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RESEARCH ARTICLE

Analysis of genetic variability for yield and its components in sesame (*Sesamum indicum* L.)

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SUMMARY

One hundred and twenty four F_4 families of sesame derived from straight and reciprocal crosses made between E-8 (commercial cultivar) and Tamil Nadu Local (land race) were evaluated during *Kharif*, 2010 to assess genetic variability, heritability (broad sense) and genetic advance for ten quantitative characters. Analysis of variance revealed highly significant difference among the F_4 families for days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, distance from ground to first capsule and number of seeds per capsule. High GCV and PCV were observed for branches per plant, capsules per plant and seed yield per plant. High heritability coupled with high genetic advance as per cent mean was observed for plant height, branches per plant, capsules per plant, capsule length, distance from ground to first capsule, seeds per capsule, 1000 seed weight and seed yield per plant.

Key Words : Sesame, F_4 families, Genetic variability, Heritability, Genetic advance

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Sesame (*Sesamum indicum* L.) is one of the important indigenous oilseed crops. It is mostly grown for its seed. Sesame seed is highly nutritive (oil 50%, protein 25%) and its oil contains an anti-oxidant called sesamol which imparts to it a high degree of resistance against oxidative rancidity (Ashri, 1989). Globally, China and India are the major sesame producers.

In any crop, existence of variability is essential for resistance to biotic and abiotic factors as well for wider adaptability. Selection is also effective when there is sufficient genetic variability among the individuals of a population. Thus, the knowledge on the amount of variation and its heritable portion present in the source population is pre-requisite for any successful breeding programme aimed at improving yield and other characters. During this study, an attempt was made to compute the proportion of genotypic variability, heritability in broad sense as well as genetic advance with respect to ten quantitative characters.

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MATERIALS AND METHODS

One hundred and twenty four F_4 families of sesame derived from straight and reciprocal crosses made between E-8 (a white seeded, an agronomicaly superior cultivar) and Tamil Nadu Local (a brown seeded land race; TNL) were evaluated along with eight checks in augmented design during *Kharif*-2010 at University of Agricultural Sciences, Raichur, Karnataka. Of one hundred and twenty four F_4 families, one hundred and three families were from straight cross (E-8 x TNL) and twenty one families were from reciprocal cross (TNL x E-8). Observations on ten quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule

length, distance from ground to first capsule, number of seeds per capsule, 1000 seed weight and seed yield per plant were recorded on five randomly selected plants in each family. The estimates of variability such as genotypic co-efficient of variability (GCV) and phenotypic co-efficient of variability (PCV) were calculated by following the method suggested by Burton and Devane (1953). Heritability in broad sense and genetic advance were computed based on formula given by Hanson *et al.* (1956) and Johnson *et al.* (1955), respectively.

RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed highly significant differences among the F_4 families for the characters days to 50 per cent flowering, days to maturity, plant height, number of branches, number of capsules per plant, distance from ground to first capsule, number of seeds per capsule and seed yield per plant indicating the presence of considerable amount of genetic variation in the material for its effective management through selection to identify the superior families. These characters also had high value of range while capsule length and 1000 seed weight exhibited medium value of range.

The estimates of genetic parameters like GCV, PCV, heritability and genetic advance as per cent of mean are presented in Table 2. There was a close correspondence between the estimates of PCV and GCV for all the characters studied except days to 50 per cent flowering which indicates minimal environmental effects in expression of these characters. PCV and GCV values were high for number of branches per plant, number of capsules per plant and seed yield per plant indicating the presence of greater variability for these characters among F_4 families. Higher GCV suggests that these characters are under the influence of genetic control and, therefore, simple selection can be practiced for further improvement of these characters. These results are in accordance with findings of Solanki and Gupta (2003), and Gangarde *et al.* (2009). Moderate PCV and GCV were recorded for plant height, capsule length, distance from ground to first capsule, number of seeds per capsule and 1000 seed weight. These results are in agreement with findings of Parameshwarappa *et al*. (2009) and Chowdhury *et al*. (2010).

Table 1: Mean sum of squares for ten quantitative characters in F_4 families of sesame

Source of variation	Blocks	Entries	Checks	Checks vs. entries	Error
Days to 50 per cent flowering	1.041	28.97**	16.26	619.08**	0.85
Days to maturity	0.04	44.60**	18.55	1333.25**	0.99
Plant height (cm)	18.37	266.64**	587.26	1242.77**	2.28
Number of branches per plant	0.66	3.69**	2.57	48.94**	0.09
Number of capsules per plant	20.15	2502.41**	955.42	54617.89**	2.07
Capsule length (cm)	0.01	0.06	0.20	0.05	0.003
Distance from ground to first capsule(cm)	6.00	44.12**	72.50	830.39**	1.04
Number of seeds per capsule	0.66	93.71**	280.85	30.14**	2.19
1000 seed weight (g)	0.004	0.22	0.28	4.52*	0.005
Seed yield per plant (g)	1.09	69.08**	41.27	938.75**	0.12

* and ** Indicate significance of value at P=0.05 and 0.01, respectively

Table 2: Genetic parameters for ten quantitative characters in F_4 families of sesame

Characters	Range		Mean	Coefficient of variation		h^2(%)	GAM
	Min	Max		PCV	GCV		
Days to 50% flowering	31	52	38.62	21.46	12.76	35.28	15.63
Days to maturity	90	114	100.92	6.43	6.16	92.95	12.23
Plant height (cm)	43	121	87.92	16.80	16.57	97.25	33.66
Number of branches per plant	1	10	3.58	38.90	38.40	97.42	78.17
Number of capsules per plant	13	232	93	47.76	47.75	99.96	98.35
Capsule length (cm)	1.9	3.0	2.48	13.96	13.37	91.66	26.18
Distance from ground to first capsule (cm)	17	44	34.33	17.76	17.82	99.98	36.70
Number of seeds per capsule	52	92	67.16	14.17	13.68	93.25	27.23
1000 seed weight (g)	1.00	3.22	2.46	19.49	17.24	78.26	31.43
Seed yield per plant (g)	1.18	38.74	16.50	45.26	45.24	99.91	93.15

PCV- Phenotypic coefficient of variation, h^2- Heritability in broad sense, GCV- Genotypic coefficient of variation, GAM- Genetic advance as per cent of mean

Days to maturity showed low PCV and GCV which is in accordance with findings of Shadakshari *et al.* (1995) and Ganeshan (2005).

Estimates of heritability and genetic advance as per cent mean in combination are more important for selection than heritability alone. High heritability coupled with high genetic advance as per cent mean was observed for plant height, number of branches per plant, number of capsules per plant, capsule length, distance from ground to first capsule, number of seeds per capsule, 1000 seed weight and seed yield per plant. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance. Hence, phenotypic selection would be effective for these characters. Similar results have been reported by Reddy *et al.* (2001), Hamid *et al.* (2003), Babu *et al*. (2005) and Sudhakar *et al.* (2007). High heritability with moderate genetic advance was recorded for days to maturity which might be due to predominance of non additive gene action. These results are in accordance with Parameshwarappa *et al.* (2009). Days to 50 per cent flowering had moderate heritability as well as genetic advance as per cent mean indicating the non additive gene action.

The present study suggested that, selection for superior yielding types based on number of branches per plant, number of capsules per plant and seed yield per plant would be effective as these characters had high GCV, heritability and genetic advance as per cent mean.

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