Biological Forum – An International Journal **15(4): 166-172(2023)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Studies on Yield Attributes in Relation to Genetic Parameters in Sesame (*Sesamum indicum* L.) Genotypes

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(Received: 09 February 2023; Revised: 27 February 2023; Accepted: 14 March 2023; Published: 20 April 2023)
(Published by Research Trend)

ABSTRACT: A field investigation was carried out to study the genetic variations of seventeen yield and yield contributing traits in 36 genotypes of sesame. The analysis of variance revealed significant differences among the genotypes for all the studied characters. Phenotypic variances were found higher than the corresponding genotypic variances for all the characters. Among all the quantitative traits, five traits manifested higher genotypic as well as phenotypic variances and present the purview of genetic improvement through direct selection. The estimation of PCV along with GCV was high for seven traits while, it was moderate for other five traits. The characters *viz*. plant height, stem height from base to first branch, number of capsules per plant, 1000 seed weight, stover yield per plant, biological yield per plant and protein content showed high estimates of heritability combined with high genetic advance indicating, least environmental ascendancy and preponderance of additive gene effects. Although, productivity is low in sesame but searching the traits of importance and incorporating them for the genetic enhancement in sesame can be considered as a criterion for improving seed yield in breeding programs of sesame. So, these characters can be considered as a benchmark in breeding programmes for refined improvement in seed yield of sesame.

Keywords: Sesame, Genetic variability, GCV; PCV and Seed yield.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is an important and very ancient oilseed crop cultivated extensively in Asian countries and drier part of Africa (Iwo *et al*., 2007). It is an annual oilseed crop of the pedaliaceae family in the tropics and warm sub tropics, where it is usually grown in small patches (Agrawal *et al*., 2018). Sesame is described as the "Queen of oilseeds" because of its high nutritional value oil and other health benefits. Its seed contains 40-63% oil which have significant amount of oleic and linoleic acids (Abate and Mekbib 2015). Sesame seed is the readily available source of protein and also contains high amount of sulfur containing amino acids (Abate *et al*., 2015). Its stability due to antioxidant *i.e.* sesomin and sesamolin leads its industrial application in the developing countries for improving the shelf life of canned products. Sesame mainly grown in the states like Gujarat, Uttar Pradesh, Andhra Pradesh, Tamil Nadu, Karnataka, West Bengal, Bihar and Assam. Being largely self-sufficient in production, still sesame productivity is declining (Agrawal *et al*., 2018). Despite the economic importance for food, oil and medicine, the yield potential of sesame is not spectacular due to its cultivation in sub-marginal lands and non-availability of superior high yielding varieties due to lack of an appropriate breeding program (Manjeet *et al.* 2020). Sesame has different development stages of capsules because plant growth is originally indeterminate. Capsules on middle low position of stem are ripen almost enough but those of late bloom high on the stem remain immature (Doo *et al*., 2003). So, when we make crosses, genetic parameters should be well defined (Kader *et al*., 2022). The favourable outcome of any crop improvement program is basically depend on the nature and magnitude of genetic variability present in crop and the selection of that crop with high variability as parent, so that desired character amalgamation can be pick out to enhance the yield. Phenotypic selection of parents based on their performance only may not always be a reliable source for hybrids development. Since, phenotypically superior genotypes may yield inferior hybrids or poor recombinants. Hence, it is essential to select parents on the basis of their genetic worth, *i.e*., heritability along with genetic advance for selection. Genetic information on heritability and genetic advance for yield contributing characters would be of great value enable development of new genotypes (Mangi *et al*., 2007). Heritability provides information on the transmissibility of character from one generation to another and helps plant breeders for the selection of elite genotypes from diverse genetic populations (Patidar *et al*., 2018). So, its estimates along with genetic advance would be more useful in predicting grain yield than heritability estimates alone (Johnson *et al*., 1955). Genetic advance is indicative of additive gene action and it is the only genetic variance which response to the selection and it also provides information about the expected gain in a character from one cycle of selection (Dutta *et al*., 2013). Hence, keeping in view the above facts, the present study was carried out with the objectives to look into the extent of genetic variations in yield and yield contributing traits in sesame genotypes.

MATERIAL AND METHODS

The field experiment was conducted at research farm of department of Genetics & Plant breeding, SASRD, Medziphema, Nagaland and were evaluated during *kharif* seasons of 2019 and 2020. To study the variability, the experiment was planned in randomised block design with three replications by adapting a spacing of 30 cm between rows and 10 cm between plants. The experimental material comprised of thirty-six genotypes of sesame from different parts of the country. Recommended package of practices for sesame in Nagaland was followed along with the required plant protection measures to raise a good healthy crop. After seed treatment seeds from each genotype were sown in hills on raised bed along with furrows by dibbling at a depth of 2-3cm. Thinning of plants was done after 15 days of sowing. The observations on all the traits except for days to 50% flowering and days to 80% maturity were recorded based on 5 randomly taken plants per plot. Days to 50% flowering and 80% maturity were recorded on plot basis. To test for statistically significant differences between the genotypes, the pooled data over two years were subjected to analysis of variance by using INDOSTAT statistical package. The phenotypic and genotypic variances, coefficients of variation and heritability in broad sense for each character were estimated by the formula suggested by Singh and Chaudhary (1985) as follows:

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{Mst} - \text{EMS}}{\text{r}}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

MSt = Mean sum of squares due to treatment

EMS = Error mean sum of squares

r = number of replications

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) computed as:

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$= \frac{\sigma 2g}{\bar{X}} \times 100$$

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$= \frac{\sigma 2p}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = Mean of character

Heritability in broad sense (H) was derived based on the formula given by Hanson *et al.* (1956). Genetic advance was obtained by the formula prescribed by Johnson *et al.* (1955).

$$h^2 \text{ (broad sense)} = \frac{\sigma 2g}{\sigma 2p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

h^2 = Heritability (broad sense)

Genetic advance (GA) = K. σ_p. h^2

$$= K \cdot \sigma_p \cdot \frac{\sigma 2g}{\sigma 2p}$$

Where,

K = Selection differential at 5% level intensity *i.e.* 2.06 which is constant

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

Genetic advance as per cent of mean GA (%)

$$\text{GA (\%)} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

$\bar{X}$ = Mean of the character

RESULTS

Analysis of variance for yield contributing characters revealed the presence of significant differences among the genotypes for all the characters (Table 1). The genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean were estimated for thirty-six genotypes of sesame and are presented in Table 2. Variability estimates based on the genetic parameters present considerable variations for all the studied traits. In the present study, high phenotypic and genotypic variances were observed for the traits, *viz*., days to 50% per cent flowering, days to 80% physiological maturity, plant height, stem height from base to first branch, number of capsules per plant, number of seeds per capsule, stover yield per plant, biological yield per plant and oil content. While moderate estimates of phenotypic and genotypic variances were found for the characters *viz.* protein content and seed yield per plant. Traits internodal length, capsule length, number of branches per plant, relative water content, harvest index and 1000 seed weight exhibited low phenotypic and genotypic variances. The wide gap of variability between σ^2p and σ^2g which also denotes environmental variance (σ^2e) was recorded for the number of capsules per plant (363.70), plant height (189.50), stem height from base to first branch (138.87), biological yield (110.70) and stover yield per plant (49.50). While narrow gap of variability as environmental variances was observed for capsule length (0.02), 1000 seed weight (0.08), number of branches per plant (1.00), protein content (1.64), internodal length (1.77), oil content (6.43) and harvest index (7.97).

From the Table 2, it was observed that phenotypic coefficient of variation (PCV) was higher in magnitude than the corresponding genotypic coefficient of variation (GCV) for all the traits. It indicates the influence of environmental factors on these parameters and lower the scope of improvement in them through selection (Fig. 1a). Stem height from base to first branch, number of capsules per plant, number of branches per plant, 1000 seed weight, stover yield per plant, biological yield per plant and seed yield per plant exhibited high (>20%) magnitude of PCV and GCV. Moderate PCV and GCV (10-20%) were recorded for days to 50% flowering, plant height, internodal length, oil content, protein content while, number of seeds per capsule and harvest index exhibited moderate PCV only. It indicates there is scope for improvement of these traits by selection (Agrawal *et al*., 2018). Rest of the traits exhibited low (<10%) magnitude of PCV and GCV *i.e.,* days to 80% physiological maturity, capsule length and relative water content while low GCV were recorded for number of seeds per capsule and harvest index.

The estimates of heritability in broad sense (>60%) were found high for protein content, 1000 seed weight, oil content, plant height, stover yield per plant, number of capsules per plant, biological yield per plant and stem height from base to first branch. While the traits number of branches per plant, days to 50% flowering and days to 80% physiological maturity, internodal length, capsule length, harvest index and seed yield per plant, number of seeds per capsule showed moderate heritability and relative water content is the only trait which showed low heritability. Genetic advance as per cent of mean for the studied traits ranged 8.21 to 65.38%. The characters *viz*., number of capsules per plant (65.38%), stover yield per plant (61.77%), biological yield per plant (58.65%), seed yield per plant (54.53%), stem height from base to first branch (48.54%), number of branches per plant (46.82%), 1000 seed weight (37.44%), protein content (30.10%), plant height (27.13%) and internodal length (23.44%) exhibited high genetic advance as per cent of mean (>20%) while oil content (18.68%), days to fifty per cent flowering (15.63%), harvest index (11.56%) and number of seeds per capsule (10.57%) showed moderate genetic advance as per cent of mean (Fig. 1 b). However, the traits capsule length (8.93%), days to 80% physiological maturity (8.21%) and relative water content (2.69%) exhibited low genetic advance as per cent of mean.

The parameters like, plant height, stem height from base to first branch, number of capsules per plant, 1000 seed weight, stover yield per plant, biological yield per plant and protein content exhibited high heritability accompanied with high genetic advance as per cent of mean, indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose (Panse, 1957). While the trait oil content showed high heritability with moderate genetic advance as per cent of mean. However, moderate estimates of heritability coupled with high to moderate genetic advance as per cent of mean was recorded for seed yield per plant, internodal length, number of branches per plant, days to 50% flowering, harvest index and number of seeds per capsule. This indicates genotypic variance for these traits is probably owing to both additive and non-additive type of gene effects. Capsule length and days to 80% maturity reported moderate heritability with low genetic advance as per cent of mean similar to Abate *et al*. (2015) for days to 80% physiological maturity. Relative water content is the only trait which exhibited low heritability coupled with low genetic advance as per cent of mean.

DISCUSSION

Sesame is globally an important oilseed crop. Understanding of the underlying genetic mechanisms which influence seed and oil yields is important for developing improved sesame genotypes. This will enable selection of high-performing cultivars for direct production, industrial use and breeding programmes. This present findings examined genetic parameters as variance components, heritability and genetic advance of seed yield and their contributing traits in thirty-six genotypes of sesame. Variability in studies traits were also reported by Shekhawat *et al*. (2013); Singh *et al*. (2018); Gupta *et al*. (2020); Patidar *et al*. (2020); Kant *et al*. (2021). The magnitude of phenotypic variances was found higher than the corresponding genotypic variances for all the studied characters indicates the influence of environment on the expression of these characters. Such type of result was also reported by Abate *et al*. (2015); Mohanty *et al*. (2020) in their studies. Similarly, findings of high phenotypic and genotypic coefficient of variation in traits *viz*. stem height from base to first branch, number of capsules per plant, number of branches per plant, 1000 seed weight, stover yield per plant, biological yield per plant and seed yield were in agreement with the earlier reports of Gidey *et al*. (2013); Vanishree *et al*. (2013); Singh *et al*. (2018), Padmaja *et al*. (2020, 2017); Haibru *et al*. (2018); Mohanty *et al*. (2020); Gupta *et al*. (2021) for number of branches per plant, number of capsules per plant, number of seeds per capsule, stover yield per plant and seed yield per plant. Moderate GCV and PCVfor days to 50% flowering and plant height, oil content, number of seeds per capsule, internodal length andprotein content, 1000 seed weight, oil content, stover yield per plant, number of capsules per plant, biological yield per plant and stem height from base to first branch are in conformity with the findings of Bharathi *et al*. (2014); Mahmoud *et al*. (2015); Kumari *et al*. (2020); Kadvani *et al*. (2020); Jadhav and Mohrir (2012); Kumar *et al*. (2022).

Heritability values guide the expected response to selection in a segregating population. Understanding of inheritance pattern of different traits are vital to improve selection response in sesame breeding and cultivar development programmes. According to Robison *et al*. (1949), heritability greater than 60% are considered high, values from 30 to 60% medium whereas values less than 30% are regarded as low. In the present study, heritability in a broad sense was higher for protein content, 1000 seed weight, oil content, plant height, stover yield per plant, number of capsules per plant, biological yield per plant and stem height from base to first branch. The results are in conformity with the findings of Alake *et al.* (2010); Jadhav and Mohrir (2012); Thirumalarao *et al*. (2013); Vanishree *et al.* (2013); Bharathi *et al*. (2014); Padmaja *et al.* (2020 & 2017); Abate *et al.* (2015); Patidar *et al.* (2020); Gogoi and Sarma (2019); Saravanan *et al.* (2020); Kalaiyarasi *et al*. (2019); Manjeet *et al*. (2020); Kiruthika *et al.* (2018); Mohanty *et al*. (2020); Kadvani *et al*. (2020). High heritability values provide a measure of genetic advancement through phenotypic selection (Johnson *et al.*, 1955). In the present study, high heritability with high genetic advance were computed for seven traits. Conversely, Gupta *et al*. (2021); Jamir *et al.* (2020); Kadvani *et al.* (2020); Padmaja *et al.* (2017 & 2020) reported high heritability and high genetic advance for number of capsules per plant, 1000 seed weight; Kalaiyarasi *et al.* (2019); Jadhav and Mohrir (2012) for plant height, number of capsules/plant and 1000 seed weight; Gupta *et al.* (2021); Gogoi and Sarma (2019) for 1000-seed weight; Kumari *et al*. (2020) for plant height, number of capsules per plant, 1000 seed weight and protein content; Iwo *et al.* (2007) for number of capsule per plant; Kant *et al.* (2021); Divya *et al.* (2018) for plant height and number of capsules per plant; Bindu *et al.* (2014); Saxena and Bisen (2016); Teklu *et al.* (2017) for plant height; Manjeet *et al*. (2020); Mohanty *et al.* (2020) for biological yield; Kumar *et al*. (2022) for plant height, number of capsules per plant, oil content and seed yield per plant. Singh *et al.* (2018); Kadvani *et al.* (2020); Patidar *et al*. (2020) reported oil content with high heritability with moderate genetic advance. On the other hand, Teklu *et al.* (2014); Kadvani *et al.* (2020) observed moderate heritability with high to moderate genetic advance for number of seeds per capsule; Singh *et al.* (2018) for number of branches per plant and seed yield per plant; Saravanan *et al.* (2020); Patidar *et al*. (2020) for seed yield per plant.

Table 1: Analysis of variance for 17 characters in sesame.

Sr. No.	Characters	Mean sum of squares		
		Replication (d.f.=2)	Treatment (d.f.=35)	Error
1.	Days to 50% flowering	18.22	162.63**	18.22
2.	Days to 80% physiological maturity	3.25	171.85**	19.28
3.	Plant height	15.33	2447.45**	189.50
4.	Internodal length	0.84	16.19**	1.77
5.	Stem height from base to first branch	25.21	1408.02**	138.87
6.	Number of capsules per plant	4.67	4178.93**	363.70
7.	Capsule length	0.00	0.16**	0.02
8.	Number of seeds per capsule	6.51	145.81**	20.65
9.	Number of branches per plant	0.13	9.47**	1.00
10.	1000 seed weight	0.02	2.17**	0.08
11.	Seed yield per plant	1.08	633.69**	49.50
12.	Biological yield per plant	3.17	1254.55**	110.70
13.	Harvest index	0.13	45.95**	7.97
14.	Relative water content	14.07	68.84**	33.15
15.	Oil content	1.03	135.29**	6.43
16.	Protein content	1.08	64.15**	1.64
17.	Seed yield per plant	0.55	118.74**	13.92

Table 2: Component of genetic parameters for yield and its contributing traits in sesame.

Sr. No.	Characters	Variance			Coefficient of variation			h^2 (Broad Sense) in %	GAM (%)
		$\sigma^{2}p$	$\sigma^{2}g$	$\sigma^{2}e$	PCV	GCV	ECV		
1.	DFF	42.29	24.07	18.22	13.33	10.06	8.75	56.90	15.63
2.	DPM	44.71	25.43	19.28	7.01	5.29	4.60	56.90	8.21
3.	PH	565.83	376.32	189.50	19.80	16.15	11.46	66.50	27.13
4.	IL	4.18	2.40	1.77	19.77	15.00	12.88	57.60	23.44
5.	SHBB	350.40	211.53	138.87	39.04	30.33	24.57	60.40	48.54
6.	NCP	999.57	635.87	363.70	49.89	39.79	30.09	63.60	65.38
7.	CL	0.04	0.02	0.02	8.25	5.98	5.68	52.60	8.93
8.	NSC	41.51	20.86	20.65	10.21	7.24	7.20	50.30	10.57
9.	NBP	2.42	1.41	1.00	38.90	29.73	25.08	58.40	46.82
10.	TSW	0.43	0.35	0.08	22.20	20.09	9.45	81.90	37.44
11.	SYP	146.86	97.37	49.50	45.23	36.82	26.26	66.30	61.77
12.	BY	301.35	190.64	110.70	45.00	35.79	27.28	63.30	58.65
13.	HI	14.30	6.33	7.97	12.67	8.43	9.46	44.30	11.56
14.	RWC	39.10	5.95	33.15	8.58	3.35	7.90	15.20	2.69
15.	OC	27.91	21.48	6.43	11.79	10.34	5.66	77.00	18.68
16.	PC	12.06	10.42	1.64	16.91	15.72	6.24	86.40	30.10
17.	SYYP	31.39	17.47	13.92	47.57	35.48	31.68	55.60	54.53

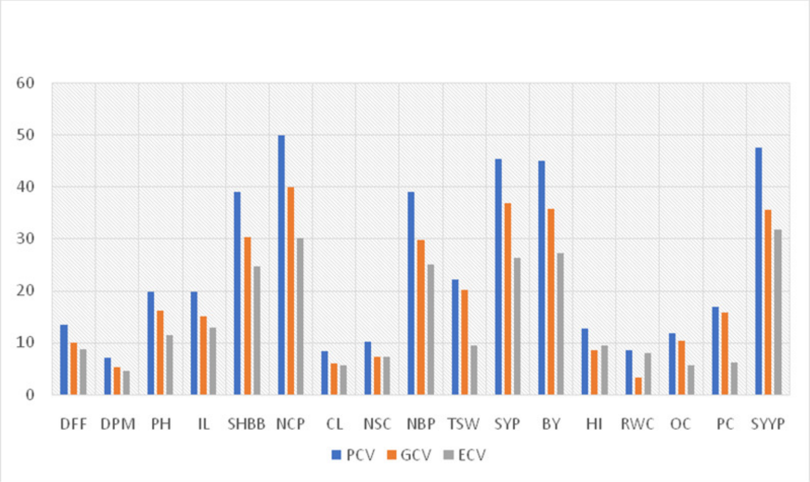

Fig. 1 (a) Genetic parameters (PCV, GCV and ECV) of seventeen morpho-physiological and quality traits in sesame.

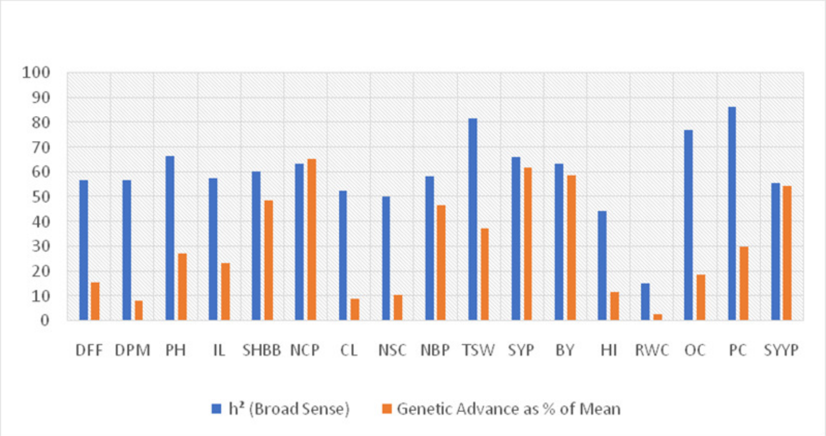

Fig. 1 (b) Genetic parameters (Heritability and Genetic advance as per cent of mean) of seventeen morpho-physiological and quality traits in sesame.

CONCLUSIONS

The traits with high heritability and high genetic advance as percent of mean are governed by the additive gene action where simple selection is effective for breeding programmes. Considering the above result the quantitative trait number of capsules per plant and 1000 seed weight had direct effect on seed yield per plant. Thus, on the basis of the forgoing discussions the traits *viz*., plant height, stem height from base to first branch, number of capsules per plant, 1000 seed weight, stover yield per plant, biological yield per plant and protein content to be given more importance during selection programme for improving seed yield in breeding programs of sesame. There is a big challenge of capsules shattering problems at the ripening stage of capsules in sesame especially if there is high temperature and high humidity at that time. So this could be included in the future study of sesame.

Acknowledgement. Authors are thankful to School of Agricultural Sciences and Rural Development, Nagaland University, Medziphema, Nagaland for providing necessary support and facilities and also to the AICRP on Sesame and Niger, JNKVV, Jabalpur (MP) for supplied Sesame germplasm collections for the study. The authors gratefully acknowledge the financial support in the form of fellowship to the University Grants Commission for this study.

Conflict of Interest. None.

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How to cite this article: Preeti Kumari Pankaj Shah and H.P. Chaturvedi (2023). Studies on Yield Attributes in Relation to Genetic Parameters in Sesame (*Sesamum indicum* L.) Genotypes. *Biological Forum – An International Journal, 15*(4): 166-172.