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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR THE PHENOTYPIC TRAITS IN SESAME (*Sesamum indicum* L.) GENOTYPES

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Sesame (*Sesamum indicum* L.) also known as Til or Gingelly, is one of the most important oilseed crop of tropical and temperate regions. It belongs to the order Tubiflorae, family Pedaliaceae. It is referred as "Queen of oilseeds" due to its resistance to oxidation and rancidity, also plays an important role as an industrial food crop because of its high nutritional value. The seeds of sesame contains 40 to 63 per cent oil which is rich in antioxidants and has a significant amount of oleic and linoleic acids (1). Gingelly seed is consumed as a source of calcium, potassium, tryptophan and methionine. It is also used in pharmaceutical as well as cosmetic industries (2). The success of any crop improvement programme essentially depend on the nature and magnitude of genetic variability present in the crop. The knowledge of nature and magnitude of genetic variability is of immense value for planning efficient breeding programme to improve the yield potential of the genotypes.

The experimental material used in the present investigation comprised of sixty genotypes of sesame which were obtained from All India Coordinated Research Project on Sesame and Niger (ICAR), JNKVV Campus, Jabalpur, Madhya Pradesh. They were selected on the basis of duration, suitable for *Kharif* season and yield. The following are raised along with two check varieties Swetha Thil and Rajeshwari obtained from RARS, Jagtial. The experiment was laid out in Randomized Block Design (RBD) with three replications during *kharif,* 2015. Each genotype was sown in four rows of 4 meter length with inter row spacing of 30 cm and intra row spacing of 10 cm. Sowing was done by dibbling and all the recommended package of practices were followed to raise a healthy crop and necessary prophylactic measures were adopted against pests and diseases. Observations were recorded for yield, yield attributing characters on five randomly selected competitive plants for each entry in each replication. The mean data obtained at each location was considered for final statistical analysis. Days to 50% flowering was recorded on plot basis. Observations were recorded and the data was subjected to statistical analysis.

The analysis of variance (Table-1) showed highly significant differences among the genotypes under study for all the ten traits *viz.,* days to 50% flowering, days to maturity, 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), harvest index (%) and seed yield per plant (g), indicating the presence of considerable genetic variability among the experimental material under study.

The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values. Among the all traits number of branches plant 23.06% and 24.63% exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by number of capsules per plant (21.53% and 22.30) and harvest index (20.22% and 21.03), suggest that these characters are under the influence of genetic control. Therefore, these characters can be relied upon and simple selection can be practiced for further improvement. These results are in agreement with those of (3). Moderate phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) values were recorded for Plant height, number of seeds per capsule, 1000-seed weight and seed yield per plant The results are in conformity with the findings of (1). Days to 50% flowering, days to maturity and capsule length recorded a low phenotypic and genotypic co-efficient of variation (3).

Table-1 : Analysis of variance for ten characters in 62 genotypes of sesame.

Character	Mean sum of squares		
	Replications (df=2)	Treatments (df=61)	Error (df=122)
Days to 50% Flowering	2.14	17.74**	1.78
Days to maturity	14.77	25.34**	5.99
Plant Height (cm)	19.97	485.12**	15.10
No. of branches/plant	0.04	2.06**	0.09
No. of capsules/plant	8.09	251.49**	6.02
Capsule length (cm)	0.01	0.14**	0
No. of seeds per capsule	1.45	332.81**	8.31
1000 seed weight (g)	0.02	0.31**	0.01
Seed yield/plant (g)	0.12	2.54**	0.27
Harvest index (%)	0	136.51**	3.58

** Significant at 1% level, * Significant at 5% level

Table- 2 : Mean, range, variability, heritability (broad sense), genetic advance and genetic advance as per cent mean for ten characters in 62 sesame genotypes.

Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance at 5%	Genetic advance as per cent mean at 5%
		Min	Max	Genotypic	Phenotypic			
Days to 50% flowering	41.48	36.00	46.33	5.56	6.42	74.90	4.11	9.91
Days to maturity	94.98	90.67	110.00	2.67	3.71	51.80	3.76	3.96
Plant height (cm)	80.70	60.00	108.00	15.51	16.24	91.20	24.62	30.51
Number of branches per plant	3.51	2.20	5.47	23.06	24.63	87.70	1.56	44.50
Number of capsules per plant	42.01	29.30	60.67	21.53	22.30	93.10	17.98	42.80
Capsule length (cm)	2.60	2.23	3.20	8.19	8.87	85.30	0.40	15.59
Number of seeds per capsule	56.01	37.93	72.80	18.56	19.26	92.90	20.64	36.85
1000 seed weight (g)	2.68	2.13	3.83	11.87	12.44	91.00	0.62	23.32
Seed yield per plant (g)	5.32	3.75	6.99	16.34	19.10	73.1	1.53	28.78
Harvest index (%)	32.90	21.92	48.50	20.22	21.03	92.50	13.18	40.07

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, number of seeds per capsule, 1000-seed weight, seed yield per plant and harvest index .This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance. Hence, are amenable for simple selection. Similar findings were reported by (3). Capsule length had high heritability coupled with moderate genetic advance as per cent of mean indicating that the characters were governed by both additive and non-additive gene action. These results are in accordance with (4). High heritability coupled with low genetic advance was recorded for Days to 50% flowering indicating non- additive gene action. These results are in conformity with the findings of (3). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the traits studied indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits (Table-2).

The results showed that there were highly significant differences among the genotypes for all characters studied. Number of branches per plant exhibited highest PCV and GCV values followed by number of capsules per plant and harvest index. 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, number of seeds per capsule, 1000-seed weight, seed yield per plant and harvest index indicating the influence of additive gene action, as such simple selection would be effective for improvement of these traits.

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