0346	-0.0157	-0.5653	<b>-0.1113</b>	-0.1507	-1.1820
HI	-0.0253	0.0802	0.0194	0.0047	0.0509	-0.0088	0.0019	0.1840	0.0831	<b>0.2017</b>	0.5918

Residual effect= SQRT (1-1.0432), Numbers in bold indicate direct effects DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsules per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

that selection of parents for hybridization should not be based on geographical diversity only, but it should have a base of both geographical origin as well as genetic divergence. Similar findings have been reported by Jadhav and Mohrir [31], Gogoi et al. [32], Mohan [33], Ramprasad et al. [34], Soudharya et al. [35], Swathy et al. [36] and Mohanty et al. [37].

Intra and inter cluster distance (Table 5 with Fig. 1) between all possible pairs of ten clusters were computed with the help of method given by Singh and Chaudhary [38]. The intra cluster distance ranged from 6.63 to 5.46. The cluster II exhibited maximum intra cluster distance (6.63) followed by the cluster I (6.19) and cluster III (5.46). The intra cluster distance was zero for cluster IV, V, VI, VII, VIII, IX and X indicating that genotypes within this cluster were similar. The inter cluster distance ranged from 16.51 to 4.35. The inter cluster distance between cluster III and X (16.51) was maximum followed by cluster III and VIII (14.41), III and IX(14.12) and II and VI (13.49). The minimum inter cluster distance was observed between cluster IV and V (4.35) followed by that of clusters IV and VI (4.55), IV and VII (4.79), V and VII(5.02) and V and VI(5.68).

In general, intra-cluster distance values were lower than the inter-cluster distances which indicated substantial diversity present among the genotypes studied. Thus, the genotypes

included within a cluster tended to diverse less from each other.

Cluster mean for the eleven characters are presented in Table 6. Cluster I had a mean values greater than over all mean for Oil content and harvest index, but for the rest of traits it had mean values lower than the overall mean. Cluster II had a mean values greater than the overall mean for days to 50% flowering and oil content. Cluster III exhibited the lowest mean value for most of the traits viz., capsule length, capsule width, 1000 seed weight and harvest index. Cluster IV depicted mean value for second highest mean value for capsule width and 1000 seed weight. The lowest mean value for days to maturity, plant height and oil content was noticed in cluster IV. Cluster V depicted highest mean value for days to 50% flowering whereas second highest mean value for plant height and seed yield per plant. Cluster VI showed highest mean value for capsules per cluster. Besides this, it had lowest mean value for leaf area. Cluster VII exhibited second highest mean values for capsule length, capsule width and capsules per cluster. Cluster VIII depicted highest mean value for days to maturity and seed yield per plant. Cluster IX depicted highest mean value for leaf area and harvest index. Cluster X showed highest mean value for most of traits viz. plant height, capsule length, capsule width and 1000 seed weight whereas lowest mean value for days to 50% flowering.

**Table 5. Inter and intra cluster D<sup>2</sup> values for different clusters**

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	<b>6.19</b>									
II	9.11	<b>6.63</b>								
III	8.72	9.65	<b>5.46</b>							
IV	7.62	12.12	11.42	<b>0.00</b>						
V	7.44	10.39	11.02	4.35	<b>0.00</b>					
VI	8.14	13.49	11.85	4.55	5.68	<b>0.00</b>				
VII	7.95	10.90	12.44	4.79	5.02	6.61	<b>0.00</b>			
VIII	8.70	11.47	14.41	9.05	8.48	9.47	7.41	<b>0.00</b>		
IX	9.53	10.72	14.12	11.69	10.63	11.39	8.39	5.91	<b>0.00</b>	
X	11.15	13.44	16.51	8.41	7.95	9.99	7.27	9.17	12.04	<b>0.00</b>

Numbers in bold indicate intra cluster D<sup>2</sup> values

**Table 6. Cluster means for yield and yield contributing traits of sesame genotypes**

Cluster	DFP	DM	PH	CL	CW	CC	LA	SW	OC	HI	SYP
I	38.66	94.23	103.58	2.97	1.11	5.11	42.95	3.21	39.62	23.88	5.23
II	40.28	94.44	106.39	2.98	1.06	3.96	52.73	3.12	40.86	18.39	4.19
III	40.37	94.73	100.72	2.76	0.87	5.09	40.48	2.90	42.23	14.77	3.11
IV	39.33	91.33	98.20	3.30	1.33	6.33	39.97	3.73	36.93	20.47	7.23
V	43.00	94.17	111.70	3.17	1.27	6.13	43.87	3.37	38.77	18.53	7.73
VI	41.83	98.33	108.90	3.17	1.30	7.27	36.57	3.27	36.13	24.50	7.03
VII	39.67	91.50	101.77	3.33	1.33	7.00	49.13	3.70	38.30	22.73	6.67
VIII	38.33	101.50	106.13	3.23	1.17	4.73	48.00	3.53	38.10	33.53	8.00
IX	40.50	97.17	109.13	2.97	1.07	6.07	55.17	3.23	38.43	34.57	5.57
X	38.00	96.00	115.53	3.80	1.80	5.33	47.27	3.80	37.27	24.40	7.67
Over all mean	40.00	95.34	106.21	3.17	1.23	5.70	45.61	3.39	38.66	23.58	6.24

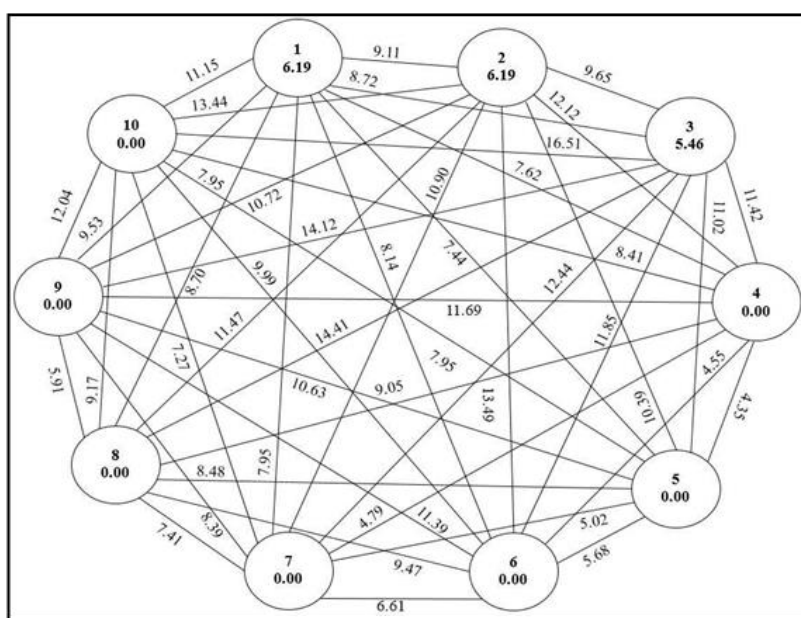


Fig. 1. Cluster diagram indicating inter and intra cluster distance

Table 7. Percentage contribution of each character towards divergence

Sr.No.	Source	Times Ranked 1st	Contribution%
1	DFF	5	0.58 %
2	DM	1	0.12 %
3	PH	8	0.93 %
4	CL	9	1.05 %
5	CW	62	7.20 %
6	CC	183	21.25 %
7	LF	270	31.36 %
8	SW	8	0.93%
9	OC	2	0.23 %
10	HI	165	19.16 %
11	SYP	148	7.19 %

DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsules per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

It could be concluded that high yielding genotypes coupled with desirable traits like plant height, capsule length, capsule width, capsules per cluster, 1000 seed weight, harvest index and seed yield per plants could be selected as parents for hybridization programme from cluster X, IX, VI and VIII. Intercrossing genotypes from these clusters might result in wide array of variability for exercising effective selection.

The component of  $D^2$  due to each character variable was ranked in descending order of magnitude, rank-I being assigned to the highest value. The percent contribution of different characters to diversity is presented in Table-7. The present study revealed that leaf area (31.36%), capsules per cluster (21.25%), harvest index (19.16%), capsule width (7.20%), seed yield per plant (7.19%) and capsule length (1.05%) were the main contributors to the total

divergence. These six characters accounted for 87.21% of total divergence. The contribution of remaining five characters was negligible to small [39].

#### 4. CONCLUSION

The analysis of variance revealed the presence of sufficient variability among the genotypes for different characters. Maximum range of variation was observed for plant height followed by leaf area and days to maturity indicating the presence of wide variation for the characters. The values of phenotypic coefficient of variation were higher than genotypic coefficient of variation indicating the less influence of environmental factors in most of the characters. The highest genotypic coefficient of variation was observed for seed yield per plant followed by capsules per cluster and harvest index which indicated the presence

of wide genetic variation for these characters. High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for the traits viz., capsule width, capsules per cluster, leaf area, harvest index and seed yield per plant indicating that these characters are under the control of additive gene effect. Therefore, further improvement in these traits using pure line selection would be worthwhile. The seed yield per plant was found to be significant and positively correlated with days to maturity, capsule length, capsule width, capsules per cluster, 1000 seed weight and harvest index at genotypic and phenotypic levels. The oil content had highly significant and negative association with seed yield per plant. Path coefficient analysis showed days to 50% flowering, days to maturity, plant height, capsule length, capsule width, 1000 seed weight and harvest index positive direct effects on seed yield per plant. Hence, these traits were considered as the most important yield contributors and due emphasis should be given while attempting seed yield improvement in sesame. The genetic diversity analysis revealed the formation of ten clusters suggested the presence of wide genetic diversity among the forty-two genotypes studied. The geographic diversity was not associated with genetic diversity. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that leaf area followed by capsules per cluster, harvest index, capsule width, seed yield per plant and capsule length were the main contributors to the total divergence. These six characters accounted for more than 87.21% of total divergence in the material studied. Based on the maximum genetic distance, it is advisable to attempt intercrossing of the genotypes from cluster X, IX and VIII, which may lead to broad spectrum of favorable genetic variability for yield improvement in sesame. The present study suggested that days to maturity, capsule length, capsule width, capsules per cluster, 1000 seed weight and harvest index should be considered as selection criteria for yield improvement in sesame.

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## COMPETING INTERESTS

Authors have declared that no competing interests exist.

## REFERENCES

1. Bedigian D, Smyth CA, Harlan JR. Patterns of morphological variation in *Sesamum indicum* (L.). *Econ. Bot.*, 1986;40: 353-365.
2. Quarrie S, Peki QS, Radosevi R, Rancic D, Kaminska A. Dissecting a wheat QTL for yield present in a range of environments: From the QTL to candidate genes. *J. Exp. Bot.*, 2006;57: 2627-2635.
3. Wattoo FM, Saleem M, Ahsan, M, Sajjad M, Ali W. Genetic analysis for yield potential and quality traits in maize (*Zea mays* L.). *Am.-Eurasian J. Sustain. Agric.*, 2009;6(6): 721-732.
4. Dewey DR, Lu KH. Correlation and path coefficient analysis of components of crested wheat grass seed production. *J. Agron.*, 1959;51: 515- 518.
5. Mukhtar MS, Rahman M, Zafar Y. Assessment of genetic diversity among wheat (*Triticum aestivum* L.) cultivars from a range of localities across Pakistan using random amplified polymorphic DNA analysis. *Euphytica*. 2002;128: 417-425.
6. Mumtaz SA, Naveed M, Shinwari ZK. Assessment of genetic diversity and germination pattern in selected cotton genotypes of Pakistan. *Pak. J. Bot.*, 2010;42(6): 3949-3956.
7. Pandey SK, Das A, Rai P, Dasgupta T. Morphological and genetic diversity assessment of sesame (*Sesamum indicum* L.) accessions differing in origin. *Physiol. Mol. Biol. Plants*. 2015;21(4):519-529.
8. Valarmathi G, Kumar M, Saravana NA. Genetic variability and correlation studies for seed related traits in sesame (*Sesamum indicum* L.). *Sesame and Safflower Newsletter*. 2004;19.
9. Raghuwanshi SS, Kachadia VH, Vachhani JH, Jivani LL, Malav AK, Bhati SS. Selection indices in groundnut (*Arachis hypogaea* L.). *Electron. J. Plant Breed.*, 2015;7(1):140-144.
10. Sarwar G, Haq MA. Evaluation for genetic parameters and disease resistance in sesame. *J. Agric. Res.*, 2006;3:44-46.

11. Gawali CW, Bhoite KD, Pardeshi SR, Mhaske BM, Wagh MP. Study of genetic variability and correlation studies in sesame (*Sesamum indicum* L.). Agril. Sci. Digest. 2007;27: 282-284.
12. Sumathi P, Muralidharan V. Analysis of genetic variability, association and path analysis in the hybrids of sesame (*Sesamum indicum* L.). Trop. Agric. Res. Ext. 2010;13(3): 63-67.
13. Gidey YT, Kebede SA, Gashawbeza GT. Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. Intern. J. Plant Breed. Genet. 2012;7: 2-14
14. Bharathi D, Rao VT, Mohan YC, Bhadru D, Venkanna V. Genetic variability studies in sesame (*Sesamum indicum* L.). Intern. J. Appl. Biol. Pharmac. Technol. 2014; 5: 31-33.
15. Abate M, Mekbib F. Assessment of genetic variability and character association in Ethiopian low-altitude sesame (*Sesamum indicum* L.) genotypes. J. Adv. Stud. Agric. Biol. Environ. Sci., 2015a;2(3): 55-66.
16. Iqbal A, Akhtar R, Begum T, Dasgupta T. Genetic estimates and diversity study in sesame (*Sesamum indicum* L.). IOSR J. Agric. Veter. Sci., 2016;9: 1-5.
17. Mandal RK, Suman SJ, Ojha RK, Ram, S. Genetic variability in the germplasm of sesame (*Sesamum indicum* L.). Environ. Ecol., 2010;28(4): 2556-2561.
18. Gayathri G. Heterosis breeding in sesame (*Sesamum indicum* L.). Ph.D. (Ag) thesis, Kerala Agricultural University, Thrissur. 2011;180.
19. Gidey YT, Kebede SA, Gashawbeza GT. Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. Int. J. Plant Breed. Genet., 2013;7 (1): 21-34.
20. Reddy PAV, Sekar MR, Ranganatha ARG, Dhanraj A. Genetic variability and heritability for seed yield and its components in sesame (*Sesamum indicum* L.). J. Oilseeds R., 2001;18(2): 173-175.
21. Krishnaiah G, Reddy KR, Sekar MR. Variability studies in sesame. Crop Res., 2002;24(3): 501-504.
22. Mohanty TA, Singh UK, Singh SK, Kushwaha N, Singh D. Study of genetic variability, heritability and genetic advance in sesame (*Sesamum indicum* L.) genotypes. Int. J. Curr. Microbiol. App. Sci., 2020a;9(02): 347-356.
23. Rao VT, Bharathi D, Mohan C, Venkanna V, Bhadru D. Genetic variability and association analysis in sesame (*Sesamum indicum* L.). Crop Res., 2013;46:122-125.
24. Abhijatha A, Arya K, Madhukar K, Gogineni S. Evaluation of sesame (*Sesamum indicum* L.) genotypes to the shaded uplands of southern region. Int. J. Curr. Microbiol. Appl. Sci., 2017;6(7): 332-339.
25. Patil MK, Lokesha R. Estimation of genetic variability, heritability, genetic advance, correlations and path analysis in advanced mutant breeding lines of sesame (*Sesamum indicum* L.). J. Pharmacogn. Nat. Prod., 2018;4: 151.
26. Bhuvan J, Sharma MK. Character association studies in sesame (*Sesamum indicum* L.) under rainfed condition. Adv. Plant Sci., 2004;17(1):313-316.
27. Yol E, Karaman E, Furat, S, Uzun B. Assessment of selection criteria in sesame by using correlation coefficients, path and factor analyses. Australian J. Crop Sci., 2010;4(8): 598-602.
28. Fazal A, Mustafa HSB, Hasan EU, Anwar M, Tahir MHN, Sadaqat HA. Interrelationship and path coefficient analysis among yield and yield related traits in sesame (*Sesamum indicum* L.). Nat. sci., 2015;13(5): 27-32.
29. Bamrotiya MM, Patel JB, Malav A, Chetariya CP, Ahir D, Kadiyara J. Genetic variability, character association and path analysis in sesame (*Sesamum Indicum* L.). Int. J. Agric. Crop Sci., 2016a;8(54): 2912-2916.
30. Rao CR. Advanced Statistical Methods in Biometrical Research, John Wiley and Sons, New York. 1952;357-369.
31. Jadhav RS, Mohrir MN. Genetic divergence analysis in sesame (*Sesamum indicum* L.). Electron. J. Plant Breed., 2013;4(1): 1090-1092.
32. Gogoi LR, Singh SK, Sarma RN. Assessment of genetic diversity in indigenous sesame genotypes. Int. J. Curr. Microbiol. Appl. Sci., 2018;7(6):1509-1520.
33. Mohan YC. Variability and genetic divergence in sesame (*Sesamum indicum* L.). Int. J. Appl. Biol. Pharma. Tech., 2014b;5(3):222-225.
34. Ramprasad E, Jatothu SSJL, Yamini KN, Dangi KS. Analysis of genetic diversity in sesame (*Sesamum indicum* L.) advanced

- breeding lines and varieties collected from major breeding centers in India. Electron. J. Plant Breed., 2019b;10 (3): 1269-1274.
35. Soundharya B, Hemalatha, V, Shobha R, Edukondalu B. Genetic divergence studies in sesame (*Sesamum indicum* L.) genotypes. Int. J. Curr. Microbiol. Appl. Sci. 2017b;6(9): 2615-2619.
36. Swathy V, Premnath A, Viswanathan PL, Raveendran M, Manonmani S. Determination of genetic divergence based on morphological traits in sesame (*Sesamum indicum* L.). Electronic J. Plant Breed., 2018;9(2):747-752.
37. Mohanty TA, Singh, UK, Singh SK, Singh D, Kushwaha N. Assessment of genetic diversity in sesame (*Sesamum indicum* L.) based on agro-morphological traits. Curr. J. Appl. Sci. Technol. 2020b;39(25): 101-107.
38. Singh BS, Choudhary RK. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. 1977;20-35.
39. Tanwar A, Bisen R. Genetic diversity analysis in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. Electronic J. Plant Breed. 2018;9(1):9-17.

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