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Heritability and genetic advance for seed yield and its attributes in sesame (*Sesamum indicum* L.)

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Abstract

The present investigation was accomplished in summer 2023 at Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The experimental material consisted of six families, each having six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were evaluated in Compact Family Block Design with three replications during summer, 2023 at Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The observations were recorded for twelve different characters. The high heritability coupled with high genetic advance was observed in cross I for plant height; cross III for number of branche per plant; cross IV for number of branche per plant, seed yield per plant, oil content and oleic acid content. While low heritability coupled with low genetic advance observed in cross II for 1000 seed weight and linoleic acid content; cross III for days to maturity, number of seed per capsule and oil content; cross IV for plant height and capsule length; cross V for days to flowering, number of capsule per plant, number of seed per capsule, 1000 seed weight, seed yield per plant, oleic acid content and linoleic acid content; cross VI for plant height and oil content. The presence of high heritability coupled with high genetic advance, moderate heritability with high genetic advance or low heritability with high genetic advance, indicate that the role of additive gene action. So, selection may be effective in these crosses.

Keywords: Heritability, genetic advance, gene action

Introduction

Sesame (*Sesamum indicum* L) is one of the oldest and self pollinated oilseed crops. Sesame ($2n = 2x = 26$) commonly known as gingelly, til, benniseed and simsim belongs to the order Tubiflorae and family *Pedaliaceae*. It is called as the "Queen of oil seeds" because of its excellent qualities of the seed, oil and meal. Sesame seed contain about 40-52 percent oil, 20-27 percent protein, 6-7 percent moisture, 16 percent carbohydrate and 6-8 percent crude fiber. Heritability expresses the relative amount of heritable portion of variation, however its estimate along with genetic advance is more useful in predicting the resultant effect of selecting the best individual. Both broad and narrow-sense heritability estimates were important, but when segregating generations are available, the calculation of narrow-sense heritability provides a more precise result. Hence, in the present investigation, narrow-sense heritability may be more helpful in selecting segregating populations. That is why the genetic advance was calculated based on narrow-sense heritability to ascertain more reliable results and improvement in the mean genotypic value of selected families over that of the base population.

Materials and Methods

The present investigation carried out to study the six crosses (G. Til 4 × AT 502, G. Til 5 × HT 2, G. Til 6 × Thilak, IC 199434 × N 32, MB 1-2 × G. Til 2 and VRI 2 × AT 413). These were obtained by crossing twelve sesame lines. The F_1 hybrids were generated during summer, 2022. Backcrossing was done in *kharif*, 2022 with their respective parents. Selfing of F_1 was also done in the same season (*kharif*, 2022) to get F_2. The experimental material consisted of six families, each having six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were evaluated in Compact Family Block Design with three replications during summer, 2023 at Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The observations were recorded for twelve different characters *viz*., days to flowering, days to maturity, plant height (cm), number of branch per plant, number of capsule per plant, capsule length (cm), number of seed per capsule, 1000 seed weight (g), seed yield per plant (g), oil content (%), oleic acid content (%) and linoleic acid content (%). The narrow-sense heritability calculated using the methodology suggested by Warner (1952) [9]. The expected genetic advance represents the shift in a population mean towards the superior side under some selection pressure after a single generation of selection. It was calculated using the methodology suggested by Johnson *et al.* (1955) [2].

Results and Discussion

The analysis of variance between generations within each family showed significant differences between six generation means for all the studied characters in all six crosses with the exception of 1000 seed weight in Cross III (G. Til 6 × Thilak). For majority of the characters under study, mean sum of squares revealed significant differences among generations in all the crosses, indicating a high level of variability in the experimental material.

The narrow-sense heritability for seed yield per plant ranged from 16.80 percent in cross V to 121.30 percent in cross IV. Cross III (67.51%) and cross IV (121.30%) exhibited high heritability. The cross I (36.14%) showed medium heritability, whereas cross V (16.80%) showed low heritability. The genetic advance varied from 3.34 percent in cross V to 34.25 percent in cross IV. Cross IV (34.25%) exhibited high genetic advance. The cross III (15.72%) indicated moderate genetic advance, whereas cross I (7.29%) and cross V (3.34%) showed low genetic advance. A perusal of data presented in table 2 showed that cross IV exhibited high heritability coupled with high genetic advance, indicating the role of additive gene action and small influence of the environment. The crosse III had high heritability coupled with moderate genetic advance. The cross I indicated moderate heritability with low genetic advance, While cross V explicated low heritability coupled with a low genetic advance.

High heritability coupled with high genetic advance was also reported by Kadvani *et al.* (2020) [3], Manjeet *et al.* (2020) [4], Thouseem *et al.* (2022) [8], Parihar *et al.* (2022) [6] and Mitkari *et al.* (2023) [5]. High heritability coupled with moderate genetic advance was reported by Iqbal *et al.* (2016) [1]. Low heritability coupled with a low genetic advance was reported by Pavani *et al.* (2020) [7].

The high to low estimates of narrow-sense heritability was observed for seed yield per plant and its components. The high heritability observed by cross I (G. Til 4 × AT 502) for plant height, number of seed per capsule, 1000 seed weight and linoleic acid content; cross II (G. Til 5 × HT 2) for plant height, number of capsule per plant, capsule length and oil content; cross III (G. Til 6 × Thilak) for plant height, number of branch per plant and seed yield per plant; cross IV (IC 199434 × N 32) for days to maturity, number of branch per plant, number of capsule per plant, 1000 seed weight, seed yield per plant, oil content and oleic acid content; cross V (MB 1-2 × G. Til 2) for plant height and capsule length; cross VI (VRI 2 × AT 413) for number of capsule per plant, capsule length and linoleic acid content. The higher estimates of heritability indicated that these traits were comparatively less affected by environment and their phenotype is a good reflection of genotype and thus possessed paramount importance in making a selection of superior genotype based on the phenotypic performance of these metric traits, but in case of lower heritability, pedigree or progeny test can be employed to improve it.

The high genetic advance was reported in cross I (G. Til 4 × AT 502) for plant height; cross IV (IC 199434 × N 32) for number of branch per plant, seed yield per plant, oil content and oleic acid content; cross III (G. Til 6 × Thilak), cross V (MB 1-2 × G. Til 2) and cross VI (VRI 2 × AT 413) for number of branche per plant.

The high heritability coupled with high genetic advance was observed in cross I for plant height; cross III for number of branche per plant; cross IV for number of branche per plant, seed yield per plant, oil content and oleic acid content. While low heritability coupled with low genetic advance observed in cross II for 1000 seed weight and linoleic acid content; cross III for days to maturity, number of seed per capsule and oil content; cross IV for plant height and capsule length; cross V for days to flowering, number of capsule per plant, number of seed per capsule, 1000 seed weight, seed yield per plant, oleic acid content and linoleic acid content; cross VI for plant height and oil content.

The high to low narrow-sense heritability and genetic advance were observed for most of the characters. The presence of high heritability coupled with high genetic advance, moderate heritability with high genetic advance or low heritability with high genetic advance, indicate that the role of additive gene action. So, selection may be effective in these crosses. When high heritability with moderate genetic advance, moderate heritability with moderate genetic advance or low heritability with moderate genetic advance present, which indicated presence of both additive and non-additive gene action, so improvement through reciprocal recurrent selection. The high heritability coupled with low genetic advance or moderate heritability coupled with low genetic advance present, which indicated that there is a preponderance of non-additive gene action and heterosis breeding may be rewarding. While low heritability coupled with a low genetic advance present, which means the environmental effects highly influence for this character and selection would be ineffective in these crosses.

Table 1: Estimates of heritability and genetic advance for days to flowering, days to maturity, plant height (cm), number of branch per plant, number of capsule per plant and capsule length (cm) in six crosses of sesame

Particulars	Estimates (%)					
	Days to flowering	Days to maturity	Plant height	Number of branch per plant	Number of capsule per plant	Capsule length
Cross I (G. Til 4 × AT 502)						
Heritability (ns)%	-	42.02	84.88	-	36.91	43.17
Genetic Advance%	-	1.71	20.48	-	4.88	7.70
Cross II (G. Til 5 × HT 2)						
Heritability (ns)%	59.37	40.56	80.34	-	103.57	93.79
Genetic Advance%	4.19	2.02	17.10	-	10.04	17.27
Cross III (G. Til 6 × Thilak)						
Heritability (ns)%	-	3.25	89.23	69.85	38.97	-
Genetic Advance%	-	0.16	13.08	45.42	3.74	-
Cross IV (IC 199434 × N 32)						
Heritability (ns)%	38.87	67.94	28.29	68.75	121.08	18.07
Genetic Advance%	2.89	4.01	3.28	44.89	15.77	2.76
Cross V (MB 1-2 × G. Til 2)						
Heritability (ns)%	11.47	52.88	110.27	44.30	10.72	138.39
Genetic Advance%	0.82	2.95	14.58	26.86	1.38	19.98
Cross VI (VRI 2 × AT 413)						
Heritability (ns)%	58.99	34.51	17.41	47.24	77.15	69.64
Genetic Advance%	4.32	1.75	2.02	27.17	7.47	10.63

Table 2: Estimates of heritability and genetic advance for number of seed per capsule, 1000 seed weight (g), seed yield per plant (g), oil content (%), oleic acid content (%) and linoleic acid content (%) in six crosses of sesame

Particulars	Estimates (%)					
	Number of seed per capsule	1000 seed weight	Seed yield per plant	Oil content	Oleic acid content	Linoleic acid content
Cross I (G. Til 4 × AT 502)						
Heritability (ns)%	78.01	70.53	36.14	47.01	38.67	104.95
Genetic Advance%	7.38	6.76	7.29	2.35	2.87	11.12
Cross II (G. Til 5 × HT 2)						
Heritability (ns)%	44.24	9.98	-	69.03	-	10.24
Genetic Advance%	3.97	0.82	-	3.66	-	0.81
Cross III (G. Til 6 × Thilak)						
Heritability (ns)%	23.12	-	67.51	17.23	43.59	-
Genetic Advance%	1.83	-	15.72	1.26	3.48	-
Cross IV (IC 199434 × N 32)						
Heritability (ns)%	-	67.72	121.30	183.25	187.54	-
Genetic Advance%	-	6.60	34.25	45.76	51.59	-
Cross V (MB 1-2 × G. Til 2)						
Heritability (ns)%	8.60	25.20	16.80	41.46	6.56	9.19
Genetic Advance%	0.69	2.20	3.34	2.62	0.53	0.70
Cross VI (VRI 2 × AT 413)						
Heritability (ns)%	55.59	-	-	2.59	-	86.27
Genetic Advance%	4.55	-	-	0.17	-	8.69

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