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Research Article

Estimation of Variability Parameters in Three Diverse Species of Sesame Along with their Intra and Inter Specific Hybrids

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ABSTRACT

Sesame known as the "queen" of oil seed crops is one of the oldest oilseed crops cultivated worldwide. The present investigation was carried out for the estimation of different variability parameters, such as ANOVA (Analysis of Variance), phenotypic and genotypic coefficient of variation, heritability and genetic advance in twelve diverse genotypes of Sesamum indicum, S. mulayanum and S. radiatum along with their twenty three intra and inter specific hybrids for twelve physiological and yield component characters at the Experimental Farm area of the Department of Crop Improvement CSKHPKV, Palampur. ANOVA revealed the presence of sufficient genetic variability for all the characters under study. Moderate PCV (10-20%) was observed for five characters viz., harvest index, plant height, branches per plant, seed yield per plant and capsules per plant whereas, it was low (<10%) for remaining characters. GCV was moderate (10-20%) for four characters viz., plant height, harvest index, branches per plant and seed yield per plant thus, indicating that the phenotypic expression of these characters represent a true picture of their genotypic expression also, while the remaining characters exhibited low GCV (<10%). High heritability coupled with high genetic advance was observed for plant height and harvest index which indicated the presence of high additive gene action while high heritability with moderate genetic advance was observed for seed yield per plant, number of capsules per plant and days to flower initiation stipulating the presence of both additive and non additive gene actions thus, providing scope for improvement of these traits through hybridization and selection.

Keywords: *Phenotypic and Genotypic coefficient of variation, Heritability, Genetic advance, Sesame.*

INTRODUCTION

Oilseed crops are the backbone of agricultural economy of India from time immemorial. They are essential components of human diet being next to food grains, rich sources of energy and the earners of fat soluble vitamins A, D, E and K.

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Sesame (*Sesamum indicum* L.), a member of the family Pedaliaceae also known as sesamum, til, gingelly, simsin, gergelim is the most ancient oilseed crop and one of the oldest cultivated plant in the world dating back to 3050-3500 B.C. Asia has a rich diversity of cultivated sesame while Africa is prosperous in wild relatives (Sharma et al., 2014). Sesame seeds contain 50 per cent oil and 20-25 per cent protein. The oil contains 47 per cent oleic acid, 39 per cent linoleic acid, 39 per cent mono unsaturated and 46 per cent poly unsaturated fatty acids. Though sesamum occupies a prominent place among oilseeds, its production is comparatively less as compared to other oilseed crops. The major constraints identified for most of the countries including India are, instability in yield, lack of wider adaptability, growing on marginal land non–synchronous maturity etc. Yield is the most important trait for any crop improvement programme. Since it is a complex trait controlled by many genes, yield can be enhanced by improving the yield contributing traits. The success of any crop improvement program depends upon the nature and magnitude of genetic variability present in the crop. In sesame high level of polymorphism has been reported in its morphology (Sarkar & Saha, 2014). Therefore characterization and evaluation are the important pre-requisites for effective utilization of germplasm and also to identify sources of useful genes for initiating any systematic breeding programme. Therefore, the present investigation was carried out for obtaing the first hand information, so as to select suitable genotypes for direct and indirect use in sesamum improvement programme.

MATERIALS AND METHODS

Experimental material for the present study (Table 1) consisted of sesame (*Sesamum indicum* L.) genotypes comprised of five diverse cultivars *i.e.* TKG-371, Punjab Til No.1, BTLK-03-9, LTK-4 and Local Black and five *Sesamum mulayanum* (IC-557175, IC-557209, IC-557247, IC-557174 and IC-557273) and two *Sesamum radiatum* (IC-557261 and IC-557265) accessions. *Sesamum indicum* genotypes were sown during *kharif*, 2012 at Experimental Farm, Department of Crop Improvement, CSK HPKV, Palampur. Staggered sowing was done at 15 days interval to synchronize flowering, starting from second week of July to second week of August. Mechanical scarification of seeds of some wild annual species of sesame was done prior to sowing to speed up the germination and later kept for germination in petriplates in incubator at 25±2°C. The germinated seedlings were transferred to the pots. Intra and interspecific hybrids were developed by random mating of cultivated genotypes and wild annual sesame species. Hybrids together with their parents were evaluated during *kharif*, 2013 at the Experimental Farm, Department of Crop Improvement, Palampur. The F_1 hybrid salong with their parents were raised in pots containing mixture of soil, sand and vermicompost in 2:1:1 ratio, in a completely randomized design (CRD) with equal replications. The average weekly meteorological data recorded at Agrometeorological Laboratory of Department of Agronomy, CSKHPKV, Palampur during cropping period. Randomly five competitive plants were selected for recording biometrical measurements on days to flower initiation, days to 50% flowering, days to 75% maturity, plant height, number of capsules per plant, Internode length, seeds per capsule, branches per plant, 1000-seed weight, seed yield per plant, biological yield per plant and harvest index. The analysis of variance was done as per CRD Cochran and Cox (2006). The genotypic and phenotypic coefficients of variation were estimated following Burton and De Vane (1952). Heritability in broad sense (h^2_{bs}) and genetic advance was calculated as per the formula given by Burton and De Vane (1952) and Johnson et al. (1955). The traits were classified as having high (>20 per cent), moderate (10 to 20 per cent) or low (<10 per cent) range of variation as per the method suggested by Sivasubramanian and Menon (1973). Range of heritability was categorized as high (>61 per cent), medium (31 to 60 per cent and low (<30 per cent) suggested by Jhonson et al. (1955).

RESULTS AND DISCUSSION

Analysis of variance for twelve yield contributing characters are presented in (Table 2) which revealed the presence of significant differences among the genotypes for all the characters under study. The estimates of PCV were higher than their corresponding GCV for all characters studied (Table3) which indicated that the apparent variation is not only due to the genotypes but, also due to the influence of environment. Therefore, caution has to be exercised in making selection for these characters on the basis of phenotype alone as environmental variation is unpredictable in nature. PCV was found to be moderate (10-20%) for five characters *viz.*, harvest index, plant height, branches per plant, seed yield per plant and capsules per plant whereas, it was low (<10%) for remaining characters. While, moderate GCV (10-20%) was observed for four characters *viz.*, plant height, harvest index, branches per plant and seed yield per plant thus, indicating that the phenotypic expression of these characters represent a true picture of their genotypic expression also. Low GCV (<10%) was observed for remaining characters which emphasized the need for generating more variability for these characters.

Low variability for characters like days to 50 per cent flowering and days to 75 per cent maturity has also been reported by Krishnaiah et al. (2002). Similar results on PCV and GCV were given by various workers such as Saravanan and Nadarajan (2003), Solanki and Deepak (2003) and Anitha vasline et al. (2000). Low phenotypic and genotypic coefficients of variation for the characters such as days to 50 per cent flowering and days to maturity were also recorded by various workers (Sudhakar et al., 2007; Shadakshari et al., 1995; & Krishnaiah et al., 2002) and oil content (Sudhakar et al., 2007; & Shadakshari et al., 1995). Low coefficient of variation for number of seeds per capsule was reported by Thangavelu et al. (2000). In the present study, heritability was high (>70%) for most of the traits studied viz., plant height, days to 50 per cent flowering, days to 75 per cent maturity, days to flower initiation, seed yield per plant, number of capsules per plant and harvest index. Moderate heritability (50-70%) was observed for branches per plant, biological yield per plant and seed per capsule. While low heritability (<50%) was observed only for internode length and 1000-seed weight. Reddy et al. (2001) and Krishnaiah et al. (2002) reported similar results. Capsule length and oil content showed high heritability with low genetic advance. These results are in conformity with the findings of Reddy et al. (2001) and Sudhakar et al. (2007). Khan et al. (2001) reported high heritability (>90 per cent) for plant height, number of branches per plant, number of capsule per plant, number of seeds per capsule, 1000-seed weight and seed yield per plant.High heritability values of these traits indicated that the variation observed was mainly under genetic control and less influenced by the environment.Genetic advance expressed as percent of mean was observed to be high (>25%) for plant height and harvest index. It was moderate (10-25%) for seed yield per plant, branches per plant, number of capsules per plant and days to flower initiation while it was low (<10%) for characters such as days to 50 per cent flowering, seeds per capsule, days to 75 per cent maturity, biological yield per plant, internode length and 1000-seed weight.

High heritability with moderate genetic advance was observed for seed yield per plant, number of capsules per plant and days to flower initiation which indicated the presence of both additive and non additive gene action in the inheritance thus, providing scope for improvement of these traits through hybridization and selection. High heritability with low genetic advance was observed for days to 50 per cent flowering and days to 75 per cent maturity which indicated the role of non-additive gene action involving both dominance and epistatic effects in the inheritance and selection would be less effective for these traits. Low heritability with low genetic advance was observed for internode length and 1000-seed weight indicating that selection for these traits would not be that effective. Kiruthika et al. (2018), Bharathi et al. (2014), Desawi et al. (2014), Parameshwarappa et al. (2009) and Chandrashekhara and Reddy (1993) reported similar results for different characters in sesame.

Table 1: List of Parents and hybrids used in the study

S.No.	Genotypes
	S. indicum
1	TKG-371
2	Punjab Til No.1
3	LTK-4
4	BTLK-03-9
5	LOCAL BLACK
	S. mulayanum
6	IC-557175
7	IC-557209
8	IC-557247
9	IC-557174
10	IC-557273
	S. radiatum
11	IC-557261
12	IC-557265
	S. indicum* x *S. indicum
13	TKG-371x Punjab Til No.1
14	TKG-371 x Local Black
15	Punjab Til No.1 x TKG-371
16	Punjab Til No.1 X BTLK-03-9
17	LTK-4 x BTLK-03-9
18	LTK-4 x Local Black
19	BTLK-03-9 x TKG-371
20	BTLK-03-9 x Local Black
21	Local Black x TKG-371
	S. indicum* x *S. mulayanum
22	Punjab Til No.1x IC-557273
	S. mulayanum* x *S. indicum
23	IC-557247 x Punjab Til No.1
24	IC-557247 x LTK-4
25	IC-557174 x TKG-371
26	IC-557174 X Punjab Til No.1
27	IC-557273 x Local Black
	S. mulayanum* x *S. mulayanum
28	IC-557247 x IC-557175
29	IC-557174 x IC-557247
30	IC-557273 x IC-557174
	S. radiatum* x *S. indicum
31	IC-557261 x LTK-4
32	IC-557265 X LTK-4
	S. radiatum* x *S. mulayanum
33	IC-557261 x IC-557247
	S. radiatum* x *S. radiatum
34	IC-557261 X IC-557265
35	IC-557265 x IC-557261

Table 2: Analysis of variance of parents and their hybrids for different characters in sesame

Characters		Mean sum of squares due to	
		Genotypes	**Error**
	df	**34**	**70**
Days to flower initiation		29.76*	1.01
Days to 50 per cent flowering		28.90*	0.89
Days to 75 per cent maturity		65.91*	2.13
Plant height (cm)		1040.18*	15.53
Internode length (cm)		0.57*	0.17
Branches per plant		7.67*	1.24
Numbers of capsules per plant		32.26*	2.53
Seeds per capsule		13.33*	2.52
1000-seed weight (g)		0.04*	0.02
Seed yield per plant (g)		0.28*	0.02
Biological yield/ plant (g)		2.94*	0.52
Harvest index (%)		17.06*	1.65

*Significant at $P \leq 0.05$

Table 3: Estimates of parameters of variability for different characters in sesame genotypes and their hybrids

Characters	PCV (%)	GCV (%)	Heritability h^2bs (%)	Expected genetic advance (% of mean)
Days to flower initiation	6.52	6.20	90.30	12.14
Days to 50% flowering	5.28	5.04	91.20	9.91
Days to 75% maturity	4.75	4.53	90.70	8.88
Plant height (cm)	14.50	14.20	96.00	28.66
Internode length (cm)	8.60	5.71	44.00	7.79
Branches per plant	14.09	11.49	66.50	19.34
Number of capsules per plant	10.20	9.14	80.40	16.87
Seeds per capsule	7.67	5.90	59.20	9.34
1000-seed weight (g)	6.95	3.75	29.20	4.06
Seed yield per plant (g)	12.48	11.30	82.10	20.97
Biological yield/ plant (g)	7.02	5.45	60.40	8.76
Harvest index (%)	16.18	14.11	76.10	25.38

CONCLUSION

The higher estimates of PCV than GCV for all characters studied indicated that the apparent variation was not only due to the genotypes, but, also some environmental interaction/ influence. The moderate GCV values indicated that the phenotypic expression of characters represent a true picture of their genotypic expression also. High heritability values were recorded for most of the traits studied *viz*., plant height, days to 50 per cent flowering, days to 75 per cent maturity, days to flower initiation, seed yield per plant, number of capsules per plant and harvest index. High heritability coupled with high genetic advance indicated the presence of high additive gene action for plant height and harvest index while high heritability with moderate genetic advance observed for seed yield per plant, number of capsules per plant and days to flower initiation indicated the presence of both additive and non additive gene action, thus, providing scope for improvement of these traits through intra and interspecific hybridization and selection.

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