



RESEARCH ARTICLE

ASSESSMENT OF GENETIC DIVERGENCE IN SESAMUM BASED ON
MORPHO-ECONOMIC CHARACTERS

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ABSTRACT

A set of sesame genotypes including popular ruling varieties was characterized for genetic diversity based on 14 agro-economic traits including seed yield. The test genotypes were separated into five clusters. Principal component (PC) analysis revealed that first two PC axes explained 85.8% of the total multivariate variation. Number of capsules/plant contributed maximum to genetic divergence followed by number of seeds/capsule, 500-seed weight and seed yield/plant. Cluster V revealed comparatively dwarf plant type while Cluster II and Cluster IV were shown to have tall stature. Besides, genotypes under Cluster V had shown capsule bearing from lower height indicating possibility of more scope for increased number of capsules/plant. Cluster II bore longer and bold capsule resulting highest number of seeds/capsule (87.80) coupled with increased 500-seed weight (1.43gm). Pratap formed a mono-genotypic cluster (Cluster II) and it was highly divergent from B 67, TC 25, RT 103, TMV 5 and E 8; while, E 8 exhibited tremendously high genetic distance from RT 103 followed by TC 25, Pratap and T 13. Thus, parental combination of either Pratap or E 8 with above genotypes may result heterotic performance and reveal wide array of transgressive segregants in segregating populations following recombination breeding.

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INTRODUCTION

Sesame (*Sesamum indicum L.*, Family: Pedaliaceae) is the oldest oilseed crop and considered as the queen of high quality vegetable oil (44-58%) for human consumption as it contains high levels unsaturated fatty acids and antioxidants e.g., sesamol, sesamin, sesamolin and sesaminol (Nupur et al., 2010). Therefore, sesame oil is claimed to reduce blood cholesterol, high blood pressure and play an important role in preventing atherosclerosis, heart diseases and cancers (Miyahara et al., 2001). Besides, sesame oil is rich in carbohydrate (13.5%), protein (18-25%), calcium and phosphorus and used as a source of biodiesel with superior environmental performance (Ahmed et al., 2010). Its unique semi-drying property makes it suitable for use in paint formulation (Bedigian 2003). It is also useful in the manufacture of soaps, cosmetics, perfumes, insecticides and pharmaceutical products.

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Owing to high nutritive value, sesame seeds are added as food ingredients in bread, cakes, cookies, margarine and other confectioneries (Iman et al., 2011). Chlorosesamone-an active principle derived from root extracts of sesame has antifungal properties (Hasan et al., 2000). India shares largest area (35%) under sesame and ranked second largest producer of sesame seeds (13.1%) in the world with an estimated production of 636,000 metrictonnes, but suffers a serious setback in terms of productivity (368kg/ha) even less than world average (489kg/ha). In fact, sesame gained less attention for intensive cultivation as compared to other important oilseed crops in India and it is preferentially cultivated in less fertile marginal lands owing to its tolerance to drought stress. Besides, land races and improved varieties cultivated in India are still low yielding. Variation and selection are the two basic requirements of genetic improvement in any crop. Without variation, selection becomes ineffective. Therefore, development of high yielding sesame cultivars requires a thorough knowledge of the existing genetic variation. Genetic diversity is the diversity of the sets of genes carried by different genotypes of a species. High levels of morphological genetic diversity do exist in sesame (Arriel et al., 2007).

Knowledge on genetic diversity helps to monitor and predict probable genetic gains through utilization of germplasm in hybridization programme. Therefore, assessment of genetic diversity in a set of breeding materials is a pre-requisite to distinguish the genotypes into genetically close and divergent types. Further, it is also possible to assess the contribution of different component traits to the total divergence. Many workers have noted a close correspondence between genetic divergence of the parental varieties as measured by D^2 -statistic and degree of heterosis in crosses. Besides, the genotypes which are genetically distant enough with regard to traits contributing sizeable genetic divergence are expected to generate wide range of genetic variation in recombination breeding and pave the way for greater scope for recovery of transgressive segregants (Maurya and Singh, 1978). Besides, heterosis has been reported by many workers in different oilseed crops when parents are chosen through genetic diversity (Singh *et al.* 2007 in mustard; Dong *et al.*, 2003 in soybean; Pasquet *et al.*, 2002 in groundnut; Khan *et al.* 2013 in linseed; and Yousuf *et al.*, 2011 in rapeseed). Therefore, an attempt has been made to quantify the magnitude and nature of genetic divergence in the present set of sesame genotypes for their possible use in further breeding programme.

MATERIALS AND METHODS

Twelve popular genotypes of sesame collected from different states of India were tested in RBD with three replications. Each test genotype was grown in five rows of 3.5m length with a spacing of 30x10 cm.

Observations on days to initial flowering, days to cessation of flowering, duration of flowering, days to maturity, height to first capsule(cm), plant height(cm), number of primary branches/plant, number of capsule/plant, capsule length(cm), capsule breadth(cm), number of seeds/capsule, 500-seed weight(gm), oil content(%) and seed yield/plant(gm) were recorded. The data were subjected to statistical method of analysis of variance (Panse and Sukhatme, 1985). Genetic divergence among the 12 genotypes was estimated using Mahalanobis D^2 - statistic and the genotypes were grouped into different clusters using Tocher's method as described by Rao (1952). The relative contribution of different characters to the total genetic distance between each pair of genotypes was calculated as per method of Singh and Chowdhury (1985) and principal component (PC) analysis as per Hotelling (1933).

Table 1. D^2 -values for all possible combinations involving 12 genotypes for 14 characters in sesame

Genotypes	Vinayak	TC 25	CST 785	Pratap	BS 5-18-6	RT 103	TMV 5	T 13	Madhabi	Phule Til-1	E8
B67	252.11**	257.52**	150.48**	1038.36**	87.27**	368.68**	63.30**	160.30**	234.32**	204.36**	539.73**
Vinayak		467.18**	211.20**	486.40**	95.88**	631.85**	348.61**	394.61**	18.22	258.18**	198.51**
TC25			76.23**	944.84**	281.41**	38.40**	284.39**	119.24**	405.26**	134.55**	1093.43**
CST 785				651.05**	125.86**	152.42**	171.85**	84.04**	199.95**	41.76**	682.85**
Pratap					673.70**	997.80**	1044.6**	748.09**	492.85**	518.09**	894.11**
BS 5-18-6						416.14**	216.99**	189.40**	84.17**	173.97**	329.88**
RT 103							367.14**	137.93**	545.13**	187.11**	1391.44**
TMV 5								178.25**	346.00**	173.43**	707.39**
T 13									350.83**	82.42**	900.89**
Madhabi										256.19**	275.19**
Phuletil 1											728.00**

Table 2. Contribution of different characters towards genetic divergence in sesame

Characters	Number of times ranked first	% -contri-bution of traits	Co-efficients of Eigen vectors	
			Z ₁	Z ₂
Days to initial flowering	2	3.03	-0.1167	-0.0152
Days to cessation of flowering	1	1.51	-0.0231	0.0464
Period of flowering	3	4.54	-0.0001	0.0003
Days to maturity	2	3.03	-0.0901	0.0336
Plant height	4	6.06	-0.0590	0.0327
Height to first capsule	3	4.54	-0.0616	0.0016
No of primary branches	1	1.51	-0.0414	-0.2116
No of capsules per plant	15	22.72	0.9257(I)	0.6312(I)
Capsule length	6	9.09	-0.1667	0.2044(V)
Capsule breadth	4	6.06	-0.2757	-0.0354
No of seeds per capsule	10	15.15	0.2901(II)	0.6089(II)
500 Seed weight	8	12.12	0.0761 (III)	0.2881(III)
Oil content	2	3.03	-0.0004	0.2268(IV)
Seed yield per plant	5	7.57	0.0061 (IV)	-0.0623
Lamda value			$\lambda_1 = 1161.82$	$\lambda_2 = 651.71$
% of variation accounted for			54.972	30.836

Table 3. Clustering pattern of 12 sesame test genotypes

Clusters	Number of genotypes	SI. No. of genotypes	Name of the genotypes
I	3	1,6,9	B67, BS 5-18-6, T 13
II	1	5	Pratap(C50)
III	3	2,4,10	Vinayaka, CST 785, Madhabi
IV	3	8, 11, 12	TMV 5, Phuletil 1,E8
V	2	3,7	TC25, RT 103

RESULTS AND DISCUSSION

Nature of genetic divergence

The estimates genetic distances for paired genotypic combinations have been presented in Table 1. The D^2 -values for all possible 66 combinations ranged from 18.12 (between Vinayak and Madhabi) to as high as 1391.44 (between RT 103 and E 8). Barring one non-significant combination for D^2 -values (between Vinayak and Madhabi), all the rest of combinations had revealed significant genetic divergence at even 1% level of significance indicating presence of wide range of genetic diversity in the present set of test genotypes. In context, Vinayak and Madhabi were genetically most close to each other ($D^2=18.22$) due to similarity in almost all agro-economic traits.

Table 5. Cluster means of 12 sesame test genotypes

Clusters	I (3)	II (1)	III (3)	IV (3)	V (2)
I	<u>1.884</u>	7.262	3.567	4.858	3.920
II		<u>0.000</u>	6.480	6.128	7.649
III			<u>1.464</u>	3.903	3.268
IV				<u>2.451</u>	5.351
V					<u>1.285</u>

Table 4. Average intra (diagonal) and inter-cluster distance in 12 Sesame test genotypes

Clusters	I (3)	II (1)	III (3)	IV (3)	V (2)
Days to initial flowering	37.11	40.47	35.22	40.22	30.17
Days to cessation of flowering	63.33	71.67	62.78	70.22	62.67
Period of flowering	26.22	31.00	27.56	30.00	32.50
Days to maturity	76.00	83.67	75.89	81.33	70.33
Plant height	92.06	106.07	97.31	110.23	94.15
Height to first capsule	52.96	65.75	54.49	68.66	50.76
No of primary branches	1.20	0.10	1.59	1.87	1.50
No of capsules per plant	13.93	11.47	17.22	18.56	16.73
Capsule length	2.29	2.97	2.64	2.45	2.42
Capsule breadth	0.79	1.07	0.79	0.80	0.79
No of seeds per capsule	57.78	87.80	68.58	61.83	62.43
500 Seed weight	1.40	1.43	1.33	1.40	1.43
Oil content	49.56	52.03	52.18	50.30	54.68
Seed yield per plant	2.23	2.88	3.15	3.19	2.87

Similarly, genotype combinations e.g., TC 25/RT 103 (38.40%), CST 785/Phule Til-1 (41.76%), B67/TMV 5(63.30%), T13/Phule Til-1 (82.42%), CST 785/T13(84.04%), BS 5-18-6/Madhabi (84.17%), and B67/BS 5-18-6 (87.27%) showed considerable homology ($D^2 < 100.00$) than rest of the *inter se* combinations. Homology in character expression in the above paired test materials can be attributed to similar ancestry or similar selection pressure in the segregating populations during the course of development of the breeding materials. Among different *inter se* paired genotypic combinations, Pratap had high genetic distance from B 67, TC 25, RT 103, TMV 5 and E 8 using D^2 . Similarly, E 8 exhibited tremendously high genetic divergence from RT 103 followed by TC 25, Pratap and T 13. Thus, these highly divergent parental genotypic combinations may result heterotic combinations and could reveal wide array of transgressive segregants in segregating populations following recombination breeding.

Contribution of characters to genetic divergence

Selection and choice of parents mainly depends upon contribution of characters towards divergence (De *et al.* 1988). The relative contribution of different characters to the total divergence was assessed from percentage contribution based on number of times each characters ranked first (Table 2) as well as in terms of the magnitude of the coefficients of first two Eigen vectors (Z_1 and Z_2). Higher coefficients of Eigen vectors for a certain trait indicate the relatedness of that trait to respective PC-axes (Sneath and Sokal, 1973). The first and second Eigen vectors (Z_1 and Z_2) accounted for 54.97% and 30.83% of total genetic variation respectively indicating importance of above genetic parameters to assess relative contribution of each component traits and seed yield/plant towards genetic divergence. Number of capsules/plant had maximum percentage contribution to genetic divergence followed by number of seeds/capsule, 500-seed weight and seed yield/plant indicating their relative importance in choice of genotypes for hybridization programme. The above agro-economic traits seem to be the contributing factors for genetic divergence among the present set of test materials as also revealed from the magnitude of Eigen vectors (Z_1 and Z_2). This corroborates the findings of Sudhakar *et al.* (2006), Rao (2004) and Chaudhary *et al.*, (2010). Rodge *et al.* (2003) reported highest contribution (14.9%) of seeds per capsule towards divergence followed by 1000- seed weight and plant height; while seed yield showed very low (0.11-2.2%) contribution towards divergence among the varieties. In contrast, Anuradha and Reddy (2005); and Raghuvanshi and Duhoon (2005) revealed importance of days to flowering and days to maturity in terms of contribution to divergence among the genotypes.

Group constellation or clustering pattern

Grouping of test genotypes into different clusters was made based on D^2 -values between all possible pairs of genotypes following Tocher's method. In the present investigation, the total twelve parental genotypes were grouped into five distinct genetic clusters (Table 3). Begum *et al.*, (2011) studied the genetic diversity of 50 sesame (*Sesamum indicum* L.) genotypes through Moahalanobis's D^2 and the genotypes under this study fall into five clusters. Sudhakar *et al.* (2006) analysed genetic divergence among 62 sesame genotypes by D^2 -statistics based on 9 traits related to productivity and the genotypes were grouped into 13 clusters with Cluster I as the largest genotypic group containing 31 genotypes. In the present investigation, Cluster I, Cluster III and Cluster IV contained three parental genotypes each indicating genetic proximity of the test genotypes grouped in different clusters. Grouping of more number of genotypes in above clusters might have resulted due to similar selection pressure favouring identical expression of characters influencing grain yield during the course of development of the breeding materials. In this context, Cluster V included two genotypes (TC 25 and RT 103) and the Cluster II was shown to be a mono-genotypic cluster which included the highly divergent genotype "Pratap". Rodge *et al.* (2003) analysed genetic divergence among 36 sesame varieties by D^2 values ranging from 47.4 to 7487.7 based on 10 characters and the varieties were grouped into 7

clusters with 23 varieties included in cluster I. Similarly, Rao (2004) grouped 72 sesame genotypes into 10 clusters using 7 characters including yield. Using some other set of materials, Anuradha and Reddy (2005) grouped 71 diverse germplasm lines of sesame into 6 clusters considering 12 characters including yield.

Intra and Inter-cluster distance

The inter-cluster distances were of higher magnitude than intra-cluster distances (diagonal values) between any combination of clusters indicating ample amount of genetic variation in the genotypes between clusters. A perusal of the Table 4 indicated lowest intra-cluster distance (0.00) in Cluster-II and its maximum value in Cluster-IV (2.451) indicating that the Cluster-II is composed of only single genotype while Cluster-IV may be designated as comparatively most heterogeneous cluster. In case of inter-cluster distance, the possible 10 combinations of five genetic clusters may be arranged in descending order of magnitude of statistical distance. The inter-cluster distances varied from a minimum value of 3.268 between Cluster -III and Cluster-V to the maximum value of 7.649 between Cluster -II and Cluster-V. Cluster II maintained very high genetic distances i.e., 7.649 and 7.262 respectively from both the cluster I as well as Cluster V. Hence, hybridization of parental genotypes of Cluster I as well as Cluster V with those of Cluster II may result heterotic crosses and may generate transgressive segregants in the selfing generations. As a follow of step, selection of parents from such divergent groups should be based on grain yield *per se* performance or on the basis of component traits, which would compliment with each other for the expression of final output. Thus, it evidences that divergent clusters had large differences among them for more number of characters where as clusters having closeness among them contained genotypes with more of similarity for many characters. However, other practical considerations like reaction to diseases and insect-pests, maturity duration etc. should also be taken into account while choosing genotypes as parents from different clusters. Sudhakar *et al.* (2006) and Anuradha and Reddy (2005) pointed out that selection of parents should be done from two clusters having wide inter-cluster distance to get more variability and high heterotic effect.

Characteristic features of clusters:

Early flowering and early maturity genotypes with comparatively more flowering period are desirable. In this context, Cluster V was estimated to have lowest days to initial flowering, days to cessation of flowering and days to maturity but highest cluster mean value for period of flowering (Table 5) indicating possibility for proportionately higher partitioning of assimilates in terms of bearing more number of capsules. Cluster V revealed comparatively dwarf plant type while Cluster II and Cluster IV were shown to have tall stature. Besides, genotypes under Cluster V were shown to start bearing of capsules from lower height indicating possibility of more scope for increased number of capsules/plant. In general, number of primary branches, number of capsules, number of seeds/capsule and 500-seed weight are considered as important

yield contributing traits. In the present investigation, highest number of primary branches and number of capsules/plant was revealed in Cluster IV which was estimated to have highest seed yield. On similar consideration, Cluster III also revealed high seed yield comparative to Cluster IV. Capsule length and capsule breadth usually result increased number of seeds/capsule while, bold capsule is associated with seed size. In the present pursuit, Cluster II bore longer and bold capsule resulting highest number of seeds/capsule (87.80) coupled with increased 500-seed weight (1.43gm). Cluster V revealed highest oil content in addition to typical traits e.g., dwarf plant type, lowest height to first capsule, increased seed size coupled with erstwhile mentioned early flowering, early maturity and increased flowering period. Cluster II was a mono-genotypic group that included cv. Pratap exhibiting late maturity plant type with increased 500-seed weight and above desirable capsule characteristics. Crossing of this elite genotype with that of cluster IV and Cluster V might open a possibility of increasing grain yield in sesame.

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