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GENETIC DIVERSITY STUDIES FOR YIELD AND YIELD CONTRIBUTING TRAITS IN SESAME (*Sesamum indicum* L.)

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ABSTRACT

Fifty seven genotypes along with three checks were studied for genetic diversity using Mahalanobis D^2 statistics, to find the extent of deviation of these genotypes from the checks and to select the best genotypes for further use in breeding programme. Fifty seven genotypes along with three checks were raised during *kharif* 2014-15 in two replications and data were recorded for days to 50% flowering, days to maturity, plant height (cm), number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight (g) , seed yield plant^{-1} (g) and oil content (%). Considerable variability existed among the genotypes for all characters studied from the significant mean squares due to genotypes. The genotypes were grouped into eight clusters indicating the presence of wide range of diversity among them. Number of seeds capsules^{-1}, number of capsules plant^{-1}, 1000 seed weight, oil content and seed yield plant^{-1} contributed maximum towards genetic divergence. Fifty seven genotypes and three checks were grouped into eight clusters. The intra cluster distance ranged from 0.000 in Cluster V, VII and VIII to 103.87 in IV and the average inter cluster distance was ranged from D^2=678.90 between cluster VI and cluster VIII to (D^2=65.04) between cluster VII and cluster VIII. The grouping of genotypes into different clusters clearly showed that many of genotypes were highly deviating from the checks. The genotypes belonging to distant clusters and exhibiting high performance in the desirable direction for number of capsules plant^{-1}, number of seeds capsule^{-1} , plant height and 1000 seed weight were identified as the potential parents for sesame hybridization programme. This study resulted in identification of parents to be crossed in four set of crossing programme. It is inferred from this study that the genotypes ES-36-A, IS-3197-A and KMR-302-A should be crossed with KMR-83-A, S-0484 and SI-3273-A in the first set, the genotypes NIC-16227-A, NIC-10621, IS-562-A, IS-101-1-4849 and AKT-64 should be crossed with SI-3273-A and RJS-147-1-84 in the second set and the genotypes KMS-48-A, TKG-22, GRT-839-A should be crossed with S-0484 and SI-3273-A in the third set ES-1144-B, Pragati and KMR-4 should be crossed with SI-3273-A, NIC-16227-A, NIC-10621 and S-0233 in the forth set's.

(Key words: Genotypes, inter cluster distance, genetic diversity)

INTRODUCTION

Sesame (*Sesamum indicum* L.) occupies vital position in Indian agriculture and probably one of the ancient oilseed crop known and used by man. It is referred as "queen of oilseed". India rank first, both in the area and production of sesame in world. The sesame seed is a rich source of edible oil. Its oil content generally varies from 46 to 52% (Anonymous, 2013). Sesame was cultivated on area of 17.78 lakh ha with production of 8.11 lakh tonnes and productivity of 456 kg ha^{-1} during 2014-15 in the country (Anonymous, 2015). In Maharashtra, area was 0.278 lakh hectares with 0.48 lakh tonnes production and productivity of 172 kg ha^{-1}. In Vidarbha, area under sesame was 0.066 lakh hectares with 0.011 lakh tonnes production and productivity of 167 kg ha^{-1} (Anonymous, 2013). The oil extracted from sesame is of high quality, resistant to oxidation and rancidity even when stored at ambient air temperature.

The future prospects for increasing area under sesame seem to be limited. Therefore, the main thrust to increase production has to be on increasing the yield unit^{-1} area, by adopting improved technology and increasing area under high yielding varieties (Gill, 1987). The study of diversity among the available germplasm is useful to plan sesame breeding programme because success of breeding programme depends on selection of superior lines of diverse origin. The development of sesame varieties with high yield potential and high oil content assumes greater importance in sesame improvement programme. Therefore, the information on genetic variation for yield and yield related agronomic characters is prerequisite to initiate the sesame breeding programme for development of varieties with high yield potential. Hence, the present investigation was conducted with the objectives to estimate the genetic variation and diversity among sesame germplasm for yield and important yield contributing traits and to identify the

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desirable and potential genetically diverse genotypes for sesame breeding programme.

MATERIALS AND METHODS

The experiment was carried out at farm Agricultural Botany Section, College of Agriculture, Nagpur during *kharif* 2014-15. The experimental material consisted of 57 genotypes with 3 checks were planted in randomized block design with two replications in plot size of 20 m x 25 m. The row to row and plant to plant distance was maintained at 30 cm x 15 cm. All recommended package of practices was applied to maintain good crop. The data was recorded on nine characters, *viz*., days to 50% flowering, days to maturity, plant height (cm), number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight (g), seed yield plant^{-1} (g) and oil content (%). Mahalanobis (1936) D^2 statistics was used for assessing genetic divergence among all the genotypes. The clustering of D^2 values was done by using Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The mean square due to genotypes were highly significant for all nine characters studied viz., days to 50% flowering, days to maturity, plant height, number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight, seed yield plant^{-1} and oil content (Table 1) indicating the presence of considerable genetic variation among the genotypes for characters studied. This allows the further estimation in the experimental material. The wide variability for number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight, plant height and yield contributing characters in sesame were also observed by Tripathi *et al.* (2013). The analysis of dispersion (Table 2) for the test of significance of differences in the mean values based on Wilk's criterion revealed highly significant differences among the genotypes for the aggregate of nine characters (X^2=585.72 at 531 d.f.). Therefore, the data were further evaluated for D^2 and cluster analysis. The D^2 values obtained for 60 genotypes in all possible combinations were 3600 which were too large for presenting, hence the table showing D^2 values were not presented. Shekhawat *et al.* (2013) reported significant divergence among the 55 genotypes for all the nine characters studied for genetic divergence in sesame.

The 60 genotypes on the basis of D^2 statistics were grouped into 8 clusters (Table 3). The cluster I and IV were largest comprising of 16 genotypes in each cluster. Cluster II comprising of 14 genotypes. Cluster III comprising 7 genotypes followed by cluster VI comprising 4 genotypes. Cluster V, VII, VIII were the smallest comprising of single genotype in each cluster. The check Pragati grouped into cluster I along with 15 genotypes. While the check TKG-22 grouped into cluster III along with 6 genotypes and the check AKT-64 grouped into cluster IV along with 15 genotypes. This indicates that there were many germplasm which were highly diverse from the check and hence offers good scope for improvement. Similar to this result Shekhawat *et al.* (2013) grouped 55 genotypes into 14 clusters; Parameshwarappa *et al.* (2010) grouped 64 genotypes into 9 clusters. The number of clusters into which genotypes were grouped is often noticed to vary with set of genotypes used for cluster analysis depending on the extent of distance from one another.

Average intra and inter cluster distance among nine characters were worked out by Tocher's method and data are presented in table 4. The inter cluster distance in most of the cases were higher than the intra cluster distance. The intra cluster distance ranged from 0.000 to 103.87. Cluster IV possessed highest intra cluster distance (D^2=103.87) followed by cluster VI (88.33) and cluster III (66.94). The average inter cluster distance was maximum between cluster VI and cluster VIII (D^2=678.90), followed by cluster V and VI (D^2=514.80), cluster VI and VII (D^2=456.23) and cluster II and VI (D^2=428.61) suggesting more variability in genetic makeup of genotypes included in these clusters. The inter cluster distance was found to be minimum between cluster VII and cluster VIII (D^2=65.04). Widely diverged clusters remain distinct in different environment. Therefore, the genotypes belonging to the distant clusters may be used in hybridization programmed for obtaining a wide spectrum of variation among the segregates. These findings are in conformity with the finding of Parameshwarappa *et al.* (2010), who also reported selection of divergent clusters.

The data regarding contribution of each character towards genetic divergence are presented in table 5. Contribution of number of capsules plant^{-1} was maximum (48.76%) followed by 1000 seed weight (30.34%), oil content (11.81%), number of seeds capsule^{-1} (7.06%), days to 50% maturity (0.73%), seed yield plant^{-1} (0.68%), number of branches plant^{-1} (0.34%), days to maturity (0.23%) and plant height (0.06%). This indicates that character like number of seeds capsule^{-1}, 1000 seed weight, oil content, number of capsules plant^{-1} were important traits contributing towards genetic divergence. In agreement with present result Tripathi *et al.* (2013) studied the contribution of individual characters towards total divergence and reported that per cent contribution was highest for number of capsules plant^{-1} (56.55%), followed by 1000 seed weight and oil content. Nayak *et al.* (2011) also reported highest contribution towards genetic divergence for days to maturity followed by days to 50% flowering, number of seeds capsule^{-1} and number of capsules plant^{-1}.

The data regarding cluster means for all nine characters are presented in table 9. The comparison of cluster means for nine characters under study marked considerable genetic difference between groups. Overall study for cluster mean considering all the nine characters indicated that cluster V possessed the highest cluster mean for days to 50% flowering, plant height and 1000 seed weight. Cluster IV possessed the highest cluster mean for days to maturity. Cluster VI possessed the highest mean for number of seeds

capsule^{-1}. Cluster VII possessed the highest cluster mean for number of branches plant^{-1} and seed yield plant^{-1}. Cluster VIII possessed the highest cluster mean for number of capsules plant^{-1} and oil content. The variance for cluster means was maximum for number of capsules plant^{-1} (510.43) followed by number of seeds capsule^{-1} (36.67), plant height (20.09), oil content (13.37), 1000 seed weight (7.14), days to maturity (6.76), days to 50% flowering (2.85), number of branches plant^{-1} (0.04), and seed yield plant^{-1} (0.05). Cluster means based on correlated data are used to know relative importance of characters in causing genetic divergence. In the present study the result of standard deviation of cluster mean indicated that number of capsules plant^{-1}, number of seeds capsule^{-1}, plant height, oil content, 1000 seed weight, days to maturity, days to 50% flowering and seed yield plant^{-1} were important source of variation which suggested that these characters were highly responsible for genetic divergence in the present material. Thus, from this study it can be reported that parents may be selected for hybridization on the basis of number of capsules plant^{-1}, number of seeds capsules^{-1} and plant height. Nayak *et al.* (2013) observed above mentioned characters for genetic divergence of sesame.

According to Bhatt (1970) the mean statistical distance may be considered arbitrarily as a guideline and crosses between parents belonging to different clusters having same or higher inter cluster distance than the mean statistical $\overline{D}$ stance may be attempted. In the present study all possibie combinations beyond mean inter cluster distance (= 91.67) from different clusters were arranged in descending order of their magnitude of genetic distance and promising 25 cluster combinations are presented in table 7. Other practical considerations like number of capsules plant^{-1}, number of seeds capsule^{-1} and plant height were also taken into account while choosing the genotypes from selected cluster combinations, as these characters were found to important for primary selection based on cluster mean, cluster variances and contribution of characters towards genetic divergence.

Based on the above criteria crossing between parents in four sets i.e. (i) Crossing of ES-36-A, IS-3197-A and KMR-302-A with KMR-83-A, S-0484 and SI-3273-A, (ii) Crossing of NIC-16227-A, NIC-10621, IS-562-A, IS-101-1-4849 and AKT-64 with SI-3273-A and RJS-147-1-84, (iii) Crossing of KMS-48-A, TKG-22, GRT-839-A with S-0484 and SI-3273-A and (iv) Crossing of ES-1144-B, Pragati and KMR-4 with SI-3273-A, NIC-16227-A, NIC-10621 and S-0233 were suggested.

Table 1. Analysis of variance for the experimental design

Source of variation	d.f	Mean sum of square								
		Days to 50% flowering	Days to maturity	Plant height	Number of branches plant^{-1}	Number of capsules plant^{-1}	Number of seeds capsule^{-1}	1000 seed weight	Seed yield plant^{-1}	Oil content (%)
Replications	1	0.83	4.80	11.04	0.00	1.37	1.11	0.00	0.03	0.01
Genotypes	59	8.67**	23.61**	46.63**	0.22**	59.05**	48.89**	0.01**	0.05**	0.84**
Error	59	2.14	4.60	12.37	0.07	2.55	0.39	0.02	0.01	0.25

** Significant at 1% level

Table 2. Analysis of dispersion

Source of variations	df	Sum of squares	Mean sum of squares
Genotypes	59	3.0457E+03	5.1623E+01**
Error	58	1.4212E+05	2.4503E-03
Total	117	3.0457E+03	2.6032E+01

** Significant at 1% level

Table 3. Distribution of 60 germplasms of sesame in different clusters

Clusters	Total number of germplasm	Name of germplasms
I	16	ES-144-B-B, SP-1184-A, GLT-8, KMR-4, NIC-8600-A, SI-1170-A, NIC-16387-A, SI-178-B, IS-205, IS-2, IS-184, KIS-352-A, IS-32359, IS-731, **Pragati**, IS-93-B
II	14	NIC-16227-A, NIC -10621, IS -562-A, NIC-17890-A, IC -204550, SI -506-A, NIC-16190-A, KMR-4-259-A, NIC-16327, IS-24-A, IS-471, IS-110613, IS-80-B, NIC-54-164-B
III	7	KMR-48-A, IC-1025-A, GRT-839-A, **TKG-22**, NIC-8538-A, SI-1782-A, IS-673
IV	16	SI-8459, **AKT-64,** IS-101-1-4849, SI-2531-C, KIS-300-A, NIC-1615-B, NIC-16391, IS-157-A, IS-153-3, SI-2039-A, KMS-423, IS-505, S-0233, KMR-83-A, NIC-9862-A, IS-8484
V	1	S-0484
VI	4	ES-36-A, IS-3197-A, NIC-7835-A, KMR-302-A
VII	1	SI-3273-A
VIII	1	RJS-147-1-84-A

Table 4. Average intra and inter cluster distance D^2 values

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**42.503**	106.320	69.537	123.190	272.380	197.912	132.013	237.538
II		**62.268**	164.453	188.598	200.007	428.611	78.317	128.596
III			**66.935**	160.598	328.940	193.391	167.853	290.103
IV				**103.865**	190.477	211.024	188.216	330.539
V					**0.000**	514.790	181.764	315.557
VI						**88.327**	456.228	678.895
VII							**0.000**	65.039
VIII								**0.000**

$\bar{D}$ = 91.67 Bold figures are average intra cluster distance

Table 5. Contribution of different characters towards genetic divergence

Sr .No	Characters	Times ranked 1st	Per cent contribution
1	Days to 50% flowering	4	0.23
2	Days to maturity	13	0.73
3	Plant height	1	0.06
4	Number of branches plant^{-1}	6	0.34
5	Number of capsules plant^{-1}	125	7.06
6	Number of seeds capsule^{-1}	863	48.76
7	1000 seed weight	537	30.34
8	Seed yield plant^{-1}	12	0.68
9	Oil content (%)	209	11.81
	Total	**1770**	**100**

Table 6. Cluster means for nine quantitative characters

CLUSTERS	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant^{-1}	Number of capsules plant^{-1}	Number of seeds capsule^{-1}	1000 seed weight (g)	Seed yield plant^{-1}	Oil content (%)
I	40.47	89.63	75.45	1.88	19.26	35.23	3.19	0.30	45.79
II	40.46	89.18	75.27	1.86	19.24	29.69	3.24	0.30	45.35
III	39.36	89.00	75.70	1.39	16.26	35.63	3.19	0.30	46.32
IV	40.22	90.84	79.89	1.91	25.41	37.73	3.29	0.29	45.97
V	42.50	90.50	81.33	2.00	14.90	31.91	3.46	0.24	45.74
VI	40.63	88.50	76.13	1.73	21.65	44.88	3.20	0.30	46.26
VII	36.50	82.50	72.40	2.10	21.70	28.48	3.27	0.40	46.64
VIII	40.50	89.00	66.70	1.70	28.00	25.89	3.22	0.25	46.71
S.D	1.68	2.60	4.48	0.60	22.59	6.05	2.67	0.22	3.65
Variance	2.85	6.79	20.09	0.04	510.43	36.67	7.14	0.05	13.37

Table 7. Selection of parents for hybridization

Sr. No	Cluster combination	D^2 Values	Cross combination	Traits
			ES-36-A	-No. of seeds capsule^{-1}
1	VI X VIII	678.89	IS-3197-A X KMR-83-A	-plant height
			KMR-302-A	-1000 seed weight^{-1}
			ES-36-A	-1000 seed weight
2	V X VI	514.79	S-0484 X IS-3197-A	-No.of seeds capsule^{-1}
			KMR-302-A	-No.of capsules plant^{-1}
			ES-36-A	
3	VI X VII	456.23	IS-3197-A X SI-3273-A	- No. of capsules plant^{-1}
			KMR-302-A	-1000 seed weight
			NIC-16227-A	- No.of capsules plant^{-1}
4	II X VII	428.61	NIC-10621 X SI-3273-A	-1000 seed weight
			IS-562-A	-No. of seeds capsule^{-1}
			AKT-64	-plant height
5	IV X VIII	330.54	IS-101-1-4849 X RJS-147-1 -84-A	-No.of seeds capsule^{-1}
			SI-2531-C	-No of capsules plant^{-1}
			S-0484 X GRT-839-A	-No.of seeds capsule^{-1}
6	III X V	328.94		-1000 seed weight
				-No of capsules plant^{-}
			S-0484 X RJS-147-1-84-A	-1000 seed weight
7	V X VIII	315.56		-No.of seeds capsule^{-1}
				-No.of capsules plant^{-1}
			KMR-48-A	-No.of seeds capsule^{-1}
8	III X VIII	290.10	TKG-22 X RJS-147-1- 84-A	-1000 seed weight
			GRT-839-A	-No.of capsules plant^{-1}
			ES-144-B	-1000 seed weight
9	I X V	272.38	Pragati X S-0484	-plant height
			KMR-4	-No.of capsules plant^{-1}
			ES-144-B	-No.of capsules plant^{-1}
		237.54	Pragati X RJS-147-1-84-A	-No.of seeds capsule^{-1}
10	I X VIII		KMR-4	-1000 seed weight
			AKT-64 KMR-302-A	-No.of capsules plant^{-1}
			IS-101-1-4849 X IS-3197-A	-No. of seeds capsule^{-1}
11	IV X VI	211.02	NIC-16391 ES-36-A	-1000 seed weight
			NIC-16227-A	-No. of seeds capsule^{-1}
			NIC-10621	-1000 seed weight
			IS-562-A X S-0484	-oil content

--Contd.---

Sr. No	Cluster combination	D^2 Values	Cross combination	Traits
12	II X V	200.01	KMR-4-259-A	-No.of capsules plant^{-1}
			IS-24-A	
			ES-144-B ES-36-A	-No.of seeds capsule^{-1}
13	I X VI	197.91	Pragati X KMR-302-A	-1000 seed weight
			KMR-4 IS-3197-A	
			KMR-48-A ES-36-A	-No.of seeds capsule^{-1}
			TKG-22 X KMR-302-A	-No.of capsules plant^{-1}
14	III X VI	193.39	GRT-839-A IS-3197-A	-1000 seed weight
			AKT-64	-No.of capsules plant^{-1}
			KMS-423 X S-0484	-1000 seed weight
15	IV X V	190.48	S-0233	-No.of seeds capsule^{-1}
			NIC-16227-A KMS-423	-No.of seeds capsule^{-1}
16	II X IV	188.60	NIC-10621 X AKT-64	-1000 seed weight
			IS-562-A S-0233	-plant height
			AKT-64	-1000 seed weight
			IS-101-1-4849 X SI-3273-A	-No.of capsules plant^{-1}
17	IV X VII	188.22	NIC-16391	-No.of seeds capsule^{-1}
				-No.of capsules plant^{-1}
18	V X VII	181.76	S-0484 X SI-3273-A	-1000 seed weight
				-No.of seeds capsule^{-1}
19	III X VII	167.85	KMR-48-A	-No.of capsules plant^{-1}
			TKG-22 X SI-3273-A	-No.of seeds capsule^{-1}
			NIC-16227-A KMS-423	-No. seeds capsule^{-1}
20	II X IV	164.60	NIC-10621 X AKT-64	-1000 seed weight
			IS-562-A S-0233	-plant height
			KMR-48-A KMS-423	-No.of capsules plant^{-1}
21	III X IV	160.60	TKG-22 X AKT-64	-1000 seed weight
			GRT-839-A S-0233	-No.of seeds capsule^{-1}
			ES-144-B	-No.of capsules plant^{-1}
22	I X VII	132.01	Pragati X SI-3273-A	-No.of seeds capsule^{-1}
			KMR-4	-1000 seed weight
			NIC-16227-A	-No.of seeds capsule^{-1}
23	II X VIII	128.60	NIC-10621 X RJS-147-1-48-A	-1000 seed weight
			IS-562-A	-Plant height
			ES-144-B KMS-423	-No.of capsules plant^{-1}
24	I X IV	123.19	Pragati X AKT-64	-Plant height
			KMR-4 S-0233	-No.of seeds capsule^{-1}
			ES-144-B NIC-16227-A	-No.of seeds capsule^{-1}
25	I X II	106.32	Pragati X NIC-10621	-No.of capsules plant^{-1}
			KMR-4 IS-562-A	-1000 seed weight

$\overline{D}$=91.67

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