

## Original Research Article

### Genetic Variability, Path analysis and divergence studied in Sesame (*Sesamum indicum* L.)

#### ABSTRACT

The study was conducted during *rabi*, 2020 at the Niger Research Station, Navsari Agricultural University, Vanarasi, Ta. Vansda to assess the information on genetic variability, character association and path analysis among 42 genotypes of sesame (*Sesamum indicum* L.). 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 day of maturity, capsule length, capsule width, capsules per cluster, 1000 seed weight and harvest index at 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<sup>2</sup> analysis indicated wide genetic diversity among the forty-two genotypes which were grouped into ten clusters indicating there is no formed relationship between geographical diversity and genetic diversity. Cluster III and X showed the maximum intercluster 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 attributes and cluster IX for two important characters. Genotypes from these clusters may produce progenies with high genetic variation.

**Keyword-** Genetic variability, Heritability, Genetic advance, Path analysis, *Sesamum indicum* L.

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## Introduction

Sesame (*Sesamum indicum* L.) is one of the most important ancient cultivated oilseed crops grown in Asia and Africa. It belongs to the 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 Oilseed". The crop is highly tolerant to drought, grows well in most of the well-drained soils and various agroclimatic regions, and is well adapted to different rotations. Sesame is a 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 oilseed crop being a rich source of protein (18–25%), carbohydrate (13.5%), minerals and polyunsaturated fatty acid (Bedigian, 1986). Variation is a prerequisite to start a breeding programme in any crop. Genetic variability is necessary for continued genetic improvement of crop species. Biometrical techniques to evaluate the genetic variability and extent of heritability of economic characters serve as useful tools in evaluating these segregating populations. Variation and selection are two basic essentials 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 (Quarrie, 2006) and more particularly by yield-related traits which are greatly influenced by both genetic and environmental factors (Wattoo, 2009). If information on genetic variability is available then the selection based on yield component traits is advantageous. Phenotypic and genotypic correlation coefficients and yield components and their contribution in path analysis provide information on their relative importance in determining the yield (Dewey and Lu, 1959).

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Genetic diversity is a fundamental element in plant breeding which provides information about genetic relatedness among elite breeding material (Mukhtar *et al.*, 2002). Genetic diversity among landraces will help in the selection and breeding of high yielding, good quality cultivars that will increase production (Mumtaz *et al.*, 2010). 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 programs and also significant to improve sesame varieties. Diversity analysis based only on morphological characters are prone to environmental bias due to biotic influences and also complex genetic structure of different morphological traits (Pandey *et al.*, 2015).

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## 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, Navsari, Ta. Vansda, Dist. Navsari, Gujarat. The seeds were sown at 60 cm between rows and 15 cm between plants in the row. Total area of experimental unit was  $24.5\text{m}^2$ . 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 row 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 observations were recorded on five randomly selected plants from each genotype on different

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characters viz. days to 50% flowering, daystomaturity,plantheight(cm),capsulelength (cm), capsule width (cm), capsulespercluster,leafarea(cm<sup>2</sup>),1000seedweight (g), oil content (%), harvest index(%)andseedyieldperplant(g).ThephenotypicandgenotypiccoefficientofvariabilitywascomputedasperBurtonandDe vane (1953). Heritability (h<sup>2</sup>) in broadsense and genetic advance percent of meanwascalculatedforeachcharacteraccordingtothemethodsuggestedbyJohnson(1955).Correlationcoefficientsforyieldandyieldcomponentswereevaluatedusing the formula suggested by PanseandSukhatme(1987).

## ResultsandDiscussion

The ~~present~~ experimental ~~result material~~ 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, plantheight, 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. daystomaturity and oil contents 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. there is ample scope to identify high yielding traits possessing genotypes. Similar results in related to sesame for most of the characters were also reported by Valarmathi (2004) Raghuwanshi (2005); Sarwar and Haq (2006), Gawali (2007),

Parameshwarappa (2009) for days to 50% flowering, plantheight, capsule length, 1000 seed weight and seed yield per plant; Sumathian and muralidharan (2010), Gidey *et al.* (2012), Bharathi *et al.* (2014), Abate and Mekbib (2015a) and Iqbal *et al.* (2016).

The estimates of genotypic (GCV) and phenotypic (PCV) coefficients of variability (Table-2) indicated that the values of PCV were higher than GCV for all-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. Highest estimates of GCV in sesame have been also reported for seed yield per plant by Valarmathi (2004), Mandal *et al.* (2010), Gayathri (2011) and Gidey (2013).

Highest 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.* (2001), Krishnaiah *et al.* (2002); for harvest index by Mohanty (2020a).

The correlation coefficients between seed yield per plant and ~~its eleven yield~~ component characters and among themselves were estimated at genotypic and phenotypic levels and are presented in Table-3 as Genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlations

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coefficient are described as under this table. In general, the values of genotypic correlations coefficient were higher than their corresponding phenotypic correlations coefficient. This indicated that though 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).

Such positive interrelationship between seed yield per plant and these attributes has also been reported in sesame by several researchers.

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UNDER PEER REVIEW

Table 1: Analysis of variance for different characters in sesame

Source of Variation	d.f.	MSS					
		Days to 50% flowering (DF)	Days to maturity (DM)	Plant height (cm) (PH)	Capsule length (cm) (CL)	Capsule width (cm) (CW)	Capsules per cluster (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				
		Leaf area (cm <sup>2</sup> ) (LA)	1000 seed weight (g) (SW)	Oil content (%) (OC)	Harvest index (%) (HI)	Seed yield per plant (g) (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

\* and \*\* indicate significance at 5% and 1% level of probability, respectively

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

<b>DF</b> ≡ Daysto 50% flowering	<b>DM</b> ≡ Daysto maturity	<b>PH</b> ≡ Plantheight(cm)	<b>CL</b> ≡ Capsulelength(cm)
<b>CW</b> ≡ Capsulewidth(cm)	<b>CC</b> ≡ Capsulespercluster	<b>LA</b> ≡ Leaf area(cm <sup>2</sup> )	<b>SW</b> ≡ 1000 seedweight(g)
<b>OC</b> ≡ Oilcontent(%)	<b>HI</b> ≡ Harvestindex(%)	<b>SYP</b> ≡ Seed yieldperplant(g)	

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Table 2: Range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percent of mean for different characters of sesame.

Sr. No.	Characters/Traits	Range	Mean	Coefficient of variance		Heritability- h <sup>2</sup> (%)	Genetic Advance (GA)	Genetic Advance as percent Mean (GAM)
				GCV (%)	PCV (%)	h <sup>2</sup> (%)	GA	GAM
1	Days to 50% flowering (DFE)	35.33 – 43.33	39.45	4.38	6.86	40.69	2.27	5.75
2	Days to maturity (DM)	85.67 – 101.50	94.58	2.31	5.60	17.00	1.86	1.96
3	Plant height (cm) (PH)	88.40 – 116.90	104.47	5.27	8.54	38.06	6.99	6.69
4	Capsule length (cm) (CL)	2.57 – 3.80	3.00	6.76	9.23	53.69	0.31	10.20
5	Capsule width (cm) (CW)	0.77 – 1.80	1.10	16.26	18.42	77.95	0.33	29.57
6	Capsules per cluster (CC)	2.27 – 7.27	5.03	24.42	26.36	85.82	2.34	46.61
7	Leaf area (cm <sup>2</sup> ) (LA)	36.30 – 56.43	45.21	12.62	13.60	86.02	10.90	24.11
8	1000 seed weight (g) (SW)	2.70 – 3.80	3.21	7.72	10.07	58.80	0.39	12.20
9	Oil content (%) (OC)	36.13 – 44.07	39.88	2.81	6.50	18.69	1.00	2.50
10	Harvest index (%) (HI)	11.17 – 34.57	21.90	23.17	25.30	83.85	9.57	43.70
11	Seed yield per plant (g) (SYP)	2.03 – 8.00	5.07	27.24	30.14	81.65	2.57	50.70

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

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

Characters		DFE	DM	PH	CL	CW	CC	LA	SW	OC	HI	SYP
DFE	$r_g$	<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>	1.079**	<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, DFE=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsule per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant.

<b>DFE</b> = Daysto 50%flowering	<b>DM</b> =Daysto maturity	<b>PH</b> =Plantheight(cm)	<b>CL</b> =Capsulelength(cm)
<b>CW</b> = Capsulewidth(em)	<b>CC</b> =Capsulespereluster	<b>LA</b> =Leaf area(em <sup>2</sup> )	<b>SW</b> =1000 seedweight(g)
<b>OC</b> = Oilcontent(%)	<b>HI</b> =Harvestindex(%)	<b>SYP</b> =Seed yieldperplant(g)	

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Table 4: Genotypic path coefficients 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 indicated direct effects

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

<b>DF</b> = Daysto 50% flowering	<b>DM</b> = Daysto maturity	<b>PH</b> = Plantheight(em)	<b>CL</b> = Capsulelength(em)
<b>CW</b> = Capsulewidth(cm)	<b>CC</b> = Capsulespercluster	<b>LA</b> = Leaf area(cm <sup>2</sup> )	<b>SW</b> = 1000 seedweight(g)
<b>OC</b> = Oilcontent(%)	<b>HI</b> = Harvestindex(%)	<b>SYP</b> = Seed yieldperplant(g)	

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Table5: Interand intracluster  $D^2$  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 intracluster  $D^2$  values

Fig1. Cluster diagram indicating intra and inter-cluster distance

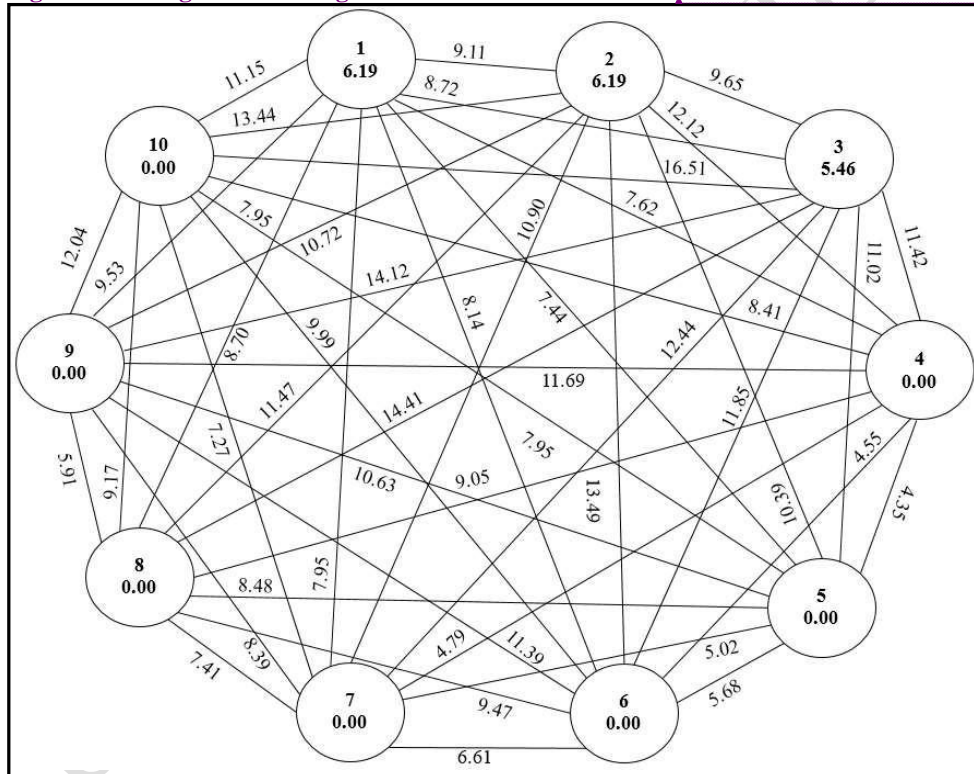


Figure 1. Cluster diagram indicating inter and intra cluster distance

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Table6:Cluster means for yield and yield contributing traits of sesame genotypes

Cluster	DFE	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

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Table7:Percentage contribution of each character towards divergence

Sr.No.	Source	Times Ranked 1st	Contribution%
1	Days to 50% flowering DFF	5	0.58 %
2	Days to maturity DM	1	0.12 %
3	Plant height (cm) PH	8	0.93 %
4	Capsule length (cm) CL	9	1.05 %
5	Capsule width (cm) CW	62	7.20 %
6	Capsules per cluster CC	183	21.25 %
7	Leaf area (cm <sup>2</sup> ) LF	270	31.36 %
8	1000 seed weight (g) SW	8	0.93 %
9	Oil content (%) OC	2	0.23 %
10	Harvest index (%) HI	165	19.16 %
11	Seed yield per plant (g) SYP	148	7.19 %

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

The positive genotypic association has been reported between seed yield per plant and capsule length by Parmeswarappa *et al.* (2009), Rao *et al.* (2013), Abhijatha *et al.* (2017), Patil and Loksha (2018); for seed yield per plant and 1000 seed weight by Bhuvan and Sharma (2004), Yol *et al.* (2010), Fazal *et al.* (2015), Imran and dash (2018); for seed yield per plant and harvest index by Gidey *et al.* (2013), Bamrotiya *et al.* (2016a) and Patil and Loksha (2018), respectively. The present results on correlation coefficients revealed that, day 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 interrelationship 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.

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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 day to 50% flowering, day 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% which suggested that there might be few more component traits responsible to influence the seed yield per plant than those studied. 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.

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The Mahalanobis's  $D^2$  statistics was computed for all possible pairs of populations under investigation. Forty-two genotypes of sesame were grouped into ten clusters on the basis of relative magnitude of  $D^2$  values following Tocher's method (Rao, 1952). Cluster I was the largest cluster having twenty one genotypes. The second largest cluster II had nine while cluster III had five genotypes, respectively whereas 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 that selection of parents for hybridizations 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 (2013), Gogoi *et al.* (2018), Mohan (2014b), Ramprasad *et al.* (2019b), Soudharya *et al.* (2018b), Swathy *et al.* (2018) and Mohanty *et al.* (2020b).

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Intra and inter cluster distance (Table 5 with figure 1.) between all possible pairs of ten clusters were computed with the help of method given by Singh and Chaudhary (1977). 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

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(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 I exhibited third highest mean value for-  
oil content (39.62%). These second highest mean value for leaf area (52.73 cm<sup>2</sup>) and oil content (40.86%) whereas lowest mean value of capsules per cluster (3.96) and seed yield per plant (4.19 g) was recorded in cluster II. Cluster III exhibited the lowest mean value for most of the traits viz., capsule length (2.76 cm), capsule width (0.87 cm), 1000 seed weight (2.90 g) and harvest index (14.77%). Cluster IV depicted mean value for second highest mean value for capsule width (1.33 cm) and 1000 seed weight (3.73 g). The lowest mean value for days to maturity (91.33 days), plant height (98.20 cm) and oil content (36.93%) was noticed in cluster IV. Cluster V depicted highest mean value for days to 50% flowering (43.00 days) whereas second highest mean value for plant height (111.70 cm) and seed yield per plant (7.73 g). Cluster VI showed highest mean value for capsules per cluster (7.27). Besides this, it had lowest mean value for leaf area (36.57 cm<sup>2</sup>). Cluster VII exhibited second highest mean values for capsule length (3.33 cm), capsule width (1.33 cm) and capsules per cluster (7.00). Cluster VIII depicted highest mean value for days to maturity (101.50 days) and seed yield per plant (8.00 g). Cluster IX depicted highest mean value for leaf area (55.17 cm<sup>2</sup>) and harvest index (34.57%). Cluster X showed highest mean value for most of traits viz. plant height (115.53 cm), capsule length (3.80 cm), capsule width (1.80 cm) and 1000 seed weight (3.80 g) whereas lowest mean value for days to 50% flowering (38.00 days).

It could be concluded that highly 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.

## Conclusion

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 selecti

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For clusters, III, IV, V, VI, VII and VIII

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on criteria for yield improvement in sesame.

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