

Research Article

Selection of traits for seed yield improvement through variability parameters in sesame (*Sesamum indicum* L.) genotypes.

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Abstract

Sesame (*Sesamum indicum* L.) was renowned in the ancient ages for the stability of its healthy oil, accessibility of extraction, and drought resilience. Consequently, to produce novel varieties, the present work entails the utilization of basic metrics of variability and genetic variation. The investigation included 60 sesame genotypes and 13 quantitative characteristics. The analysis of variance revealed that genotypes were significant for all of the parameters assessed ($P > 0.05$ and $P > 0.01$). The average seed yield per plant was 6.93g, ranging from 4.84 to 9.17g. In all of the traits studied, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variance (GCV). The tense relationship between PCV and GCV values indicated that the environment had minimal impact on the expression of the traits under investigation. The no. of branches, no. of capsules/axil, capsules per plant, no. of seeds per capsule, and oil content suggested higher estimations of PCV and GCV. The heritability varied from 75.13% for seed width to 99.03% for no. of capsules/axil. The genetic advance (GA) percent means varied from 7.71 (seed length) to 110.93 (no. of capsules/axil) at 5% selection intensity. plant height, no. of branches, 1000 seed weight, capsule length, capsules per plant, no. of seeds per capsule, seed thickness, oil content, and seed yield per plant all showed substantial heredity and a high GA% mean. Because of this, the traits of additive genetic control and direct selection in sesame have a high potential for increasing its yield.

Keywords: Genotype, Genetic advance, Genotypic coefficient of variation, Phenotypic coefficient of variation Variability

INTRODUCTION

Sesame (*Sesamum indicum* L.) has been farmed since antiquity and is one of the oldest and most significant oilseed crops. It was farmed and domesticated in the Indian subcontinent over 4,000 years ago, during the Harappan and Anatolian civilizations (Iqbal *et al.*, 2016). Because of the stability of its nutritious oil, ease of extraction, and drought resilience, sesame was popular in the ancient world. Sesame is a healthy oilseed crop abundant in protein (18–25%), carbs (13.5%), minerals, and polyunsaturated fatty acids (Iqbal *et al.*, 2016). Sesame oil is preferred as a cooking medium by Indians and Africans. Sesame contains a unique antioxidant, sesamol, and high polyunsaturated fatty acids

such as oleic acid (43%), linoleic acid (35%), palmitic acid (11%), and stearic acid (7%) that have propelled it to the title of "queen of oilseed crops" (Ashri, 2018). Sesame is India's fifth most significant edible oil crop, behind groundnut, rapeseed-mustard, sunflower, and soybean. India tops the globe in sesame acreage (24%), as well as export contribution (40%) (FAOSTAT, 2020). India's sesame production is low when compared to other sesame-producing nations. Productivity increases would surely assist the Indian oil crop industry and other auxiliary sectors. One of the easiest methods to boost crop yield is to increase productivity. Any crop's genetic progress is essentially contingent on using available genetic resources. In plant breeding programs, a big germplasm supply is

always favoured since many good features will certainly stay in the population, enabling the breeding program to be exploited (Mohanty *et al.*, 2020). There has been little research on sesame genetic diversity. Several genetic metrics, including phenotypic and genotypic coefficients of variation (PCV and GCV), heritability and genetic gain may be used to determine the genetic diversity of experimental materials. A significant biometric approach is multivariate analysis. Multivariate analysis is widely employed in the selection of parents for hybridization projects in various crops, such as blackgram, where numerous quantitative variables are generally aggregated together to produce a definitive conclusion of diversity (Iqbal *et al.*, 2016). The present study used several genetic estimations and multivariate analysis to determine how distinct sesame genotypes are.

MATERIALS AND METHODS

Study area

The experimental study was performed at Student's Farm, Department of Agriculture, Loyola Academy, Secunderabad, during *kharif* 2021.

Experimental material and design

The experimental material was comprised of 60 genotypes (Table 1) seeded in a randomised full-block de-

sign (RBD) with three replications. Each genotype was grown in a 5 m long row with 30 x 10 cm spacing. The recommended agronomic practices (35:23:23 NPK/ha) were followed to ensure a successful yield. Plant height (cm), no. of branches per plant, seed yield per plant (g), 1000 seed weight (g), no. of capsules per axil, capsule length (cm), No. of capsules per plant, No. of seeds per capsule, seed length (mm), seed width (mm), seed thickness (mm), and oil content were all measured. Data was collected from five randomly chosen plants in each entry of each replication.

Statistical analysis

Panase and Sukhatme (1961) used ANOVA to analyse the data gathered for all attributes (1961). As indicated by Robinson (1966), heritability values were determined, and the percentage was classified as Low (>30 percent), Moderate (30-60 percent), and High (> 60 percent) using Hanson *et al.* (1956). According to Johnson *et al.* (1955), the genetic advance was evaluated in absolute units (GA) and as a percentage of the mean (GAM), signifying selective superiority of 5% of genotypes, and was classed as Low (0-10%), Moderate (10-20%), and High (> 20%). Burton (1952) methods were used to determine PCV and GCV in percentages, which were then classed as Low (0-10%), Moderate (10-20%), and High (> 20%). The data was computed using the R programme (RStudio) and MS-Excel.

Table 1. List of sesame genotypes used in the study

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1	EC 304231	21	RT-125	41	CHANDANA
2	AKT-101	22	JLT-7	42	YLM-17
3	AGRA BALIK	23	VINAYAK	43	YLM-4
4	EVC-122	24	CT-44	44	SWETHA
5	CT-50	25	T-78	45	KIS-304
6	TMV-4	26	TMV-7	46	GT-10
7	TMV-6	27	VRI-2	47	JLT-408
8	RT-372	28	IC 127622	48	DORG-3052
9	YLM-66	29	YLM-11	49	DORG-60KRDS
10	PHULE TIL-1	30	IC 511151	50	DORG-B7-11
11	EC-208652	31	IC 204785	51	DORG-135-011
12	CT-51	32	IC 511141	52	DORG-37-11
13	EC 301961	33	EC 346665	53	TKG-22
14	CT-35	34	EC 346829	54	DORG-BLSG-9
15	RT-351	35	EC 346370	55	IC 204550
16	CUMS-17	36	IC 500448	56	EC 370712
17	ES-21086-2	37	IC 500463	57	IC 204248
18	CHAGATAM LOCAL	38	IC 500393	58	IC 500506
19	ANAMIDI 74	39	VRI-1	59	IC 132828
20	B-67	40	MADHAVI	60	IC 129908

RESULTS AND DISCUSSION

Analysis of variance

Table 2 shows the ANOVA findings for 13 traits of 60 sesame genotypes. The mean sum of squares due to genotypes were highly significant ($P>0.05$ and $P>0.01$) for all traits suggesting that the material under investigation possessed considerable genetic diversity. There was no significant variation in replication, demonstrating that environmental error (Genotype x environment) was less prevalent. These results indicated that significant variations exist across genotypes for all traits examined, which may give breeders an excellent opportunity to recognize high-performing accessions for desirable characteristics to improve crop breeding programs. Kiruthika *et al.* (2018) and Kumar *et al.* (2022) revealed that the days to 50% flowering, No. of capsules/axil and seed yield per plant of sesame, genotypes differed significantly in their studies.

Mean performance

According to the mean values (Table 3), the genotypes had early mean performance for days to 50% flowering (40.54 days), plant height (133.07 cm), No. of branches (6.60), 1000 seed weight (3.74 g), No. of capsules/axil (3.87), capsule length (3.41 cm), capsules per plant (147.33), No. of seeds per capsule (115.07), seed length (3.75 cm), seed width (2.46 cm), seed thickness (1.51 cm), oil content (35.62%) and seed yield per plant (9.17 g). Iqbal *et al.* (2016) found identical mean performance when they provided a broad range of mean values for plant height, 1000 seed weight, capsule length, and seed output per plant. Ismaila *et al.* (2016) found similar results regarding days to 50% blooming, number of branches, 1000 seed weight, capsule length, and

capsule per plant. Mohanty *et al.* (2020) discovered similar results regarding the no. of seeds per capsule, oil content, and seed production per plant.

Estimates of variability components

Table 3 and Fig. 1 show the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (bs), and genetic advance as a percentage of means (GA%) for 60 sesame genotypes (Table 1) of 13 characteristics.

Genotypic and phenotypic coefficients of variation

Higher levels of variability in genotypes allow for crop improvement. For each of the 60 genotypes of the 13 characteristics, a phenotypic (PCV) and genotypic (GCV) coefficient of variation was determined. As a consequence, when the PCV and GCV were calculated, these parameters remained unit-free. GCV is a useful statistic for evaluating the variability of different phenotypes because it reflects the heritable genetic component of the total variance. The PCV was higher than the GCV for all of the features in this study (Table 3 and Fig. 1). This result is similar with to those of Kumar *et al.* (2022), Iqbal *et al.* (2016), Ismaila *et al.* (2016), Mohanty *et al.* (2020), Kiruthika *et al.* (2018), Singh *et al.* (2018) and Sabiel *et al.* (2015), who found that PCV was higher than GCV in sesame crop studies. This implies that the observed variation is produced not just by genotypes but also by the relevant environmental influence. This environmental impact might be attributable to soil fertility, heterogeneity, and other uncontrolled elements. The no. of branches, no. of capsules/axil, capsules per plant, no. of seeds per capsule, and oil content of the characteristics analysed all had higher (>20) estimates of phenotypic (PCV) and

Table 2. Mean sum of squares from ANOVA for sesame yield and its components of 60 genotypes

Source	Replication	Treatment	Error	Sem	CD	CV %
DoF	2	59	118			
Days to 50% Flowering	1.37	14.67**	0.50	0.41	1.14	1.74
Plant Height	70.43	952.92**	50.08	4.09	11.44	7.14
No. of branches	0.28	4.63**	0.10	0.18	0.50	9.73
1000 seed weight	0.02	0.52**	0.05	0.13	0.38	8.04
No. of capsules/axil	0.00	1.24**	0.00	0.04	0.10	5.36
Capsule length	0.04	0.31**	0.02	0.07	0.20	5.00
Capsules per plant	11.10	1697.75**	7.37	1.57	4.39	5.56
No. of seeds per capsule	4.63	751.75**	14.11	2.17	6.07	5.07
Seed length	0.00	0.14**	0.04	0.12	0.34	6.55
Seed width	0.01	0.12**	0.01	0.06	0.17	5.76
Seed thickness	0.00	0.05**	0.00	0.03	0.09	5.85
Oil content	0.14	70.80**	1.58	0.72	2.03	5.27
Seed Yield per plant	0.83	3.46**	0.32	0.33	0.91	8.14

DoF: Degree of Freedom

genotypic (GCV) coefficients of variation. A high GCV and PCV, according to Iqbal *et al.* (2016), Ismaila *et al.* (2016), Mohanty *et al.* (2020), and Kiruthika *et al.* (2018) indicate that environmental influences have less impact on the expression of such characteristics. Thus there is a greater opportunity to improve them through selective breeding. The PCV and GCV intensities were moderate (10-20) in the plant height, 1000 seed weight, capsule length, seed width, seed thickness, and seed yield per plant. Furthermore, moderate PCV and GCV levels are more impacted by hereditary characteristics, according to Iqbal *et al.* (2016), Ismaila *et al.* (2016), Kiruthika *et al.* (2018), Mohanty *et al.* (2020), and Sabiel *et al.* (2015), since environmental impacts on phenotypic expression are limited. As a consequence, these characteristics are amenable to further improvement via selection. For days to 50% flowering and seed length, PCV and GCV levels were low (>10). Iqbal *et al.* (2016), Ismaila *et al.* (2016), and Mohanty *et al.* (2016) all found similar findings. Low PCV and GCV values for characteristics indicate that the environment has a greater influence on these qualities. This suggests that phenotypic selection would be ineffective for improving genetics.

Heritability and genetic advance

Heritability determines the degree of phenotypic variation caused by additive gene activity. Heritability is a valuable indication of how well traits are handed down from parents to their offspring (Temam *et al.*, 2020). The proportion of heritable variation impacts the consistency of progeny performance in following genera-

tions. Robinson (1966) defines heritability as the possibility and degree to which improvement may be attained by selection and progress, and it can be utilised in both broad and restricted circumstances. Understanding how much improvement may be gained via selection while designing genetic modifications is useful. Genetic advance (GA) under selection refers to the increase in the average genotypic value of the chosen families over the overall population over time. Table 3 and Fig. 1 provide estimates of heritability and genetic advance as a percent of the mean (GA percent M) at 5% select in intensity for 13 quantitative and qualitative parameters of 60 sesame genotypes. The measured heritability varied from 43.09 percent to 99.03 percent from the first fruit harvest to plant height.

High (>60) estimates of heritability were recorded for all traits except seed length, suggesting that, even if environmental factors least control the characteristics, selection for their improvement may be ineffectual since heritability (bs) is assessed based on total genetic variation, which includes both total fixable (additive and AA type of epistasis) and non-fixable (dominance, AD and DD type of epistasis) variances Iqbal *et al.*, (2016), Ismaila *et al.*, (2016), Kiruthika *et al.*, (2018), Mohanty *et al.*, (2020) and Sabiel *et al.*, (2015). Seed length has moderate heritability (30-60), showing that environmental variables have a considerable impact on these characteristics and that genetic improvement via selection would be fairly challenging due to the environment's masking effects on genotypic effects (Iqbal *et al.*, 2016). Low (<30) heritability was observed there are no traits less than 30. The strong heritability values suggest that

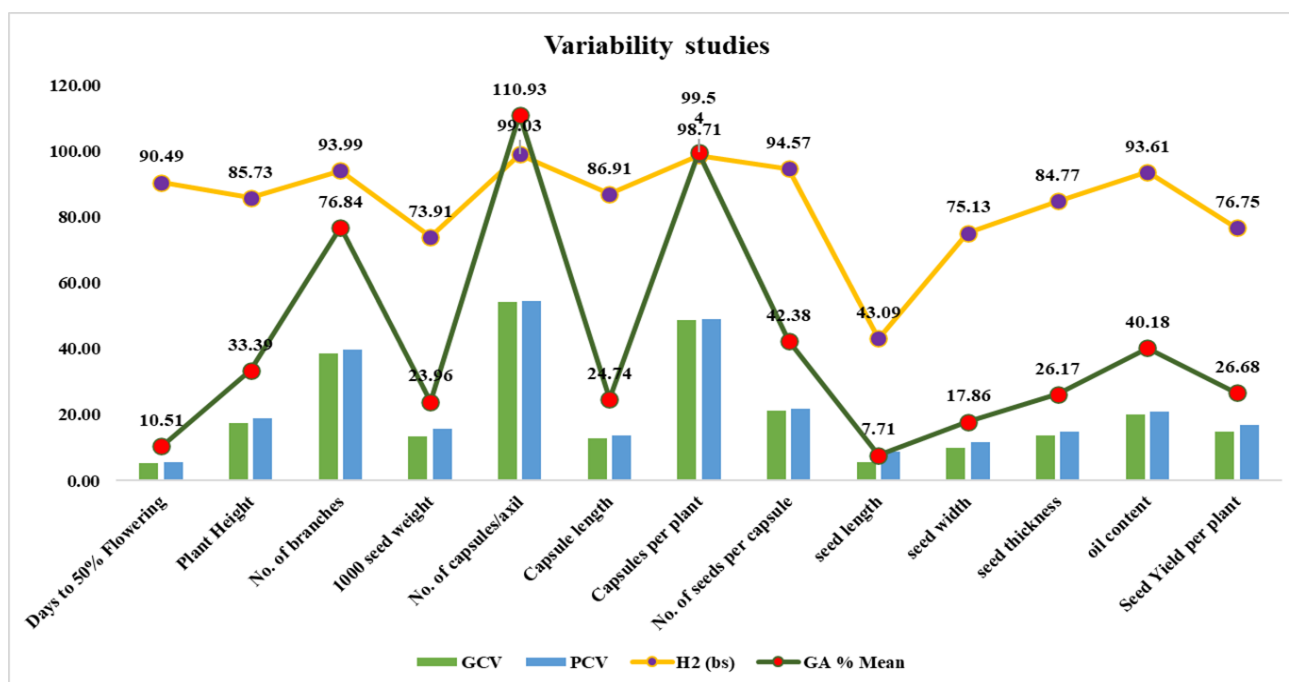


Fig. 1. Showing estimates of variability components in 60 genotypes (H_2 (bs): Heritability (broad sense); GA % M: Genetic advance % mean; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation).

Table 3. Estimates of variability components for 13 traits of 60 genotypes of sesame.

Characters	Range		Mean	Variance			Coefficient of variation		H ² (Broad Sense)	Genetic Advance	Genetic Advance as % of Mean
	Max	Min		VG	VP	GCV	PCV				
Days to 50% Flowering	46.33	35.33	40.54	4.72	5.22	5.36	5.64	90.49	4.26	10.51	
Plant Height	133.07	40.40	99.11	300.95	351.03	17.50	18.90	85.73	33.09	33.39	
No. of branches	6.60	0.20	3.20	1.51	1.61	38.47	39.68	93.99	2.46	76.84	
1000 seed weight	3.74	1.79	2.90	0.15	0.21	13.53	15.74	73.91	0.69	23.96	
No. of capsules/axil	3.87	1.00	1.19	0.41	0.42	54.11	54.38	99.03	1.32	110.93	
Capsule length	3.41	1.77	2.44	0.10	0.11	12.88	13.82	86.91	0.60	24.74	
Capsules per plant	147.33	13.93	48.81	563.46	570.83	48.64	48.95	98.71	48.58	99.54	
No. of seeds per capsule	115.07	29.33	74.12	245.88	259.99	21.16	21.75	94.57	31.41	42.38	
Seed length	3.75	2.38	3.19	0.03	0.08	5.70	8.69	43.09	0.25	7.71	
Seed width	2.46	1.46	1.86	0.04	0.05	10.00	11.54	75.13	0.33	17.86	
Seed thickness	1.51	0.73	0.91	0.02	0.02	13.80	14.98	84.77	0.24	26.17	
Oil content	35.62	6.12	23.83	23.08	24.65	20.16	20.84	93.61	9.57	40.18	
Seed Yield per plant	9.17	4.84	6.93	1.05	1.37	14.78	16.87	76.75	1.85	26.68	

programmes of sesame development for characteristics such as seed length and seed yield per plant will be implemented in the future. Backcrossing is essential to concentrate these traits in genotypes since many traits seem to be governed by alleles with additive effects (Temam *et al.*, 2020).

For seed thickness to No. of capsules/axil, the genetic progress % ranged from 7.71 to 110.93. Plant height, no. of branches, 1000 seed weight, no. of capsules/axil, capsule length, capsules per plant, no. of seeds per capsule, seed thickness, oil content, and seed yield per plant all showed high (>20) GA percent of the mean, indicating that additive genes control these parameters and that selection could help to improve them. This suggests that such features may be generated by direct selection. Among those who have contributed to this work are Iqbal *et al.* (2016), Ismaila *et al.* (2016), Kiruthika *et al.* (2018), Mohanty *et al.* (2020), and Sabiel *et al.* (2015). Days to 50% Flowering and seed width had a moderate (10–20) GA percent of the mean. In contrast, seed length exhibited a low (10) GA percent of the mean. This implies that nonadditive genes regulate the phenotypes, so heterosis breeding might be advantageous, as reported by Kiruthika *et al.* (2018).

Heritability (bs) is the only numerical assessment of the percentage of two variants, which may not result in accomplishment if the decision is only based on heritability (bs) estimates. Johnson *et al.* (1955) proposed that heritability (bs) estimates, combined with GA% of the mean, would be more successful in evaluating the effect of choosing the best accession. It contains more information than each parameter alone, demonstrates how genes interact, and can be altered (Muluken *et al.*, 2016).

Plant height, branch No., 1000 seed weight, capsule length, capsules per plant, No. of seeds per capsule, seed thickness, oil content, and seed yield per plant all demonstrated high heritability and GA percent of the mean. High heritability estimates and genetic advancements were more useful in determining the effect of selecting the optimal genotype. Mohanty *et al.* (2020) reported similar findings of high heritability and GA percent of the mean for plant height, No. of seeds per capsule, and No. of capsules/axil; Patidar *et al.* (2020) for No. of seeds per capsule; Ismaila *et al.* (2016) for No. of branches and 1000 seed weight; Kiruthika *et al.* (2018) for capsule length and oil content; Chandra Mohan (2014) for capsules per plant; Manivannan and Nadarajan (1996) for plant height and Iqbal *et al.* (2016) for capsule per plant and seed yield per plant. Days to 50% Flowering and seed width showed strong heritability (bs) and moderate GA as a percent mean. Kiruthika *et al.* (2018) and Iqbal *et al.* (2016) describe similar results. This might be because the environment seems to have a greater influence on how the qualities

manifest. There is less potential for improvement via selective breeding due to dominant and/or epistatic mechanisms of gene activation.

Conclusion

According to the analysis of variance, the mean sum of squares (MSS) due to genotypes was highly significant ($P>0.05$ and $P>0.01$) for all traits under inquiry, and suggesting considerable genetic variation among the 60 sesame genotypes for 13 traits. The average seed yield per plant was 6.93 g, ranging from 4.84 to 9.17 g. The PCV was bigger than the GCV for all characters. This implies that the observed variation is produced not just by genes but also by the proper environmental effect. Plant height, capsule length, seed thickness, and seed production per plant all exhibited moderate GCV, PCV, and high heritability (bs), and a high GA percent of the mean was more successful in evaluating the influence of picking the best accession. It provides more precise information than any of the parameters individually, as well as a manifestation of additive gene activity, and is selectable.

Conflict of interest

The authors declare that they have no conflict of interest.

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