Short Note



Study of Genetic Parameters Involving Single Stemmed Genotypes of Sesame (Sesamum indicum I)

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Eighty sesame genotypes involving single stemmed and shybranching collected from different states of the country and also from outside the country were evaluated for variability, heritability and genetic advance as per cent of mean for eight traits *viz.*, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, 100 seed weight, seed yield per plant and oil content. High GCV and PCV was observed for plant height, number of branches per plant, number of capsules per plant, and seed yield per plant suggesting that these characters are under the influence of genetic control. Hence these characters can be relied upon simple selection for further improvement. High heritability coupled with high genetic advance was observed for plant height, number of branches per plant, and seed yield per plant, number of capsules per plant, and seed yield per plant height, number of branches per plant, number of branches per plant, number of branches per plant the provement. High heritability coupled with high genetic advance was observed for plant height, number of branches per plant, number of capsules per plant, and seed yield per plant. This indicates less influence of environment in expression of these characters making them amenable for simple selection.

Key words: Sesame, variability, co-efficient of variation, heritability and genetic advance

Sesame is one of the world's oldest oilseed crop. It is the 6th most important oilseed crop grown in India on an area of 2.9 m.ha with a productivity of 332 kg/ ha. Yield in sesame needs to be augmented as the productivity in India is very low when compared to other sesame growing countries. To achieve this objective, it is essential to generate more variability. The success of any crop improvement programme essentially depends on the nature and magnitude of variability present in the crop. The knowledge on nature and magnitude of genetic variability is of immense value for planning effective breeding programme to improve the yield potential of the genotypes. The present investigation was carried out to gather information on variability, heritability and genetic advance in eighty genotypes including single stemmed genotypes of sesame.

Materials and Methods

Experimental material for the present study consists of eighty sesame genotypes involving single stemmed and shybranching collected from different states of the country and also from outside the country (Cordebergea from USA). The crop was raised during Kharif 2003 at the Department of Oilseeds, Centre for Plant Breeding and Genetics, TNAU, Coimbatore in a randomized block design with three replications. Each plot consists of two row of 4m length spaced at 30 cm between rows and 15 cm between plants. Normal recommended cultural practices and plant protection measures were followed. Ten competitive plants were randomly selected for recording biometrical measurements

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on eight traits viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, 100 seed weight, seed yield per plant and oil content. The data were subjected to statistical analysis. The phenotypic and genotypic coefficient of variability was computed as per Burton, 1952. Heritability in broad sense was computed by the formula suggested by Lush (1940). Genetic advance was worked out as per the formula given by Johnson et al. (1955).

Results and Discussion

Analysis of variance revealed high and significant variation for all the characters under study indicating considerable amount of genetic variation present in the material (Table 1). The estimates of genetic parameters like genotypic coefficient of variation,

Table	1.	Analysis	of	variance	for	different		
characters of single stemmed sesame								

Characters	Mean squares					
Gildideleis	Replication	Treatment	t Error			
Days to fifty percent						
flowering	2.03	34.30**	0.911			
Plant height (cm)	16.19	694.92**	20.46			
No. of branches per plan	t 1.33	2.08**	0.24			
No. of capsules per plant	35.82	951.99**	26.54			
100 seed weight (g)	0.0005	0.003**	0.00006			
Oil content (%)	0.69	5.75**	0.09			
Days to maturity	16.9	68.53**	0.72			
Single plant yield (g)	0.11	11.18**	0.133			

*Significant at 5%; **Significant at 1%

Characters	Mean	Range	Geno typic	Pheno typic		Phenotypic coefficient	Heritability	Genetic advance	SE
			variance	variance	of variation	of variation		as percent of mean	
Days to fifty percent flowering	41.73	34.5 - 50.5	16.70	17.15	9.79	9.93	97.34	19.90	0.95
Plant height (cm)	77.33	50.05 - 122.2	337.23	347.46	23.75	24.10	97.06	48.19	4.52
No. of branches per plant	3.89	2.0 - 6.2	0.92	1.04	24.68	26.22	88.61	47.85	0.49
No. of capsules per plant	54.65	21.35 – 109.65	462.73	475.99	39.36	39.93	97.21	79.95	5.15
100 seed weight (g)	0.27	0.21 – 0.36	0.0013	0.0013	13.03	13.18	97.73	26.53	0.008
Oil content (%)	46.69	43.39 - 49.54	2.83	2.87	3.60	3.63	98.43	7.36	0.300
Days to maturity	73.46	66.00 - 89.50	33.90	34.26	7.93	7.97	98.95	16.24	0.85
Single plant yield (g)	5.79	2.33 - 13.23	5.53	5.59	40.60	40.84	98.81	83.13	0.36

Table 2. Estimates of variability parameters for yield and its components of single stammed seasame

heritability and genetic advance are presented in Table 2. Perusal of the data indicated that the traits plant height, number of capsules per plant and days to maturity recorded highest phenotypic and genotypic variation than the other characters studied.

Though the phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters studied, the close resemblance between the corresponding estimates of PCV and GCV in almost all the characters suggested that the environment had little role in the expression of these characters. High GCV and PCV were observed for plant height, number of branches per plant, number of capsules per plant, and seed yield per plant suggesting that these characters are under the influence of genetic control. Hence these characters could be relied upon and simple selection could be predicted for further improvement. These results are in consonance with those of Reddy et al. (2001) and Sudhakar et al. (2007). The characters days to fifty per cent flowering, days to maturity and oil content recorded a low phenotypic and genotypic coefficient of variation. Similar results were reported by Sudhakar et al. (2007), and Shadakshari et al. (1995). Moderate PCV and GCV were recorded for the characters 100 seed weight.

The heritability and genetic advance estimates were interpreted as low, medium and high as per the classification of Johnson et al .(1955). Broad sense heritability ranged from 88.61 (number of branches per plant) to 98.95 per cent (days to maturity). It was high in all the characters studied. As heritability alone can not serve as an indication of the expected genetic improvement, the genetic advance is also taken into consideration. High heritability coupled with high genetic advance was observed for plant height, number of branches per plant, number of capsules per plant, and seed yield per plant. This indicated the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance, hence amenable for simple selection. Similar results were reported by Reddy et al. (2001) and Krishnaiah *et al.* (2002). High heritability with moderate genetic advance as per cent of mean was recorded for days to flowering, 100 seed weight and days to maturity indicating that these characters were also governed by additive gene action. High heritability coupled with low genetic advance as per cent of mean was recorded for oil content indicating non-additive gene action. These results are in conformity with the findings of Reddy *et al.* (2001) and Sudhakar *et al.* (2007).

Selection based on the characters, plant height, number of branches per plant, number of capsules per plant, and seed yield per plant would be effective since, they expressed high heritability with high genetic advance. This might be attributed to additive gene action conditioning their expression and therefore phenotypic selection can be relied upon.

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