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GENETIC VARIABILITY AND DIVERGENCE AMONG GENOTYPES OF SESAME (*SESAMUM INDICUM* L.)

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Abstract

Genetic variability and divergence of 23 genotypes of sesame was investigated based on 12 agro-morphological and biochemical traits. Consistently high estimates of PCV, GCV, H% and GA were observed for seed yield, plant height, capsule number and 1000-seed weight. D^2 values were estimated among genotypes and based on the values, genotypes were grouped into six clusters. There was no conspicuous relationship between geographic origin and genetic diversity of genotypes. Maximum inter-cluster distance (485.87) existed between cluster II and cluster VI. Inter-genetic distance between SI 70 (belonging to cluster II) and Rama (belonging to cluster VI) was maximum (D^2 = 492.11) amongst all comparisons. Canonical analysis revealed that characters like number of seeds per capsule, seed yield, plant height and capsule number contributed maximum towards genetic divergence**.**

Introduction

Oil seeds constitute the major agricultural crop next only to food grains. Among the edible oilseed crops, sesame occupies a unique position as it can be grown throughout the year and moreover, it's poly-unsaturated fatty acid content makes it beneficial for human health. Sesame is an ancient indigenous oilseed crop of India occupying highest acreage (29%), production (26%) and also export (40%) to the outside. Sesame is an important annual crop in the tropics and warm subtropics. Although, the crop is an ancient and having multiple benefits in cultivation, sesame is still at an early stage of breeding which is being amply demonstrated by present state of poor yield performance. Development of improved plant cultivars is restricted by limited genetic variability in the crop. Wide gene pool always aids to restructure plant types with improved traits. Cultivation of sesame in marginal and sub-marginal lands under limited input management practices has caused serious genetic erosion for yield, as local genetic resources fail to respond favourably to high input managements (Kinman and Martin 1954, Ashri 1981). In general, less or limited attention has been given to sesame for development of new accessions with high seed and oil yield with a good protein profile. Hopefully, significant breakthrough in sesame productivity can be achieved through suitable crop improvement programme designed to create wider variability and that can be profitably monitored through breeding.

Genetic variability and divergence are of great interest to plant breeders as they play a pivotal role in implementing a successful hybridization programme through selection of genetically diverse parents. Creation of variability transpires to be primary step to get desirable types. Inclusion of diverse parents in hybridization programmes serves the purpose of combining desirable genes in new recombinations (Kumar and Dubey 2003). Thus, it would be of great interest to ascertain how the different genotypes of diverse origin differ from each other genetically. Multivariate analysis being pool of several quantitative traits promotes in quantifying stable differences among the genotypes. Thus, it is utilized to assess genetic divergence along with

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the relative importance of different traits in the total divergence. Genetic divergence analysis aids in classifying genotypes into distinct genotypic classes and identifying parents for hybridization (Rao *et al*. 1981, Jatasra and Paroda 1983). It is determined by using cluster analysis, which assigns genotypes into different groups. Mahalanobis' D^2 statistic (Mahalanobis 1936) is a powerful tool in quantifying the degree of divergence at genotypic level. D^2 analysis would consolidate in identification of genetically diverse high yielding genotypes which could be useful in cross breeding programme for engendering more transgressive segregants. Use of multivariate D^2 and canonical analysis for identification and classification of genotypes has earlier been reported in many crop species like durum wheat (Gashaw *et al*. 2007), rice (Bhadru *et al*. 2012), chickpea (Syed *et al*. 2012), finger millet (Wolie and Belete 2013), bottle gourd (Gulshan Ara *et al*. 2014) including in sesame (Akbar *et al*. 2011, Saha *et al*. 2012).

Against this genesis the present investigation was designed to assess the genetic diversity among 23 genotypes of sesame and to identify genetically divergent parents for future hybridization programme.

Materials and Methods

Homogeneous seeds of 23 genotypes of sesame (*Sesamum indicum* L.) collected from different parts of the country (Table 1) were selected for the study. The experimental materials were sown at a spacing of 35 × 10 cm during 2007-08 at the Agricultural Experimental Farm, University of Calcutta, Baruipur, West Bengal, India, representing the alluvial part of coastal South Bengal (22°21′56″ N, 88°26′14″ E). A randomized block design was followed with 3 replications. Normal cultural practices were carried out.

Observations on 11 agro-morphological and phenological traits *viz.*, days to 1st flowering, flower duration (days), plant height (cm), number of branches per plant, number of capsules per plant, capsule length (cm), number of seeds per capsule, 1000-seed weight (g), days to maturity, harvest index and seed yield per plant (g) were recorded from five randomly taken plants from each replication. On the other hand, protein content (%) was estimated following the method of Jackson (1967). Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis's D^2 statistic (Mahalanobis 1936) using the statistical software MSTAT-C, version 2.1 (Michigan State University 1988). Canonical roots and clustering of genotypes based on the squared distance (D^2) values were done by Tocher's method as described by Singh and Chaudhary (1985).

Results and Discussion

A wide range of variability was observed for all the traits (Table 2). Phenotypic coefficient of variations (PCV) was in general higher than genotypic coefficient of variations (GCV) for all characters, indicating substantial role of environmental effect in the character expression. Similar findings were reported by Bhadru *et al.* (2012) in rice, Begum and Dasgupta (2014) in sesame. The present finding exhibited that PCV and GCV were consistently high for characters like seed yield per plant, number of capsules per plant and number of branches per plant, demonstrating presence of high amount of variability and low influence of environmental effect on their expression (Table 2). Therefore, selection based on phenotypic performance of these traits would be effective to bring about considerable improvement in those characters (Sharma and Sharma 2007). Heritability (H%) was highest for seed yield per plant (91.40) followed by plant height (88.70) and number of capsules per plant (86.20) (Table 2). Likewise, moderately high heritability was observed for number of seeds per capsule (70.50), 1000-seed weight (79.50) and capsule length (65.10). Genetic advance (GA) expressed as percentage of mean was maximum for 1000-

seed weight (61.57) followed by number of capsules per plant (54.30). High heritability coupled with high genetic advance were observed for number of capsules per plant and 1000-seed weight, which otherwise showed that these two characters were mostly governed by additive gene action (Panse 1957). Thus, breeding methods based on progeny testing and mass selection could be useful in improving these traits. Combining all estimates, it was revealed that seed yield per plant, plant height, number of capsules per plant and 1000-seed weight displayed consistently high estimates of PCV, GCV and H%. Such high estimates were mainly due to additive gene action.

Table 1. Serial numbers and origins of 23 sesame genotypes.

Sl. No.	Name of genotype	Origin
1	B 67	Berhampore, West Bengal
2	Rama	"
3	ACCS 65	Akola, Maharashtra
4	BT 893-1	Berhampore, West Bengal
5	BT 894-1	"
6	T 95	Kanpur, Uttar Pradesh
7	SI 70	Jabalpur, Madhya Pradesh
8	SI 1580	"
9	SI 1625	"
10	SI 1159	"
11	IC 21706	Andhra Pradesh
12	SI 1666	Jabalpur, Madhya Pradesh
13	SI 1607	"
14	SI 1731	"
15	SI 212	"
16	SI 254	"
17	SI 1211	"
18	SI 1141	"
19	SI 1162	"
20	SI 1671	"
21	SI 1729	"
22	B 9	Berhampore, West Bengal
23	B 14	"

The analysis of dispersion using Wilk's criteria, illustrated significant differences among 23 genotypes for the aggregate of 12 characters (X^2, 240 df = 682.78). This justified the need for estimation of squared distance values for the genotype combinations using these multivariates. The D^2 values computed for all possible 253 pairs of comparisons ranged from 492.11 (between Rama and SI 70) to 3.18 (between SI 254 and SI 1211).

The genotypes were grouped into six clusters (Table 3). The distribution pattern of genotypes among various clusters reflected the considerable genetic variability present in the genotypes under study. Clusters I and III each consisted of maximum number of genotypes, 10 (SI 1607, B 67, SI 1731, SI 212, SI 254, SI 1211, SI 1141, SI 1162, SI 1671 and SI 1729) and 5 (BT 893-1, ACCS 65, T 95, IC 21706 and B 9), respectively (Table 3). On the other hand, cluster II and cluster IV included 2 genotypes in each, (SI 70, SI 1580 and SI 1625, SI 1159, respectively),

whereas cluster V with 3 genotypes (BT 894-1, SI 1666 and B 14) and cluster VI with only a single genotype (Rama). The clustering pattern of the genotypes revealed that genotypes from the same state did not form the single cluster. Thus, genotypes of Jabalpur were distributed in cluster I, cluster II, cluster IV and cluster V. On the contrary, genotypes belonging to different states were grouped in the single cluster. The cluster III demonstrated that it consisted of genotypes from Berhampore, West Bengal; Akola, Maharashtra; Kanpur, Uttar Pradesh and Andhra Pradesh evincing that the geographic diversity is not always related to genetic diversity and therefore, it is not adequate as an index of genetic diversity. The present result corroborates the findings of Kumaresan and Nadarajan (2003), Parameshwarappa *et al.* (2009), Akbar *et al*. (2011), Bandila *et al.* (2011) and Gidey *et al*. (2012) in sesame. The possible reason for grouping of genotypes of different region in one cluster could be the free exchange of germplasm among the breeders of different regions, or unidirectional selection practiced by breeder in tailoring the promising cultivars of different regions (Bhadru *et al.* 2012). Genotypes from the same center of origin were distributed in different clusters (Kandamoorthy and Govindarasu 2005, Senapati and Sarkar 2005, Sabesan *et al.* 2009, Banumathy *et al.* 2010) which may be due to differential adaptation to varied agro-ecosystems. Therefore, it may be inferred that the free clustering of the genotypes having different geographic origin suggested dependence upon the directional selection pressure applied for realizing maximum yield in different regions. The nicely evolved homeostatic devices will favour constancy of the associate characters and will thus show indiscriminate clustering.

Table 2. Components of genetic variability in 23 genotypes of sesame.

Character	Range of variation	Mean	PCV%	GCV%	H %	GA
Days to flowering	29.00 - 43.00	39.61	7.11	2.99	17.70	1.03
Flower duration	31.00 - 42.00	37.94 (days)	10.56	6.00	32.30	2.67
Plant height	61.50 - 127.00	75.25 (cm)	19.46	18.32	88.70	26.75
No. of branches per plant	2.00 - 8.00	5.07	50.90	31.92	39.30	2.09
No. of capsules per plant	23.00 - 105.00	61.70	49.56	46.02	86.20	54.30
Capsule length	2.30 - 3.10	2.71 (cm)	6.44	5.19	65.10	0.23
No. of seeds per capsule	44.00 - 62.00	72.09	9.34	7.84	70.50	9.78
1000-seed weight	2.15 - 3.40	2.61 (g)	18.11	16.09	79.50	61.57
Seed yield per plant	3.91 - 15.42	12.42 (g)	57.59	55.07	91.40	13.48
Harvest index	55.36 - 101.42	82.87	4.42	2.72	37.90	2.86
Days to maturity	88.00 - 115.00	100.25	108.71	8.06	10.00	1.23
Protein%	15.26 - 20.73	17.49	13.38	0.18	15.00	0.36

Maximum inter-cluster distance existed between cluster II and cluster VI (485.87) followed by between cluster II and V (319.74), between cluster II and III (209.16) and between cluster I and VI (208.45) (Table 4). The lowest inter-cluster distance (43.24) was found between cluster V and VI, indicating a close relationship between them. In other words, genotypes of these two clusters were not genetically diverse. Thus, crossing of genotypes from these two clusters may not produce higher amount of heterotic expression in the F_1s and wide range of variability in subsequent segregating (F_2) populations (Wolie and Belete 2013). Conversely, the genotypes grouped into the same cluster displayed the lowest degree of divergence from one another resulting no transgressive segregation if crosses are made between them during hybridization programmes. Therefore, to initiate a crossing programme it is desirable that the putative parents should be chosen from those clusters which will have high magnitude of genetic distance between them as

crossing of genotypes belonging to same cluster could not be expected to yield desirable segregates. In fact, increasing parental distance implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in F_2 and F_3 generations following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors (Ghaderi *et al.* 1984). In the present study, crossing between Rama (belonging to cluster VI) and SI 70 (belonging to cluster II) (D^2 = 492.11) or between Rama and SI 1580 (belonging to cluster II) (D^2 = 479.63) would be worth attempting as they show very high genetic distance between parents and also parents were grouped in different clusters.

Table 3. Clustering pattern of 23 sesame genotypes.

Cluster	No. of genotype/s	Name of genotype/s
I	10	SI 1607 (13), B 67 (1), SI 1731 (14), SI 212 (15), SI 254 (16), SI 1211 (17), SI 1141 (18), SI 1162 (19), SI 1671 (20), SI 1729 (21)
II	2	SI 70 (7), SI 1580 (8)
III	5	BT 893-1 (4), ACCS 65 (3), T 95 (6), IC 21706 (11), B 9 (22)
IV	2	SI 1625 (9), SI 1159 (10)
V	3	BT 894-1 (5), SI 1666 (12), B 14 (23)
VI	1	Rama (2)

Figures in parenthesis indicate serial number of the genotypes.

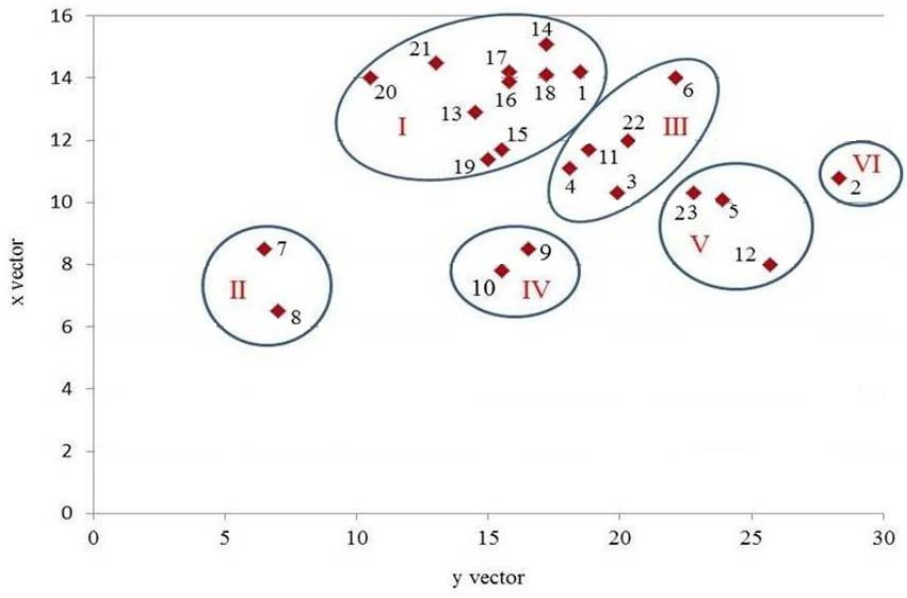

Fig. 1. Two dimensional principal components based on mean values of quantitative traits in 23 genotypes of sesame.

Canonical analysis revealed that out of the total variation 71.51% were accounted by λ_1 and 14.06% by λ_2 accounting more than 85% of the total (Table 5). The two dimensional representation of the relative position of the genotypes is given in x-y vector graph (Fig. 1). The values obtained from D^2 estimates were more or less congruent with the estimates of canonical analysis. The composition of the cluster and the relative disposition remained the same. The weights to the 12 variables given by finest three canonical vectors revealed that seed yield and plant height showed more contribution to divergence in first vector, while capsule length, number

Table 4. Inter and intra-cluster distance among 23 genotypes of sesame.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	7.85	147.31	72.53	86.49	177.46	208.45
Cluster II		8.90	209.16	108.05	319.74	485.87
Cluster III			6.43	68.55	66.63	111.43
Cluster IV				2.33	92.24	188.97
Cluster V					5.40	43.24
Cluster VI						0.00

Table 5. Canonical roots and estimates of coefficient of first three canonical vectors.

	Vector 1	Vector 2	Vector 3
Root	620.07	141.73	96.34
% of variation cum variance explained	71.51	14.06	9.58
Cum. variance exp.	71.51	85.57	95.15
Days to flowering	0.2814	–0.2161	0.3842
Flower duration	0.1986	0.0588	–0.1077
Plant height	0.5911	0.3048	0.0284
No. of branches per plant	–0.0017	0.3462	0.0430
No. of capsules per plant	–0.1642	0.3912	0.5323
Capsule length	0.0257	0.4319	–0.0189
No. of seeds per capsule	–0.1163	-0.0809	0.6787
1000-seed weight	–0.1407	-0.5109	0.0718
Seed yield per plant	0.5921	-0.2468	0.2074
Harvest index	–0.1676	0.0376	0.2082
Days to maturity	–0.2439	–0.1381	0.0387
Protein%	0.1811	–0.2204	–0.0273

of capsules per plant and number of branches per plant in vector 2 as well number of seeds per capsule and number of capsules per plant in vector 3 (Table 5). Thus combining all the vectors together it appeared that characters like number of seeds per capsule, seed yield per plant, plant height and number of capsules per plant mostly contributed to the high genetic divergence of 23 genotypes envisaging that the importance should be given on these traits for effective selection and the choice of parents for hybridization programmes. Interestingly, Kumaresan and Nadarajan (2003) observed 1000-seed weight as the major contributor for genetic variation followed by plant height and seed yield per plant in sesame. Conversely, Bandila *et al.* (2011) identified number of seeds per capsule as the highest contributor towards divergence.

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