The Bioscan 8(4): 1387-1391, 2013 (Supplement on Genetics & Plant Breeding)
AN INTERNATIONAL QUARTERLY JOURNAL OF LIFE SCIENCES
www.thebioscan.in

STUDY ON GENETIC DIVERGENCE IN SESAME (*SESAMUM INDICUM* L.) GERMPLASM BASED ON MORPHOLOGICAL AND QUALITY TRAITS

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KEYWORDS
Clustering
D^2 statistics
Sesame
Genetic divergence
Variability

Received on :
12.08.2013

Accepted on :
29.10.2013

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Abstract
The evaluation of phenotypic variability, heritability, genetic advance and diversity in germplasm collections is important for both plant breeders and germplasm curators to optimize the use of the variability available. A total of 100 sesame accessions collected from diverse ecologies of India were used in this research work. Analysis of variance revealed significant difference among genotypes for all the nine characters studied. High heritability combined with high genetic advance was recorded for seed yield/plant, number of secondary branches/plant and 1000 seed weight indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.Genetic divergence using Mahalanobis D^2 statistics was worked out and based on D^2 values the germplasm lines were grouped into eleven different clusters. Clustering was not associated with the geographical distribution instead accessions were mainly grouped due to their morphological differences. Maximum inter cluster distance was observed between cluster VI and cluster XI (134.72) followed by clusters V and XI (124.23) while, lowest divergence was noticed between cluster IV and V (9.37). Among the nine characters studied, days to 50% flowering contributed highest towards genetic divergence (21.05 %) followed by seed yield per plant (20.85 %). Cluster VI exhibited highest means for days to 50 % flowering (62.5), plant height (119.8), number of primary and secondary branches per plant (10.4, 19.3) and days to maturity (110.5). Cluster XI exhibited lowest means for days to 50 % flowering (46), plant height (81.4), number of primary branches per plant (6.7) and days to maturity (100.5). Greater genetic divergence was found between clusters VI and XI followed by clusters V and XI indicating superior and novel recombinants and explore the fullest range of variability for the characters and to realize good recombinant can be realized by mating between the lines of these clusters in a definite fashion.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is known to be the most ancient oil seed crop dating back to 3050-3500 B.C. The crop is highly tolerant to drought, grows well in most of the well drained soils and various agro climatic regions, and is well adapted to different rotations. It can set seed and yield well under fairly high temperature and can grow in stored soil moisture without rainfall and irrigation. However, continuous flooding or severe drought adversely affects the crop resulting in low yield (Mensah *et al.*, 2009). Sesame oil has highest antioxidant content and contains several fatty acids such as oleic acid (43 %), linoleic acid (35%), palmitic acid (11%) and stearic acid (7%). Though variations in climatic and edaphic conditions, according to Muhamman and Gungula (2008), affect sesame yields and performance, the major constraints identified in growing sesame in most countries are instability in yield, lack of wider adaptability, drought, non-synchronous maturity, poor stand establishment, lack of response to fertilizer application, profuse branching, lack of seed retention, low harvest index and susceptibility to insect pests and pathogens.

Genetic diversity in crop plants is essential to sustain level of high productivity. Genetic variation survives for agronomically vital characters in sesame but its production is still very low in India. Traditional sesame landraces as well as related wild species are an important source of genetic diversity for breeders and form the backbone of agricultural production. The characterization and conservation of sesame germplasm are essential for both safe guarding and the future use of existing genetic resources of sesame. Genetic diversity in sesame, based on morphological, biochemical, metabolic, and molecular markers, has been reported by many researchers worldwide (Bedigian 2010a; Tabatabaei *et al.*, 2011; Parsaeian *et al,*. 2011; Yol and Uzun 2012). However, the development of improved plant cultivars is restricted mainly due to narrow genetic pool which results into limited possibility to restructure the sesame crop. The knowledge of genetic diversity among landraces will help in the selection and breeding of high yielding, good quality cultivars that will increase production. Keeping the above points in view, this study was carried out to recognize and categorize genetic variability of 100 sesame accessions collected from diverse environmental conditions throughout India and to choose sesame germplasm with diverse agronomic performances and yield potential from these important assets.

MATERIALS AND METHODS

One hundred black seeded germplasm accessions planted in Augmented Block Design with two replications were studied

during Summer 2011 at Project Coordinating Unit (Sesame and Niger), JNKVV, Jabalpur, Madhya Pradesh. Jabalpur district is classified under "Kymore plateau and Satpura hills agro-climatic zone". The maximum temperature during the month of May and June reaches up to 40-46°C, whereas, minimum temperature goes below 6°C in the winter season. The soil of experimental area was vertisol having clayey loam texture with uniform topography. Each plot consisted of two rows each of 5 m length with row-to-row spacing of 0.45 m. All recommended package of practices were followed during the conduct of experiment. Observations were recorded on the basis of five random competitive plants selected from germplasm in every replication for seed yield and its attributing characters. Differences between genotypes for different characters were tested for significance using analysis of variance. Genotypic coefficient of variation, phenotypic coefficient of variation, heritability (broad sense) and genetic advance was measured by Burton (1968) and Hanson *et al.*, 1956 method. Genetic divergence was estimated using the Mahalanobis D^2 statistics. Character means were transformed into sets of uncorrelated variables using the pivotal condensation of common dispersion matrix according to Rao (1952). Although the D^2 statistics can handle a multidimensional situation, higher order interactions do not contribute very much in any experiment. In all the D^2 combinations, the characters were ranked on the basis of their contribution to D^2. Grouping of genotypes into different clusters was done according to Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

Analysis of variance indicated that the mean sum of squares due to genotypes were significant for all the characters except 1000 seed weight indicating considerable amount of genetic variability present amongst the material under study. The variation of different traits under study revealed the measure of free variability in the population of different genotypes, which would reflect the unforeseen impact of potential variability on yield. The traits seed yield per plant followed by number of secondary branches, 1000 seed weight and number of primary branches showed high PCV and GCV estimates. High coefficient of variation for number of branches per plant (Gidey *et al.*, 2013, Saha *et al.*, 2012, Sudhakar *et al.*, 2007, Solanki and Gupta, 2003) and seed yield per plant (Sumathi and Murlidharan (2010), Parameshwarappa *et al.*, 2009 and Sudhakar *et al.*, 2007) has also been reported. Hence, these characters can be relied upon and simple selection can be practiced for further improvement. The estimates of genotypic and phenotypic coefficient of variations were moderate for days to 50% flowering, oil content (%) and plant height. In the contrary, Parameshwarappa *et al.*, 2009 and Sudhakar *et al.*, 2007 reported low phenotypic and genotypic coefficient of variation for characters days to 50% flowering, plant height (Sumathi and Murlidharan, 2010) and oil content. Variations for days to maturity and capsule length indicated low estimates of genotypic and phenotypic coefficient of variations (Table 1).

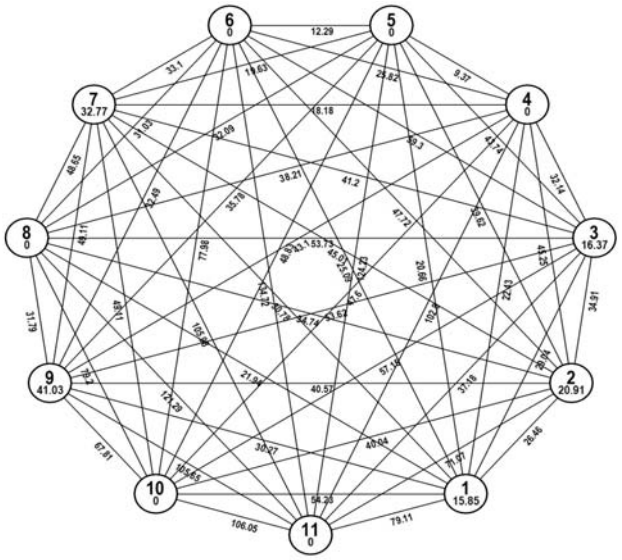
Heritability in broad sense estimates were highest for days to 50% flowering, seed yield per plant, number of secondary branches and days to maturity. The estimates were moderate for plant height, 1000 seed weight and number of primary branches (Table 1). Genetic advance as per cent of mean (GA) is more reliable index for understanding the effectiveness of selection in improving the traits because the estimates are derived by involvement of heritability, phenotypic standard deviation and intensity of selection. Thus, genetic advance along with heritability provides clear picture regarding the effectiveness of selection for improving the plant characters. As presented in Table 1, the estimate of genetic advance were recorded highest for seed yield per plant (66.4) followed by number of secondary branches (53.2); moderate for 1000 seed weight (39.1), number of primary branches (18.4), days to 50% flowering (14.7) and plant height (11.0); and low for oil content (8.2) and capsule length (0.5). Noor *et al.* (2004) had cautioned that high heritability per se is no index of high genetic gain hence should be accompanied by high genetic advance. High heritability accompanied with high genetic advance recorded for seed yield per plant and number of secondary branches per plant indicated lesser influence of environment in expression of these characters and that these characters are controlled by additive gene effect, hence, amenable for simple selection. Moderate heritability and genetic advance was recorded for 1000 seed weight. Similar results were reported by Sumathi and Murlidharan (2010), Sudhakar et.al, 2007. Low heritability accompanied with low genetic advance was observed for capsule length and oil content which may be due to non additive gene action.

Genetic divergence

Genetic divergence among 100 black coloured sesame germplasm lines was determined for seed yield, its attributing characters and quality trait. The significant estimates of 'V' statistics during the analysis revealed significant differences among mean values of different correlated variables, thus analysis of genetic divergence among the tested sesame germplasm was considered to be relevant.

Table 1: Parameters of genetic variability for morphological and quality traits of sesame

S. No.	Character	Range		Mean	GCV (%)	PCV (%)	h2 (bs)(%)	GA as %of mean
		Minimum	Maximum					
1	50 % F	46	65	56.5350	6.666	7.966	70	14.726
2	DM	100	112	106.0900	2.553	3.497	53	4.921
3	PH	81	120	104.1100	6.014	8.677	48	11.004
4	NPB	4.4350	11.600	7.6980	12.332	21.757	32	18.453
5	NSB	4.4350	27.600	15.1755	25.985	33.475	60	53.252
6	CL	2.2775	3.5200	2.8079	1.897	18.390	11	-0.517
7	SYPP	3.7000	21.6000	9.5622	31.620	39.710	63	66.468
8	1000 SW	0.7450	3.9650	2.2711	22.487	34.060	43	39.192
9	OL %	32.5200	49.3050	40.6389	6.158	12.142	25	8.246



Mahlnbobis euclidean^2 distances (not to the scale)

Figure 1: Diagram showing intra and inter cluster distances among XI clusters

Hierarchical cluster analysis based on agro morphological traits allocated the 100 sesame germplasm into eleven clusters (Fig.1). Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relations. The composition of clusters and values of inter and intra clusters distances are given in tables 2 and 3, respectively. The results revealed that the inter cluster distance in most cases was larger than intra cluster distance suggesting wider diversity among the germplasm of different groups. Cluster I possessed the maximum number of 32 genotypes followed by cluster II (29), cluster III (18), cluster IX and cluster VII in such a way that germplasm lines having minimum genetic distance were grouped in same cluster and *vice versa*. Rest of the clusters were mono-genotypic one. The range of inter and intra cluster distance was 9.37 to 134.72 and 0.00 to 32.77, respectively (Table 2). The maximum inter cluster distance was found between clusters VI and XI, followed by clusters V and XI (124.23), clusters VIII and XI (121.29), clusters X and XI (106.05), clusters VII and XI (105.98), clusters IX and XI (105.65) and clusters IV and XI (102.8). The minimum inter cluster distance was recorded between clusters IV and V followed by clusters V and VI (12.29), clusters IV and VII (18.18)

Table 2: Inter and intra cluster distances in 100 black germplasm of sesame

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**15.85**	26.46	29.04	22.43	20.66	25.09	30.78	21.94	30.27	54.23	79.11
II		**20.91**	34.91	45.25	39.62	47.72	45.01	34.74	40.57	40.04	71.07
III			**16.37**	32.14	43.74	59.30	41.20	53.73	53.62	57.15	37.18
IV				**0.00**	9.37	25.82	18.18	38.21	43.10	47.60	102.80
V					**0.00**	12.29	19.63	32.09	35.78	48.83	124.23
VI						**0.00**	33.10	31.03	32.49	77.98	134.72
VII							**32.77**	48.65	49.11	49.11	105.98
VIII								**0.00**	31.79	79.20	121.29
IX									**41.03**	67.81	105.65
X										**0.00**	106.05
XI											**0.00**

Bold figures denote the intra cluster distances

Table 3: Cluster means of seed cotton yield and its attributing characters

Cluster	50% flowering	DM	PH	NPB	NSB	CL	1000 SW	OCP	SY/P
I	58.34	106.92	105.17	7.73	15.59	2.73	7.80	2.01	40.58
II	56.47	105.03	101.96	8.27	17.75	2.80	12.84	2.51	41.63
III	51.44	104.14	99.49	6.54	11.79	2.80	7.75	2.53	40.40
IV	55.50	109.50	112.70	5.90	9.00	2.72	7.80	1.38	40.13
V	59.50	110.50	118	9.05	14.75	2.67	7.95	1.51	45.25
VI	62.50	110.50	119.80	10.40	19.30	2.65	5.35	1.87	35.16
VII	56.07	108.43	116.61	7.27	12.43	2.71	9.19	2.06	41.29
VIII	63.00	104.50	104.80	6.90	19.70	2.86	8.25	0.93	43.31
IX	61.38	107.88	105.05	8.54	15.54	3.26	8.97	2.25	37.98
X	53.00	109.50	104.50	6.9	7.30	3.06	21.60	2.67	41.00
XI	46.00	100.50	81.40	6.7	10.20	3.10	7.56	3.97	33.36

DM = Days to maturity, PH = Plant height. NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, CL-Capsule length, OCP = Oil content (%), SY/P = Seed yield per plant

Table 4: Contribution of different characters towards genetic divergence (D2) in black sesame germplasm

Source	Times ranked Ist	Contribution %
50 % days to flowering	1042	21.05
Days to maturity	448	9.05
Plant height	609	12.30
Number of primary branches per plant	183	3.70
Number of secondary branches per plant	636	12.85
Capsule length	163	3.29
Seed yield/plant	1032	20.85
1000 seed weight	591	11.94
Oil content (%)	246	4.97

Table 5: Principal Component Analysis of sesame germplasm character

Characters	I Vector	II Vector	III Vector	IV Vector
50 % days to flowering	0.6637	0.13963	0.48882	0.06710
Days to maturity	0.21649	0.36382	-0.34715	-0.09101
Plant height	0.10660	0.46713	-0.56465	0.04928
Number of primary branches/ plant	0.00736	-0.14117	-0.16730	-0.30924
Number of secondary branches/plant	0.38735	-0.31513	-0.12664	-0.76136
Capsule length	0.10175	0.07373	0.21714	0.15244
Seed yield/plant	0.47391	-0.52921	-0.42848	0.53197
1000 seed weight	-0.26905	-0.46453	-0.01173	0.03628
Oil content (%)	-0.20982	-0.09693	-0.21635	-0.04412

and clusters V and VII (19.63). The highest intra cluster distance was observed for cluster IX. It indicates that the germplasm lines of cluster IX were more diverged than any other cluster. This was also reflected in the scatter diagram. The germplasm lines belonging to the distant clusters could be used in hybridization programme for obtaining a wider range of variability.

Cluster means of germplasm for nine characters in sesame (Table 3) revealed that cluster VI had maximum plant height, number of secondary branches, days to maturity and low oil content (%). Cluster XI reported to be early maturing average plant type with highest oil content (%) and low 1000 seed weight. These clusters can be preferred in selecting germplasm lines for respective traits as they recorded good means. Clustering of germplasm was not associated with the geographical distribution and were mainly grouped due to their morphological differences. Thus, showing evidence that geographical isolation is not the only factor causing genetic diversity in sesame. Similarly, the forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material might have played and important role in the fixation of diversity among the germplasm lines. A few ecological conditions could also direct the gene flow between populations from diverse geographical origins. Although sesame has been described as a self-pollinated plant, but these are indications that show the option of natural out-crossing in sesame (Baydar & Gurel, 1999).

The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times, each of the yield component character appeared first in rank and its respective per cent of contribution towards genetic divergence was presented in Table 4. The results showed that 50% days to flowering (21.05 %) contributed highest towards genetic divergence by taking 1042 times first rank, followed by seed yield/plant (20.85 %) by 1032 times, number of secondary branches (12.85 %) by 636 times, plant height (12.30 %) by 609 times, 1000 seed wt (11.94 %) by 591 times and days to maturity (9.05 %) by 448 times. These results are in agreement with those given by Velusami *et al*., 2008 for seed yield followed by 1000 seed weight. It indicates that these characters contribute towards the genetic divergence in the present germplasm lines. On the other hand, least variation was recorded for capsule length, number of primary branches and oil per cent showing comparatively less contribution of these characters towards the genetic divergence. On the contrary, Duhoon and Raghuwanshi, 2005 reported that oil content and days to 50% flowering exhibit maximum genetic divergence. Solanki and Gupta (2003) reported that seed yield, number of capsules per plant, plant height and 1000 seed weight are the important contributing attributes. Sudhakar *et al.*, 2006 reported that1000 seed weight, number of capsules per plant, plant height, capsule length recorded negligible contribution.

Principle component analysis was also conducted and presented in table 5. It showed association in PC1 with days to 50% flowering and number of secondary branches/plant, PC2 with plant height and days to maturity, PC3 with capsule length and PC4 with seed yield per plant. Thus, re-structuring plant type with early flowering, more number of secondary/ plant, plant height and capsule length would obviously generate plants with high seed yield.

The results indicated that the germplasm lines studied had a considerable level of variability that could be exploited in future breeding programs. Hybridization between genetically diverse genotypes in sesame to generate promising breeding material has been suggested by Alarmelu and Ramanathan (1998). Greater genetic divergence was found between clusters VI and XI followed by clusters V and XI indicating that superior hybrids or recombinants can be realized by mating between the lines of these clusters in a definite fashion. Crossing between germplam belonging to the same cluster might not be expected to yield desirable segregates. This approach is however based on the assumption that suitable parents for crossing may be showing greater amount of genetic divergence. Further research on these selected germplasm will save a lot of time for the breeder in future.

Morpho-agronomic traits have some shortcomings in evaluating genetic diversity as these are phenotypic markers and genetically distant germplasm may be morphologically similar. Further research should be done with molecular markers which can be used to determine genetic distance easily and successfully. DNA markers should provide more accurate measures of genetic similarity.

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