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Research Note

Variability, heritability and transgressive segregation on yield and its components in F₂ progenies of sesame (*Sesamum indicum* L.)

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Abstract

A total of 28 F₂ progenies were studied for variability, heritability and genetic advance and ten best F₂ progenies were studied to assess the transgressive segregation on yield and its components based on their mean performance in sesame. High genotypic coefficient of variation was observed for seed yield per plant followed by number of capsules on secondary branches. High heritability was observed for 1000-seed weight, seed yield per plant, days to maturity, plant height, number of capsules on primary branches and harvest index. High heritability coupled with high genetic advance as per cent of mean was observed for seed yield per plant and number of capsules on primary branches number of capsules per plant and number of capsules on secondary branches indicating additive gene action for controlling these traits. Hence, simple selection can be practiced to improve these traits. For the character plant height the cross ACV 2 x DT 9-10-2-25 had shown more percentage of total transgressive segregants (TTS) and significant transgressive segregants (STS). The cross CO-1 x AVT 26 had shown more percentage of total transgressive segregants and significant transgressive segregants for the characters number of branches per plant, number of capsules per plant and seed yield per plant. For the character 1000-seed weight the cross TNAU 20 x TMV 6 had shown more percentage of TTS and STS.

Key words

Sesame, Variability, Heritability, F₂ progenies, Transgressive segregants

Sesame (*Sesamum indicum* L.) is an important edible oil seed crop gaining considerable importance on account of its high economic value. There is a need to develop suitable varieties for specific situations like biotic and abiotic tolerance, climate resilient types and varieties suitable for off seasons *etc.*, In order to achieve this, suitable crosses should be identified. F₂ is an ideal generation to obtain superior transgressive segregants. The segregation pattern of a cross throws light on genetic width of the crosses and helps breeder to identify superior individual plants. Success in any crop improvement programme mainly depends on the nature and magnitude of the genetic variability present in the crop. The natural variability for yield and its component traits are very narrow in a highly self pollinated crop like sesame. By proper evaluation of the extent of genetic variation available for yield and yield attributes, their heritability values and genetic advance will be of immense value to the breeders. Hence, an attempt was made to reveal the magnitude of variability, heritability, genetic advance and genetic advance as per cent of mean for fourteen characters among 28 F₂ progenies of sesame and to assess the transgressive segregation on yield and its components based on their mean performance in sesame.

Twenty eight F₂ progenies of sesame derived from 8x8 diallel cross excluding reciprocals were evaluated in a Completely Randomized Block Design with three replications. A distance of 40 cm was maintained between rows and 15 cm between plants. Observations on various quantitative characters were recorded on thirty randomly selected plants in the segregating population. The variance components, genotypic and phenotypic coefficient of variation were determined as suggested by Burton and De Vane (1953) and Johnson et al. (1955). Heritability in narrow sense (h^2) was estimated according to Falconer (1989). Due to the fact that lines were DH, narrow sense heritability was estimated by dividing genetic variance by phenotype variance. Genetic advance was calculated with the method suggested by Allard (1960) and was estimated from the following formula: $GA = K\sigma_{ph} h^2$

The ANOVA test is performed by comparing two types of variation, the variation between the sample means, as well as the variation within each of the samples using the formula $F = MST/MSE$. MST = Mean sum of squares due to treatment MSE = Mean sum of squares due to error. The experimental material consisted of eight parents and ten F₂ progenies (Co-1xTMV 6, Co-1 x DT9-10-2-25, Co-1x AVT 26, TNAU 20 x CIANNO,

TNAU 20 x TMV6, VRI-1 x DT9-10-2-25, VRI-1 x AVT 26, ACV 2xDT 9-10-2-15, ACV2 x AVT 26 and DT 9-10-2-25 x AVT 26) were used for studying the transgressive segregation. Thirty plants from each replication/entry were randomly selected and observations were recorded for the characters plant height, number of branches per plant, number of capsules per plant, 1000-seed weight and seed yield per plant. The F_2 segregants exceeding the average mean value of two parents were counted as total transgressive segregants (TTS). Among these total transgressive segregants, those which had considerably higher values than the better parental means were classified as significantly transgressive segregants (STS).

The analysis of variance revealed highly significant differences among the treatments for all the characters studied except for capsule length, indicating considerable variation in the material (Table. 1). Mean, variability, heritability, genetic advance and genetic advance as percent of mean are presented for F_2 progenies in (Table 2). Percentage of total transgressive segregants (TTS) and significantly transgressive segregants (STS) in the F_2 generation of ten cross combinations were presented in (Table.3). The genetic analysis for transgressive segregation in F_2 is helpful for determining prepotency of different crosses achieving efficiency in early generation selection and reducing population size in later generation. The transgressive segregants are produced by an accumulation of favorable genes affecting yield and yield governing characters.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) would be more precise for discussion since variances are associated with units. The magnitude of PCV in general, was higher than GCV indicating influence of the environment. Highest PCV and GCV were recorded for characters seed yield per plant, number of capsules on secondary branches, number of capsules on primary branches and number of capsules per plant. These results were in harmony with the results of Anil kumar (1999). Moderate PCV and GCV values are observed for number of capsules on main stem, number of secondary branches, number of primary branches, plant height, harvest index and 1000-seed weight. These results were in accordance with Barauh and Goud (1993). Days to 50% flowering, capsule length, days to maturity and number of seeds per capsule recorded low PCV and GCV values as also reported by Shadakshari et al., (1995).

The high heritability was observed for 1000-seed weight, seed yield per plant, days to maturity, plant height, harvest index, number of capsules on

primary branches, number of capsules per plant and number of seeds per capsule. Similar kinds of observations were reported by Anil Kumar (1999). Since heritability estimates are influenced by the environment and genetic advance would be of more reliable and useful in formulating selection criteria. High heritability coupled with high genetic advance as percent of mean are observed for the characters seed yield per plant, number of capsules on primary branches, number of capsules per plant. Further moderate heritability with high genetic advance as percent mean was recorded for number of capsules on main stem and number of capsules on secondary branches indicating that these characters are governed by additive gene action as also reported by Govindarasu et al., (1990). Hence simple selection is suggested for further improvement in these characters.

High heritability with moderate genetic advance as percent of mean was recorded for plant height, 1000-seed weight, harvest index and number of seeds per capsule indicating that these characters were less influenced by environment but governed by both additive and non additive gene action. These results were in consonance with Shadakshari et al., (1995). High heritability with low genetic advance as percent of mean was recorded for days to maturity. Low heritability with low genetic advance as percent of mean was recorded for days to 50% flowering. These were in conformity with Shadakshari et al., (1995). These results indicated the prevalence of non additive gene action for which simple selection will be less effective.

Percentage of total transgressive segregants (TTS) and significantly transgressive segregants (STS) in the F_2 generation of ten cross combinations were presented in Table.1. The genetic analysis for transgressive segregation in F_2 is helpful for determining pro potency of different crosses achieving efficiency in early generation selection and reducing population size in later generation. The transgressive segregants are produced by an accumulation of favorable genes affecting yield and yield governing characters. The highest percentage of total transgressive segregants (TTS) for plant height was observed in VTI-1 x DT 9-10-2-15 (92.2%) and significantly transgressive segregants (STS) observed in ACV 2 x DT 9-10-2-15 (86.1%). For the character number of branches per plant the cross TNAU 20 x TMV 6 had shown more percentage of total transgressive segregants (45.5%) and C0-1 x AVT 26 more percentage of significantly transgressive segregants (28.8%). Capsule number was reported to be an important yield component in sesame (Subramanain and Subramanain 1994; Vanisri *et al.* 1994) for which the highest percentage of total transgressive

segregants (90.12%) and significantly transgressive segregants (87.2%) were observed in the cross Co-1 x AVT 26. For the character 1000-seed weight highest percentage of total transgressive segregants (70.1%) and significantly transgressive segregants (65.2%) were observed in the cross TNAU 20 x TMV 6. Seed yield is the most important economic trait in sesame. Breeding for yield generally aims at the recovery of transgressive segregants (Rajavindran *et al.* 2002). The highest percentage of total transgressive segregants for seed yield per plant was observed in the cross VRI-1 x AVT 26 (62.4%) and significantly transgressive segregants for Co-1 x AVT 26 (43.2%). According to Finker *et al.* (1973), a cross with the highest mean was relatively effective in identifying superior segregants, this was true in case of Co-1x AVT 26 which shown high frequency of transgressive segregants for seed yield per plant (Mean value 43.2g) number of capsules per plant (Mean value, 87.20) and number of branches per plant (Mean value 28.8). Therefore the cross Co-1 x AVT 26 may be further advanced to get desirable segregants.

From the foregone discussion, it can be concluded that high GCV, PCV heritability and genetic advance as per cent of mean were observed for seed yield per plant, number of capsules on secondary branches and number of capsules per plant indicating the prevalence of additive gene action in the control of these characters. Hence, simple selection may be effective to improve these characters to enhance yield potential of the sesame genotypes. Based on these studies we can conclude that those crosses which gave a high frequency of transgressive segregants for seed yield per plant, number of branches per plant, number of capsules per plant, 1000-seed weight and plant height may be preferred to other crosses in a breeding programme

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Table 1. Analysis of variance of F₂ progenies for fourteen characters in sesame

S. No	Character	Mean sum of squares		
		Replications df=2	Treatments df=35	Error df=34
1	Days to 50% flowering	3.86	8.05	1.74
2	Days to maturity	2.39	84.90	1.32
3	Plant height(cm)	46.77	964.33	21.65
4	Number of primary branches per plant	0.21	2.07	0.15
5	Number of secondary branches per plant	0.43	3.71	0.24
6	Number of capsules on main stem	11.33	99.15	7.52
7	Number of capsules on primary branches	4.37	660.05	36.51
8	Number of branches on secondary branches	25.96	55.84	8.14
9	Number of capsules per plant	99.91	1420.67	100.0
10	Capsule length(cm)	0.02	0.12	0.013
11	Number of seeds per capsule	5.18	105.30	4.88
12	1000-seed weight	0.00	0.48	0.00
13	Seed yield per plant(g)	2.53	98.76	0.971
14	Harvest index (%)	39.06	309.92	10.836



Table 2. Mean, co-efficient of variation, heritability (broad sense), genetic advance and genetic advance as percent of mean for fourteen characters in 28F₂ progenies of sesame

S.No	Character	Mean	Range	Variance		Co-efficient of variation (%)		Heritability broad sense (%)	Genetic advance (GA)	Genetic advance as percent of mean (%)
				Genotypic	Phenotypic	Genotypic	Phenotypic			
1	Days to 50% flowering	32.11	30.33-35.00	1.44	3.18	3.74	5.55	45.28	1.66	5.17
2	Days to maturity	97.84	91.00-106.67	23.40	24.72	4.94	5.08	94.66	9.69	9.90
3	Plant height(cm)	108.76	91.91-160.99	246.61	268.27	14.44	15.05	91.94	31.02	28.52
4	Number of primary branches per plant	4.92	3.25-6.23	0.53	0.68	14.79	19.22	77.03	1.32	26.82
5	Number of secondary branches per plant	3.29	2.22-4.34	0.28	0.52	16.14	22.04	53.61	0.80	24.31
6	Number of capsules on main stem	23.89	16.23-43.55	22.00	29.53	19.63	22.74	74.50	8.34	34.91
7	Number of capsules on primary branches	52.04	26.14-102.19	216.73	253.24	28.28	30.57	85.58	28.05	53.90
8	Number of branches on secondary branches	12.76	6.81-26.26	14.32	22.46	29.65	37.14	63.75	6.22	48.74
9	Number of capsules per plant	91.82	53.53-172.00	467.80	567.80	23.55	25.95	82.38	40.43	44.03
10	Capsule length(cm)	3.07	2.44-3.12	0.01	0.03	3.98	5.45	53.57	0.18	5.99
11	Number of seeds per capsule	66.27	55.50-79.57	23.22	28.10	7.29	7.99	82.63	9.02	13.61
12	1000-seed weight	3.4	2.86-4.40	0.15	0.15	11.57	11.61	99.35	0.81	23.82
13	Seed yield per plant(g)	20.2	11.32-39.86	37.61	38.58	30.35	30.74	97.48	12.47	61.73
14	Harvest index (%)	67.01	49.67-84.00	99.25	110.08	14.86	15.63	90.16	19.48	29.07



Table 3. Percentage of total transgressive segregants (TTS) and significantly transgressive segregants (STS) in the F2 generation

S.NO	Crosses	Plant height		Number of branches per plant		Number of capsules per plant		1000-seed weight		Seed yield per plant	
		TTS	STS	TTS	STS	TTS	STS	TTS	STS	TTS	STS
1	Co-1xTMV6	87.7	62.2	34.4	23.3	56.6	43.3	25.4	16.3	50.4	39.2
2	Co-1x DT9-10-2-25	89.5	71.5	8.8	1.1	88.8	72.2	10.7	6.5	45.7	28.4
3	Co-1x AVT26	88.1	70.6	38.8	28.8	90.12	87.2	13.8	6.1	60.5	43.2
4	TNAU20x CIANNO	76.6	61.7	42.2	18.8	75.5	64.3	57.6	48.9	36.7	24.3
5	TNAU20x TMV6	53.3	50.3	45.5	23.1	70.0	71.2	70.1	65.2	40.5	32.1
6	VRI-1x DT9-10-2-25	92.2	34.4	15.5	2.22	43.2	28.3	40.3	28.4	52.7	40.2
7	VRI-1xAVT26	82.1	46.4	45.5	27.1	43.2	49.5	30.5	18.4	62.4	32.1
8	ACV2x DT9-10-2-25	91.5	86.1	8.8	0.0	37.3	40.1	40.9	30.3	50.7	29.7
9	ACV2xAVT26	90.7	85.4	25.5	20.1	43.4	32.4	28.4	19.3	35.4	19.5
10	DT9-10-2-25xAVT26	84.4	81.3	4.4	1.1	70.6	63.2	40.7	25.9	41.3	26.4

