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Assessment of Genetic variability, Correlation and Path Analysis in Sesame (Sesamum indicum L.)

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ABSTRACT: Studies on genetic variance, heritability, genetic advance, association, and path analysis were done on 45 genotypes of sesame for 12 variables that contribute to yield. The analysis of variance showed significant differences between the genotypes for each character, indicating that the experimental materials had enough variability. Branches per plant, capsules per plant and seed yield per plant had higher genotypic and phenotypic correlation coefficients. For branches per plant, capsules per plant, capsule length and seed yield per plant high heritability coupled with high genetic advance as percent of mean were detected, indicating that these features are controlled by additive gene action. The characters plant height, branches per plant, capsules per plant, seeds per capsule, test weight, harvest index and oil content showed significant and positive association with seed yield per plant. Therefore, simultaneous improvement of seed yield may be possible through selection of these characters. Path coefficient analysis at genotypic level indicated that capsules per plant, branches per plant, harvest index and oil content had positive direct effects and significant positive correlation with seed yield per plant. Hence, the use of these traits in sesame improvement programme would increase the seed yield.

Keywords: Variability, Heritability, Genetic advance, Sesame.

INTRODUCTION

One of the oldest oilseed crops in the world is sesame (Sesamum indicum L.), which belongs to the genus Sesamum and family Pedaliaceae. Sesamum indicum L. is the most widely cultivated species in the Sesamum genus, which has numerous species. 36 species have been identified, according to Kobayashi et al. (1990), of which 22 species have been discovered in Africa, 5 in Asia, 7 in both Africa and Asia, and 1 species in each of Crete and Brazil. The major reason for growing sesame is for its seeds. With a nearly 50% oil content and up to 25% protein, sesame seeds are exceptionally nutrientdense. Sesame oil has a long shelf life because it contains lignans, which have a great antioxidant effect. Sesamol, tocopherols, sesamolin, and their derivatives also inhibit the oxidation of the oil and give the oil a longer shelf life. The crop is mostly grown in the tropical and subtropical regions of the world, with maximum concentration and production in Asia. The major sesame growing countries in Asia are Myanmar,

India, China and to a lesser extent Afghanistan, Pakistan, Bangladesh, Indonesia and Sri Lanka. India is the second largest producer of sesame in the world after Myanmar. In India it is cultivated in an area of 15.8 lakh ha with production of 7.92 lakh tonnes (DAC&FW, 2021).

MATERIALS AND METHODS

During the summer of 2019 at the Agronomy farm, B. A. College of Agriculture, Anand Agricultural University, Anand, with a spacing of 30 cm between the rows and 10 cm between the plants, 45 sesame genotypes (Table 1) were tested in Randomized Block Design (RBD). To grow a quality crop, suggested agronomic procedures were used. The following twelve characters were recorded: days to 50% flowering, days to maturity, plant height (cm), branches per plant, capsules per plant, capsule length (cm), seeds per capsule, test weight (g), seed yield per plant (g), harvest index (%), oil content (%), and protein content (%) in each genotype across all three replications. According to standard statistical procedure given by Panse and Sukhatme (1978) analysis of variance was calculated using RBD for each character separately. Heritability (h²) in the broad sense was calculated according to the formula given by Allard, 1960. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952). Phenotypic and genotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955). The path coefficient analysis was performed as per the formula given by Wright (1921) and adopted by Dewey and Lu (1959).

Sr. No.	Genotype Name	Source	Sr. No.	Genotype Name	Source
1.	AT-253	ARS, Amreli, Gujarat	24	TC-289	AICRP, Tikamgadh, Madhya Pradesh
2.	AT-283	ARS, Amreli, Gujarat	25	MT-75	ARS, Amreli, Gujarat
3.	AT-288	ARS, Amreli, Gujarat	26	Bhachav-7	ARS, Amreli, Gujarat
4.	AT-306	ARS, Amreli, Gujarat	27	TMV-4	TNAU, Tamil Nadu
5.	AT-307	ARS, Amreli, Gujarat	28	PKVNT-11	AICRP, Nagpur, Maharashtra
6.	AT-308	ARS, Amreli, Gujarat	29	RT-46	ARS, Mandore, Rajsthan
7.	AT-314	ARS, Amreli, Gujarat	30	RT-103	ARS, Mandore, Rajsthan
8.	AT-315	ARS, Amreli, Gujarat	31	RT-358	ARS, Mandore, Rajsthan
9.	AT-324	ARS, Amreli, Gujarat	32	RT-369	ARS, Mandore, Rajsthan
10.	AT-334	ARS, Amreli, Gujarat	33	Tilak	TNAU, Tamil Nadu
11.	AT-390	ARS, Amreli, Gujarat	34	RSS-106	ARS, Amreli, Gujarat
12.	NIC-17274	AICRP, Nagpur, Maharashtra	35	SSM	ARS, Amreli, Gujarat
13.	Borda-2	ARS, Amreli, Gujarat	36	PATAN-64	ARS, Amreli, Gujarat
14.	Khadakala-4	ARS, Amreli, Gujarat	37	ABT-33	ARS, Amreli, Gujarat
15.	GT-1	ARS, Amreli, Gujarat	38	Nanabhamodara	ARS, Amreli, Gujarat
16.	GT-2	ARS, Amreli, Gujarat	39	Keriya-7	ARS, Amreli, Gujarat
17.	GT-3	ARS, Amreli, Gujarat	40	AKT-64	PDKV, Akola, Maharashtra
18.	GT-4	ARS, Amreli, Gujarat	41	AKT-101	PDKV, Akola, Maharashtra
19.	GT-5	ARS, Amreli, Gujarat	42	SVPR	TNAU, Tamil Nadu
20.	GT-10	ARS, Amreli, Gujarat	43	Tillottama	ORS, Berhampore, West Bengal
21.	TC-25	AICRP, Tikamgadh, Madhya Pradesh	44	Kayamkulam	KAU, Kerala
22.	TC-66	AICRP, Tikamgadh, Madhya Pradesh	45	Rama	ORS, Berhampore, West Bengal
23.	TC-125	AICRP, Tikamgadh, Madhya Pradesh			

Table 1: List of sesame genotypes selected for the study.

RESULT AND DISCUSSION

The results of the analysis of variance revealed significant differences between the genotypes for each attribute, indicating that the experimental materials under investigation exhibit a high degree of genetic diversity (Table 2). The estimates of genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean are shown in Table 3. It was clear that each genotype for each attribute showed a considerable amount of variation. For all the characters under study, the magnitude of the PCV (%) values were slightly larger than their corresponding GCV (%) estimates, indicating less influence of environment on the expression of characters which were in agreement with Vamshi *et al.* (2021). PCV ranged from 2.39 (oil content) to 40.86% (branches per plant), while, GCV ranged from 2.31 (days to maturity) to 40.44% (branches per plant).

Table 2: Analysis of variance for seed yield and its related traits in sesame.

	characters		Source			
Sr. No.		Replications (MSS)	Genotypes (MSS)	Error (MSS)		
	df	2	44	88		
1.	Days to 50% flowering	0.92	41.56**	5.83		
2.	Days to maturity	44.94**	19.70**	6.96		
3.	Plant height	13.16	305.22**	65.02		
4.	Branches per plant	0.16	8.38**	0.06		
5.	Capsules per plant	16.73	343.63**	16.80		
6.	Capsule length	0.50**	0.35**	0.05		
7.	Seeds per capsule	37.89*	92.58**	8.99		
8.	Test weight	0.001	0.17**	0.07		
9.	Seed yield per plant	0.12	9.22**	0.21		
10.	Harvest index	0.81	16.33**	0.74		
11.	Oil content	0.03	4.09**	0.05		
12.	Protein content	0.13	3.92**	0.08		

*, ** Significant at 5 and 1 % levels, respectively.

Table 3: Estimates of variability parameters for 12 traits in sesame.

Sr. No.	Characters	Coefficient of	variation	Heritability	Genetic advance as per cent of mean	
		PCV (%)	GCV (%)	$h_{b}^{2}(\%)$	GAM (%)	
1.	Days to 50% flowering	9.07	7.43	67.14	12.54	
2.	Days to maturity	3.75	2.31	37.91	2.92	
3.	Plant height (cm)	15.18	11.28	55.19	17.26	
4.	Branches per plant	40.86	40.44	97.88	82.46	
5.	Capsules per plant	26.26	24.44	86.64	21.57	
6.	Capsule length (cm)	16.31	13.47	66.67	22.54	
7.	Seeds per capsule	11.14	9.69	75.60	17.35	
8.	Test weight (g)	9.16	5.28	30.00	6.21	
9.	Seed yield per plant (g)	32.47	31.34	93.17	62.33	
10.	Harvest index (%)	7.48	7.00	87.69	13.49	
11.	Oil content (%)	2.39	2.35	97.12	4.77	
12.	Protein content (%)	4.75	4.62	94.12	9.23	

PCV = Phenotypic coefficient of variation GCV = Genotypic coefficient of variation

For branches per plant, capsules per plant and seed yield per plant, higher PCV and GCV magnitudes were observed. These results are in agreement with Haibru *et al.* (2018); Singh *et al.* (2018); Aboelkassem *et al.* (2021); Kumar *et al.* (2022).

Plant height, capsule length, and seeds per capsule showed moderate PCV and GCV. These findings were consistent with those made by Gangadhara *et al.* (2012); Ahmed and Ahmed *et al.* (2013).

Low PCV and GCV values were recorded for Days to 50% flowering, days to maturity, test weight, harvest index, oil content and protein content. Sumathi and Murlidharan (2010); Tripathi *et al.* (2014); Abhijatha *et al.* (2017) discovered comparable results.

The coefficients of variation do not show how much of a character is inherited; they only show the extent of variability that exists for different characters. As a result, heritability is calculated, which is a reliable indicator of how traits are passed down to offspring (Falconer, 1981). Heritability in broad sense ranged from 30.00 (test weight) to 97.88% (branches per plant). The genetic advance as per cent of mean ranged from 2.92 (days to maturity) to 82.46% (branches per plant).

Heritability estimations were high in this study for branches per plant (97.88%) followed by oil content (97.12%), protein content (94.12%), seed yield per plant (93.17%), capsules per plant (86.64%), seeds per capsule (75.60%), days to 50% flowering (67.14%) and capsule length (66.67%), demonstrating that selection based on phenotypic observations would be efficient and these traits were less influenced by the environment. Haibru *et al.* (2018) also reported similar results. Moderate heritability was noticed for plant height (55.19%) followed by days to maturity (37.91%) and test weight (30.00%).

According to Johnson *et al.* (1955), heredity taken into account with genetic progress is more accurate in forecasting the impact of selection than heritability alone. Branches per plant, capsules per plant, capsule length, and seed yield per plant all showed high heritability along with high genetic advance as a percent of mean (GAM), indicating that these traits are regulated by additive gene action and directed selection may be more successful. These conclusions are in line with those made by Aboelkassem *et al.* (2021); Kumar *et al.* (2022); Vamshi *et al.* (2021).

For days to 50% flowering, seeds per capsule and harvest index high heritability along with moderate GAM was seen, showing the role of both additive and non-additive gene activities; as a result, population improvement through reciprocal recurrent selection may be helpful. These findings are in accept those obtained by Mohanty *et al.* (2020), Singh *et al.* (2018)

High heritability coupled with low GAM was observed for oil content and protein content suggesting involvement of non-additive gene action in the expression of this trait. Vamshi *et al.* (2021), also reported similar results.

Moderate heritability coupled with moderate genetic advance as per cent of mean were observed for the plant height indicating both additive and non-additive gene action and hence, heterosis breeding may be useful. Similar outcomes were seen by Abate *et al.* (2015). Whereas, the results differed from the reports of Tripathy *et al.* (2016), as they observed moderate heritability with moderate genetic advance for the character number of primary branches, height to first capsule and seed yield.

Moderate heritability coupled with low GAM was reported for days to maturity and test weight suggesting the preponderance of non-additive gene action as well as influence of environment. Lower estimates of heritability and genetic advance was revealed for Days to maturity and capsule length by Chandra (2014).

The correlation coefficient between seed yield and yield components were worked out at genotypic and phenotypic level (Table 4). The characters days to 50% flowering, plant height, branches per plant, capsules per plant, test weight, harvest index and oil content showed significant and positive association with seed yield per plant. Therefore, by choosing these traits simultaneous improvement of seed yield may be possible. These were in conformity with the reports findings of Singh *et al.* (2018); Ramprasad *et al.* (2019); Kumar *et al.* (2022).

Because component characters are correlated with one another, correlation coefficient does not fully describe the nature of the relationship between yield and its component features. Hence, to ascertain how each independent character will affect a dependent character, path coefficient analysis is utilized and it will be also useful to work out the cause and effect relationship so that the selection will be more effective.

Path coefficient analysis at phenotypic level (Table 5) revealed that days to 50% flowering, plant height, branches per plant, capsules per plant, test weight, harvest index and oil content manifested positive direct effects and significantly positive association with seed yield per plant. At the genotypic level, path coefficient analysis (Table 6) revealed that traits such as 50%

flowering, branches per plant, capsules per plant, harvest index, and oil content showed both positive direct effects and a strong positive connection with seed yield per plant. These findings are in consonance with those of Abhijatha *et al.* (2017), Ramprasad *et al.* (2019); Kumar *et al.* (2022). Thus, it could be advocated that direct selection based on these attributes should be given more weightage in order to increase seed yield in sesame.

Character	r	Days to 50% flowering	Days to maturity	Plant height	Branches per plant	Capsules per plant	Capsule length	Seeds per capsule	Test weight	Harvest index	Oil content	Protein content	Seed yield per plant
Days to 50%	rp	1.000	0.288**	0.526**	0.556**	0.345**	0.126	0.137	0.054	0.294**	0.183*	0.204*	0.377**
flowering	rg	1.000	0.654**	0.773**	0.666**	0.437**	0.141	0.141	0.054	0.377*	0.235	0.291	0.492**
Days to	rp		1.000	0.077	0.151	0.094	0.115	0.080	0.155	0.032	-0.077	0.061	0.109
maturity	r _g		1.000	0.264	0.261	0.120	0.233	0.151	0.352 *	-0.002	-0.122	0.063	0.110
Plant	r _p			1.000	0.515**	0.437**	0.005	0.091	- 0.058	0.375**	0.353* *	0.262* *	0.490**
height	r _g			1.000	0.715**	0.741**	-0.030	0.110	0.008	0.528**	0.503* *	0.390*	0.673**
Branches	r _p				1.000	0.523**	-0.212	0.100	0.092	0.456**	0.234* *	0.116	0.566**
per plant	r _g				1.000	0.562**	-0.263	0.107	- 0.189	0.492**	0.242	0.123	0.591**
Capsules	r _p					1.000	0.006	0.098	0.129	0.471	0.327* *	0.167	0.487**
per plant	rg					1.000	-0.098	0.160	0.296	0.543**	0.361*	0.178	0.517**
Capsule	r _p						1.000	0.085	0.049	-0.171	-0.053	0.242* *	0.245**
lengui	rg						1.000	0.144	0.070	-0.244	-0.053	0.327*	-0.353*
Seeds per	r _p							1.000	0.034	0.187*	0.330* *	-0.059	0.150
capsule	rg							1.000	0.077	0.252	0.370*	-0.073	0.194
Test	rp								1.000	0.232**	-0.210	0.043	0.200*
weight	rg								1.000	0.441**	-0.352*	0.118	0.291
Harvest	r _p									1.000	0.278* *	0.056	0.840**
maex	rg									1.000	0.291	0.074	0.884**
Oil	rp										1.000	-0.025	0.302**
content	rg										1.000	-0.030	0.310**
Protein	rp											1.000	0.157
content	rg											1.000	0.179
Seed yield													1.000
per plant													1.000

Table 4: Phenotypic (r_p) and Genotypic (r_g) correlation coefficients among different characters in sesame.

*, ** Significant at 5 and 1% levels, respectively

Table 5: Phenotypic path analysis of seed yield per plant and other component characters in sesame.

Character	Days to 50% flowering	Days to maturity	Plant height	Branches per plant	Capsules per plant	Capsule length	Seeds per capsule	Test weight	Harvest index	Oil content	Protein content	Seed yield per plant
Days to 50% flowering	0.006	0.017	0.062	0.079	0.001	-0.017	-0.001	0.004	0.196	0.010	0.020	0.377**
Days to maturity	0.002	0.058	0.009	0.021	0.000	-0.015	-0.001	0.011	0.021	-0.004	0.006	0.109
Plant height	0.003	0.005	0.117	0.073	0.002	-0.001	-0.001	-0.004	0.250	0.020	0.025	0.490^{**}
Branches per plant	0.003	0.009	0.060	0.142	0.002	0.028	-0.001	-0.007	0.304	0.013	0.011	0.566**
Capsules per plant	0.002	0.005	0.051	0.074	0.004	0.011	-0.001	-0.009	0.314	0.019	0.016	0.487^{**}
Capsule length	0.001	0.007	0.001	-0.030	0.000	-0.131	-0.001	0.003	-0.114	-0.003	0.023	-0.245**
Seeds per capsule	0.001	0.005	0.011	0.014	0.000	-0.011	-0.010	0.002	0.125	0.019	-0.006	0.150
Test weight	0.000	0.009	-0.007	-0.013	0.000	-0.006	0.000	0.071	0.155	-0.012	0.004	0.200^{*}
Harvest index	0.002	0.002	0.044	0.065	0.002	0.022	-0.002	0.016	0.667	0.016	0.005	0.840**
Oil content	0.001	-0.004	0.041	0.033	0.001	0.007	-0.003	-0.015	0.186	0.057	-0.002	0.302**
Protein content	0.001	0.004	0.031	0.017	0.001	-0.032	0.001	0.003	0.038	-0.001	0.097	0.157

*, ** Significant at 5 and 1% levels, respectively, Phenotypic residual effect= 0.2145

Character	Days to 50% flowerin g	Days to maturit y	Plant heigh t	Branch es per plant	Capsul es per plant	Capsul e length	Seeds per capsul e	Test weigh t	Harve st index	Oil conte nt	Protei n conte nt	Seed yield per plant
Days to 50% flowering	0.353	-0.153	- 0.090	0.113	0.096	-0.040	0.013	0.021	0.112	0.033	0.032	0.492**
Days to maturity	0.231	-0.233	0.031	0.044	0.027	-0.066	0.014	0.135	0.000	-0.017	0.007	0.110
Plant height	0.273	-0.062	- 0.116	0.122	0.163	0.008	0.010	0.003	0.157	0.070	0.043	0.673**
Branches per plant	0.235	-0.061	- 0.083	0.170	0.124	0.074	0.010	0.073	0.147	0.034	0.014	0.591**
Capsules per plant	0.154	-0.028	- 0.086	0.096	0.220	0.028	0.014	- 0.114	0.162	0.050	0.020	0.517**
Capsule length	0.050	-0.054	0.003	-0.045	-0.022	-0.282	0.013	0.027	-0.073	-0.007	0.036	-0.353*
Seeds per capsule	0.050	-0.035	0.013	0.018	0.035	-0.041	0.090	0.030	0.075	0.052	-0.008	0.194
Test weight	0.019	-0.082	0.001	-0.032	-0.065	-0.020	-0.007	0.384	0.131	-0.049	0.013	0.291
Harvest index	0.133	0.000	- 0.061	0.084	0.120	0.069	0.023	0.169	0.298	0.041	0.008	0.884**
Oil content	0.083	0.028	0.058	0.041	0.080	0.015	0.033	0.135	0.087	0.140	-0.003	0.310**
Protein content	0.103	-0.015	0.045	0.021	0.039	-0.092	-0.007	0.045	0.022	-0.004	0.111	0.179

Table 6: Genotypic path analysis of seed yield per plant and other component characters in sesame.

*, ** Significant at 5 and 1% levels, respectively, Genotypic residual effect= 0.1600

CONCLUSION

The assessment of genetic parameters like phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean indicated that selection must be done in the traits like branches per plant, capsules per plant, capsule length and seed yield per plant indicating that these characters are controlled by additive gene action. The characters plant height, branches per plant, capsules per plant, seeds per capsule, test weight, harvest index and oil content showed significant and positive association with seed vield per plant. Therefore, simultaneous improvement of seed yield may be possible through selection of these characters. Path coefficient analysis at genotypic level indicated that capsules per plant, branches per plant, harvest index and oil content had positive direct effects and significant positive correlation with seed yield per plant. On the basis of these results it was suggested that these traits may be given more importance while making selection for higher yield potential in sesame.

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