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Research Article

VARIABILITY AND GENETIC DIVERGENCE IN SESAME (SESAMUM INDICUM L.)

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ABSTRACT: A collection of 280 sesame genotypes of different ecogeographical origin was evaluated using augumented block design along with four checks. Analysis of variance revealed the presence of significant variability among genotypes for all the characters studied. The highest heritability coupled with highest genetic advance was observed for capsules per plant indicating the predominance of additive gene effects. Whereas lower estimates of heritability and genetic advance was revealed for days to maturity and capsule length suggesting the presence of non-additive gene action for controlling these traits. Based on diversity the genotypes were grouped into 12 clusters and highest intercluster distance was observed between cluster VI & XII followed by cluster VI & IX, cluster II & VI and cluster III & IV. Among the traits studied capsule per plant and plant height contributed maximum for studying divergence while no contribution from capsule length. Hybridization involving genotypes of cluster VI with KMR 3 (cluster XII) may result in exploiting maximum heterosis to produce desirable transgressive segregants for crop improvement.

Keywords: Sesame, Sesamum indicum L., variability, genetic divergence.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is the oldest oilseeds known and used by man (Weiss, 1971). India is the largest producer and exporter of sesame in the world. However, there is an immense scope and necessity for further crop improvement. For an efficient hybridization programme selection of genetically diverse parents and superior genotypes is important, which ensures the better recombination of genes and exhibit transgressive segregants in selfing series. Hence an effort was made to assess the existing genetic diversity among the available germplasm to enable selection of better parents in hybridization programme for further crop improvement.

MATERIALS AND METHODS

A field experiment was conducted during summer, 2007 at Regional Agricultural Research Station, Jagtial in sesame utilizing 280 germplasm accessions representing different agroecological situations of India. Since the number of genotypes were more the material was raised in augumented block design with eight blocks and four checks. Each genotype was grown in one row of 3m length adopting a spacing of 30 x 10 cm. Recommended cultural practices and plant protection measures were followed to raise a good crop. The traits viz., plant height, primary branches per plant, capsules per plant and capsule length, seed yield per plant were recorded on five randomly selected plants. However, observations were made on whole plant basis for days to 50% flowering and days to maturity. The data was subjected to analysis of variance, coefficient of variations (Burton, 1952), heritability in broad sense (Lush, 1940), genetic advance (Johnson *et al.*, 1955) as per the standard statistical methods. The data was again subjected to the Mahalanobis D^2 statistic (1936) to measure the genetic divergence. The genotypes were grouped into different clusters by Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance showed that the genotypes eliminating checks were highly significant for all the traits studied (Table 1). Considerable amount of variability was also observed among four checks except for days to 50% flowering. Highest values of genotypic and phenotypic coefficient of variation were observed for primary branches per plant, capsules per plant and seed yield per plant, whereas lower values for days to maturity and days to 50% flowering. The differences between phenotypic and genotypic coefficient of variations were very low indicating little role of environment on these traits.

The highest estimate for both heritability and genetic advance for capsules per plant revealed that the character is governed mainly due to additive effects and direct selection is rewarding for improvement. Whereas lower estimates of heritability and genetic advance were observed for days to maturity and capsule length indicating the presence of non-additive gene effects in controlling these traits and simple selection would be ineffective. However, for plant height heritability was low coupled with high genetic advance indicating the predominance of additive gene effects for the trait and environmental influence might be the reason for low heritability. Adopting Tocher's procedure, group constellation resulted in distribution of 284 genotypes into 12 diverse clusters (Table 2). Cluster I was the largest, comprising 92 genotypes followed by cluster II with 66 and cluster IV with 60 and cluster V with 24 genotypes. However, cluster VIII, X, XI & XII had one genotype each, as these could not club with any other genotypes. Interestingly, the genotypes of the same origin were grouped in many clusters suggesting that the genetic diversity may not be necessarily related with geographic diversity. The possible reason could be the free exchange of germplasm among the breeders of different regions. On the other hand, the study revealed the existence of genetic diversity within the region as the cultivars of the same region could be distributed into different clusters indicating that the unidirectional selection pressure could bring the product genetically closer. Therefore selection of genotypes for hybridization should be based on genetic diversity rather than geographic diversity (Swain and Dikshit, 1997; Verma and Sachan, 2000).

Source of variation	Degrees of freedom	Days t 50% floweri	o ng	Days t maturi	o ty	Plant heig (cm)	ght	Primar branch per pla	y es nt	Capsules per plant		Capsule length (cm)		Seed yield per plant (g)	
Block (ignoring Treatments)	7	82.09	**	43.88	**	1432.17	**	28.62	**	8068.94	**	2.51	**	205.07	**
Treatment (eliminating Blocks)	283	5.13	**	4.59		233.55	**	3.39	**	1135.64	**	0.19	*	33.88	**
Checks	3	2.75		29.21	**	335.12	*	3.03	**	534.28	**	0.78	**	8.53	*
Checks+ Genotypes vs. Genotypes	280	5.16	**	4.33		232.46	**	3.39	**	1142.08	**	0.18	*	34.16	**
Block (eliminating Check+ Genotypes)	7	0.57		1.06		88.54		0.85		267.32	**	0.12		15.07	**
Entries (ignoring Blocks)	283	7.15	**	5.65	*	266.78	**	4.08	**	1328.61	**	0.25	**	38.58	**
Genotypes	279	7.17	***	5.37	*	<u>258.18</u>	**	4.10	okok:	1340.47	**	0.24	30K	38.05	**
Checks vs. Genotypes	1	15.10	×	14.43	*	2460.50	**	1.06		403.27	**	0.78	**	278.15	**
ERROR	21	1.32		2.61		82.09		0.56		23.33		0.09		2.22	
GCV		5.86		1.85		11.58		54.87		47.81		14.40		38.32	
PCV		6.54		2.64		14.22		59.37		48.27		18.38		39.60	
Heritability (Broad sense)		0.80		0.49		0.66		0.85		0.98		0.61		0.94	
Genetic Advance (5%)		4.27		2.30		21.33		3.43		70.94		0.60		11.43	
Genetic Advance as percent	t of mean	10.81		2.68		19.43		104.47		97.55		23.24		76.41	

Table 1: Analysis of variance and genetic parameters for seed vield and its component characters in Sesam											
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** Significant at 1 % level; GCV- Genotypic coeffecient of variation; PCV- Phenotypic coeffecient of variation

The intracluster distances ranged from 13.7 (cluster VII) to 28.7 (cluster IV) excluding single genotype clusters (Table 3). The maximum intercluster distance (175.7) was observed between cluster VI & XII followed by cluster VI & IX (169.2), cluster II & VI (147.0) and cluster III & IV (130.0) suggesting wide diversity between them. However, the lowest inter cluster distance (9.2) was noticed between cluster VIII & X followed by cluster X & XI (17.0) and cluster VIII & IX (20.6) indicating that the genotypes of these cluster pairs had genetic resemblance. The character contributing most to the divergence should be given emphasis while identifying cluster selection or choice of parents for hybridization. The highest contributors in this regard were capsules per plant and plant height whereas capsule length contributed nil (Table 4). These results are akin to the reports of Solanki and Gupta (2001), Manivannan and Nadarajan (1996) for plant height.

The cluster mean values for all the traits are furnished in Table 5. There was wide range of variation in the cluster mean values for most of the characters except for days to 50% flowering and days to maturity. On considering cluster means and intercluster distances, the importance of cluster VI becomes obvious, since it had highest seed yield per plant, capsule length, capsules per plant and primary branches per plant.

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The genotypes present in cluster VI can be used as potential donors in hybridization program for sesame crop improvement. Cluster XII (KMR 33) had zero branches and could be used to derive high yielding monoculm varieties. Hybridization between KMR 33 (cluster XII) with the entries of cluster VI may result in exploiting maximum heterosis with maximum genetic divergence and is likely to produce desirable transgressive segregants for further crop improvement.

Table 2: Spread	l of sesame	genotypes in	different	clusters	based	on seven	traits
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Cluster	Number of	Constrans
No.	genotyp es	Genotypes
I	92	KMR 16, KMR 18, KMR 23, KMR 26, KMR 29, KMR 41, KMR 42, KMR 49, KMR 51, KMR 59, KMR 61, KMR 67, KMR 63, KMR 73, KMR 75, KMR 78, KMR 80, KMR 108, G 6, G 8, G 13, G 22, G 23, G 43, G 51, G 54, KM 6, KM 13, KMS 4-245, KMS 4-258, KMS 4-308, KMS 4-300, KMS 5-376, KMS 5-387, KMS 5-395, SI 1847, SI 1873, SI 1925, SI 1930, SI 2000, SI 2073, SI 2334, SI 3171, SI 9641, TKG 22, NIC 7939, IS 562 B, NIC 8317, IS 39 A, IS 178 A, SI 1248, NIC 16198, NIC 17283, S 0253 B, S 0523 B, NIC 7817, IS 112, ES 22 B, IS 2, NIC 8057, IS 184, SI 3315-6, SI 1847, IS 351, KMR 87, KMS 5-380, SI 3166, IS 673, NIC 16333, IS 299 A, NIC 8279, IS 562 A, KMS 342, S 0580 A, S 0223, B 203, GKT 8336, SI 3218, S 0440, NIC 9824, IS 1547 A, S 0022 A, NIC 16328 A, 77-701 B, JLSC 1 B, S 0268 B, RJS 175-1-84, KMS 4-244, IS 9, Rajeshwari, Hima, Swetha Til
П	66	KMR 4, KMR 6, KMR 7, KMR 8, KMR 12, KMR 13, KMR 20, KMR 28, KMR 31, KMR 35, KMR 36, KMR 37, KMR 43, KMR 55, KMR 56, KMR 60, KMR 71, KMS 4-307, KMS 4-310, KMS 4-324, KMS 5-355, KMS 5-358, KMS 5-389, KMS 5-392, KMS 5-393, SI 53, SI 72/2, SI 533, SI 1804, SI 2123, SI 2174, SI 2237, SI 2323-3, SI 3079-1, SI 3113, SI 3258, SI 506-B, IS 437, IS 167, NIC 16106, NIC 8032, GSK 24, IS 859, KMR 60, NIC 16208, IS 93 B, KMS 349, IS 295, SI 889, IS 130, NIC 8283, IS 101-3 B, KIS 375, 847-1 C, IS 62-1, RJS 151, SI 2630 B, RJS 151, T-1 C, NIC 8252, ES 45 B, S 00812 A, SI 255-1, ES 234-1-84, TKG 22, RT 54
Ш	15	KMR 39, G 44, G 47, G 49, KMS 4-270, KMS 5-364, KMS 5-373, KMS 5-382, SI 63, SI 1143, SI 3256, SI 9835, JL 1-1, IS 191 A, IS 437
IV	60	KMR 24, KMR 27, KMR 30, KMR 69, KMR 74, KMR 77, KMR 79, G 1, G 12, G 16, G 19, G 20, G 52, G 55, KM 8, KM 10, KMS 4-305, KMS 4-304, KMS 5-343, KMS 5-370, KMS 5-396, SI 3234, SI 3285-2, SI 7818, IS 8480 A, GRT 8376, OLT 7, IC 9615-3, IS 101-1-84 B, IS 77 A, IS 390, IC 204832 A, SI 241, IS 723 A, NIC 8423 B, IC 43142, IS 101-1-84, NIC 8202, SP 1184 A, SI 269, SI 3280, NIC 16381, SI 780, NIC 7908, KMS 5-379, 060-7-11-5, SI 1782 A, IS 85-1, NIC 17434, ES 10 A, NIC 9853, IC 56149, NIC 8533, SI 3075, GRT 8351 B, S 0018, KMR 83 B, ES 35 B, RMR 26, Chandana
V	24	KMR 52, G 11, KMS 5-391, SI 3267, SI 3283, SI 3319, NIC 8393, RJS 175, IS 80 A, JLT 1, IS 191 B, IS 73-1-84, EC 335000, SI 3262 B, FS 131-1- 413, NIC 10644, NIC 8392, SI 2008, S 0403 C, NIC 17274 C, SI 294, SI 1865-1 B, KIS 304 B, RME 111
VI	11	G 9, G 10, G 17, G 53, SI 3315-5, IS 153 A, IS 423 C, NIC 8045, ES 31, S 0325 A, IS 157 A-1
VII	6	G 46, G 48, RT 54, EC 303446, GRT 8622 A, NIC 8368
VШ	1	G 41
IX	6	KMR 22, KMR 32, KMS 5-360, SI 1482, SI 2008, KMS 5-366
X	1	KMS 4-246 A
	1	IS 157 B
	1	KMR 33

Table 3: Average intra (diagonal) and inter cluster (above diagonal) distance values in sesame

Cluster No.	Ι	II	III	IV	V	VI	VII	VIII	IX	Х	XI	XII
Ι	20.5	35.2	32.0	36.7	73.3	121.0	41.3	55.7	53.3	56.7	57.8	75.2
II		19.7	45.7	58.0	99.2	147.0	66.9	75.1	32.2	74.2	69.5	50.9
III			22.2	51.0	82.4	130.0	35.6	74.8	54.6	76.8	80.3	91.0
IV				28.7	51.9	96.5	42.2	35.4	79.3	37.5	43.6	91.2
V					27.8	56.3	57.1	42.2	120.6	47.1	61.1	131.8
VI						25.0	102.3	79.1	169.2	83.1	96.4	175.7
VII							13.7	61.7	81.5	65.4	74.5	111.6
VIII								0.0	99.1	9.2	20.6	97.9
IX									24.6	98.5	93.7	55.5
Х										0.0	17.0	94.5
XI											0.0	82.6
XII												0.0

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Character	Times Ranked 1st	Contribution %
Days to 50% flowering	303	0.75%
Days to maturity	211	0.53%
Plant height (cm)	11626	28.93%
Primary branches per plant	66	0.16%
Capsules per plant	27429	68.26%
Capsule length (cm)	0	0.00%
Seed yield per plant (g)	551	1.37%

 Table 4: Character contribution towards genetic divergence in sesame

Table 5: Cluster mean values of seven characters in sesame

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Capsules per plant	Capsule length (cm)	Seed yield per plant (g)
Ι	39.5	85.6	112	3.2	63	2.56	13.66
II	39.1	85.8	96	2.8	39	2.44	10.23
III	39.3	85.9	134	2.9	54	2.77	12.84
IV	39.1	85.7	108	3.4	90	2.65	16.98
V	41.0	86.3	122	4.1	131	2.77	24.97
VI	41.4	86.3	124	4.8	181	3.09	26.46
VII	40.5	86.7	143	4.2	82	2.83	20.85
VIII	42.0	87.0	90	4.0	112	3.00	19.60
IX	40.2	85.7	102	2.3	16	2.25	5.82
Х	36.0	84.0	85	3.0	110	3.00	22.80
XI	42.0	87.0	72	4.0	102	2.50	19.90
XII	39.0	81.0	50	0.0	24	2.50	6.00

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