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GENETIC VARIABILITY STUDIES IN SEMI *RABI* LOCAL GERMPLASMS OF SESAME

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ABSTRACT

Thirty five sesame germplasms (collected from eastern part of Vidarbha region) along with 6 checks were evaluated and raised in randomized block design with three replications during the year 2021-22 at the experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur. The study aimed to estimate genetic parameters of variability for yield and yield contributing traits, to estimate correlation between yield and yield contributing traits and to identify superior lines based on yield and yield contributing traits. Analysis of variance revealed significant differences among all the genotypes for all the eleven characters studied. The phenotypic variance and phenotypic coefficient of variation were found greater than the genotypic variance and genotypic coefficient of variation for all the eleven characters studied. High genotypic coefficient of variation was recorded for capsule length and harvest index. Phenotypic coefficient of variation was recorded high for the characters harvest index, capsule length, and seed yield plant^{-1}. High heritability and high genetic advance was observed for characters seed yield plant^{-1}, number of branches plant^{-1}, capsule length and harvest index. Seed yield plant^{-1} was found to exhibit positive significant correlation with plant height, number of branches plant^{-1}, number of capsules plant^{-1} and number of seeds capsule^{-1}.

(Key words: Correlation, genetic advance, heritability, sesame, variability)

INTRODUCTION

Sesame (*Sesamum indicum* L.) has been under cultivation in India since ancient times. It is one of the earliest domesticated plants. Use of wild form (black) of sesame in India for religious functions is mentioned in Sanskrit. Sesame oil is rich in saturated, mono and poly unsaturated fatty acids. The traditional sesame cultivars as well as related wild species serve as good source of genetic variability for plant breeders. The study of variability helps in planning of sesame breeding programs as the success of any breeding programme is based on selection of the superior lines of the diverse origin. The knowledge of genetic variability in sesame germplasms will be useful in the selection and breeding of good yielding, quality cultivars with increased production. Genetic variability study helps in determining the variability existing in the germplasm lines. For developing a variety with high yield coupled with good yield contributing traits require the information on variation existing in the available material (Bambodkar *et al.,* 2019). For exploiting the variability existing in the germplasm lines, germplasm collections has to be evaluated to select the novel lines for use as the parents in hybridization program or directly releasing as a variety with increased productivity. Therefore, variability study had been undertaken to estimate genetic and phenotypic variability, heritability, genotypic and phenotypic coefficient of variability and genetic advance which help to determine to what extent traits have been influenced by the environment and variability among the germplasm lines (Ingle *et al.,* 2021). Correlation studies are important in plant breeding programs to understand the degree of association between the characters. Galton (1988) emphasized the relationship between the two traits. The traits with positive significant correlation with the desirable traits can serve in as alternate selection criteria in the crop improvement programs. Considering above points, the present study was carried out to estimate genetic variability among the germplasms and to find out association of characters in sesame.

MATERIALS AND METHODS

The present research work was conducted during semi *rabi* 2021-22 at research farm of Agricultural Botany Section, College of Agriculture, Nagpur. The materials required for conduction of this research consisted of 35 sesame germplasms (collected from eastern part of Vidarbha region) and 6 checks (3 checks *viz.,*RT-54, TKG-21 and GT-1

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collected from Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur). The list of the material is given in Table 1. The germplasms of sesame were raised in randomized block design with three replications with row to row and plant to plant spacing of 30 cm X 10 cm. The germplasms and checks were sown at one row plot^{-1}. All the recommended package of practices and plant protection measures were taken as per the schedules to raise a healthy crop. The observations were recorded on five randomly selected plants in each replication for eleven characters including days to 50% flowering, days to maturity, plant height (cm), number of branches plant^{-1} , number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight (g), capsule length (cm), seed yield plant^{-1} (g), oil content (%) and harvest index (%). Analysis of variance was carried out as per the standard method given by Panse and Sukhamate (1954) in order to partition the total variation of different characters under study into its components *viz.,* replications, treatments and error. The genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) were calculated according to Singh and Choudhary (1979). Heritability was calculated according to Hanson *et al.,(*1956) and genetic advance calculated as per Robinson *et al*. (1949) for different characters. The genotypic correlation were calculated according to the method of Singh and Choudhary (1979).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among all the genotypes for all the eleven characters studied, which exhibited the presence of significant amount of genetic variability among the germplasms for seed yield plant^{-1} and other yield components as shown in Table 2. Thus, it allows the further estimation of genetic parameters. Mean performance of all the germplasms for all eleven characters showed variation among the germplasms (Table 3). Days to 50% flowering ranged from 46.67 days to 68.62 days, for days to maturity 97.70 days to 126 days, for plant height at maturity from 75.84 cm to 100.60 cm, for number of branches plant^{-1} 3.17 to 6.00, for number of capsules plant^{-1} 37.93 to 56.73 , for number of seeds capsule^{-1} 29.00 to 46.00, for 1000 seed weight 2.00 g to 3.08 g , for capsule length 1.70 cm to 4.13 cm, for seed yield plant^{-1} (g) 2.47g to 6.63 g , for oil content 45.20% to 51.68 % to and for harvest index 14.48 % to 36.34%.

The phenotypic variance and phenotypic coefficient of variation was recorded greater than the genotypic variance and genotypic coefficient of variation for all the eleven characters studied (Table 4). Genotypic coefficient of variation values were found to be high (>20%) for the characters, capsule length (20.83%) and harvest index (23.73%) and moderate (10 – 20%) for the characters seed yield plant^{-1}(16.26%) and number of branches plant^{-1}(16.39%) however low (<10%) for the characters oil content (3.15%), plant height (5.39%), number of seeds capsule^{-1}(6.50%), days to maturity (6.97%), days to 50% flowering (7.88%), 1000 seed weight (9.72%) and number of capsules plant^{-1} (8.64 %).Similarly phenotypic coefficient of variation was recorded high (>20%) for the characters harvest index (25.12%), capsule length (21.70%), seed yield plant^{-1}(20.13) whereas moderate (10 – 20%) for the characters number of branches plant^{-1}(17.59%), number of capsules plant^{-1} (14.21%), number of seeds capsule^{-1}(13.42%), plant height (11.47%), 1000 seed weight (11.02%), days to 50% flowering (10.38 %) and low (<10 %) for the characters days to maturity (7.18 %), oil content (3.86 %). In accordance to these results Narayanan and Murugan (2013), Rao *et al*. (2013),Ismail and Mohmed (2018), Ranjithkumar *et al*. (2022) also observed moderate to high GCV and PCV for yield and yield components.

For enhanced efficiency in the selection, it is important to consider heritability along with expected genetic advance as a tool in the selection program. In this study the characters, number of branches plant^{-1}, harvest index (%), seed yield plant^{-1}and capsule length (cm) exhibited high heritability coupled with high genetic advance as per cent of mean, indicating additive gene action and possibility of improving these traits by simple selection. Moderate heritability coupled with moderate genetic advance as per cent of mean was noticed in days to 50% flowering and number of capsules plant^{-1}. The moderate genetic advance coupled with moderate heritability indicates the presence of less environmental influence and the existence of additive gene action in the characters expression. Hence, days to 50% flowering can be improved by selection. The characters, days to maturity and 1000 seed weight (g) showed high heritability coupled with moderate genetic advance as per cent of mean, indicating the involvement of additive and non-additive type of gene action and postponement of selection programs for the improvement of these traits. Number of seeds capsule^{-1}, oil content (%) and plant height (cm) exhibited low heritability coupled with low genetic advance as per cent of mean. This indicates the higher influence of the environment. Similarly,Mohan (2014),Ismaila and Usman (2014),Tripathy *et al.*(2014) reported high heritability coupled with high genetic advance for various characters in sesame.

Simple correlation coefficient (genotypic) of different component traits was estimated considering seed yield plant^{-1} as the dependent variable and data are presented in Table 4. Days to 50% flowering was found to be highly significant and positively correlated with days to maturity (0.667**) and 1000 seed weight (0.647**), highly significant and negatively correlated with number of branches plant^{-1} (-0.486**), number of seeds capsule^{-1} (-0.411**), however significant and negatively correlated with number of capsules plant^{-1}(-0.357*). Days to maturity was highly significant and positively correlated with 1000 seed weight (0.791**) and days to 50% flowering (0.667**), highly significant and negatively correlated with plant height (0.411**), number of branches plant^{-1}(-0.580**), number of capsules plant^{-1}(-0.450**), number of seeds capsule^{-1} (0.587**) and harvest index (-0.485**). Plant height was

Table 1. Materials used for study

Sr. no.	Name of Germplasm	Sr.no.	Name of Germplasm	Sr.no.	Name of Germplasm	Sr.no.	Name of Germplasm
1	NT 1	12	NT12	23	NT23	34	NT34
2	NT 2	13	NT 13	24	NT24	35	NT35
3	NT3	14	NT14	25	NT25		**Checks**
4	NT4	15	NT15	26	NT26	1.	AKT-64
5	NT5	16	NT16	27	NT27	2.	AKT-101
6	NT6	17	NT 17	28	NT28	3.	PKV NT-11
7	NT7	18	NT18	29	NT29	4.	RT-54
8	NT8	19	NT19	30	NT30	5.	TKG-21
9	NT9	20	NT20	31	NT31	6.	GT-1
10	NT10	21	NT21	32	NT32		
11	NT11	22	NT22	33	NT33		

Table 2. Analysis of variance for different characters

Sources of variation	Df	Mean sum of squares					
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant^{-1}	Number of capsules plant^{-1}	Number of seeds capsule^{-1}
Replications	2	3.08	8.33	2.33	0.07	34.65	4.13
Genotypes	40	70.98**	198.27**	155.93**	1.66**	80.89**	39.88**
Error	80	13.94	3.91	84.27	0.08	29.28	20.75

Sources of Variation	Df	Mean sum of squares				
		1000 seed weight (g)	Capsule length	Seed yield plant^{-1}	Oil content (%)	Harvest index (%)
Replications	2	0.03	0.01	0.01	0.06	0.44
Genotypes	40	0.24**	1.07**	2.21**	8.44**	122.74**
Error	80	0.02	0.03	0.33	1.2	4.76

* Significant at 5% level ** Significant at 1% level

Table 3. Minimum, maximum, range for different characters

Sr. no	Parameters	Min	Max	Range
1	Days to 50% flowering	46.67	68.62	21.95
2	Days to maturity	97.70	126.00	28.3
3	Plant height (cm)	75.84	100.60	24.76
4	Number of branches plant^{-1}	3.17	6.00	2.83
5	Number of capsules plant^{-1}	37.93	56.73	18.80
6	Number of seeds capsule $^{-1}$	29.00	46.00	17.00
7	1000 seed weight(g)	2.00	3.08	1.08
8	Capsule length (cm)	1.70	4.13	2.43
9	Seed yield plant $^{-1}$ (g)	2.47	6.63	4.16
10	Oil content (%)	45.20	51.68	6.48
11	Harvest index (%)	14.48	36.34	21.86

Table 4. Estimates of variability and genetic parameters for different characters

Sr. no.	Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (% over mean)
1	Days to 50% flowering	7.88	10.38	57.69	12.34
2	Days to maturity	6.97	7.18	94.31	13.96
3	Plant height (cm)	5.39	11.47	22.09	5.22
4	Number of branches plant^{-1}	16.39	17.59	86.89	31.48
5	Number of capsules plant^{-1}	8.64	14.21	37.01	10.84
6	Number of seeds capsule $^{-1}$	6.50	13.42	23.52	6.50
7	1000 seed weight (g)	9.72	11.02	77.78	17.67
8	Capsule length (cm)	20.83	21.70	92.11	41.18
9	Seed yield plant $^{-1}$ (g)	16.26	20.13	65.26	27.07
10	Oil content (%)	3.15	3.86	66.76	5.34
11	Harvest index (%)	23.73	25.12	89.20	46.18

Note: *, ** Significant at 5 per cent and 1 per cent level, rg: genotypic correlation coefficient

Table 2. Correlation coefficient estimates for different characters

Characters	Days to maturity	Plant height (cm)	Number of branches plant^{-1}	Number of capsules plant^{-1}	Number of seeds capsules $^{-1}$	1000 seed weight (g)	Capsule length (cm)	Oil content (%)	Harvest index (%)	Seed yield (g)
Days to										
50% flowering	0.667**	-0.192	-0.486**	-0.357*	-0.411**	0.647**	-0.153	-0.005	-0.301	-0.561**
Days to maturity		-0.411**	-0.580**	-0.450**	-0.587**	0.791**	-0.139	-0.092	-0.485**	-0.679**
Plant height(cm)			0.229	0.733**	0.0001	-0.300	0.099	0.101	0.178	0.343*
Number of branches										
plant^{-1}				0.266	0.506**	-0.528**	-0.048	0.222	0.196	0.351*
Number of capsules										
plant^{-1}					0.102	-0.362*	0.006	-0.095	0.266	0.405**
Number of seeds										
capsule $^{-1}$						-0.630**	0.151	0.034	0.042	0.386*
1000 seed weight(g)							-0.079	-0.220	-0.317*	-0.633**
Capsule length (cm)								-0.151	0.038	-0.003
Oil content (%)									0.203	-0.066
Harvest index (%)										0.157

highly significant and positively correlated with number of capsules plant^{-1} (0.733**) however significant and positively correlated with seed yield plant^{-1} (0.343*). Number of branches plant^{-1} was observed highly significant and positively correlated with number of seeds capsule^{-1}(0.506*) whereas significant and positively correlated with seed yield plant^{-1} (0.351*), highly significant and negatively correlated with 1000 seed weight (-0.528**). Number of capsules plant^{-1} was found highly significant and positively correlated with seed yield plant^{-1} (0.405**), significant and negatively correlated with 1000 seed weight (-0.362*). Number of seeds capsule^{-1} was observed significant and positively correlated with seed yield plant^{-1} (0.386*), highly significant and negatively correlated with 1000 seed weight (-0.630**). 1000 seed weight was found highly significant and negatively correlated with seed yield (-0.633**) whereas significant and negatively correlated with harvest index (-0.317*). The dependent variable seed yield plant^{-1} was observed to be highly significant and positively correlated with number of capsules plant^{-1} (0.405**), significant and positively correlated with number of seeds capsule^{-1} (0.386*),plant height (0.343*), number of branches plant^{-1} (0.351*), highly significant and negatively correlated with days to 50 % flowering (-0.561**), days to maturity (-0.679**) and 1000 seed weight (-0.633**). This indicates that the characters plant height, number of branches plant^{-1}, number of capsules plant^{-1}, and number of seeds capsule^{-1}can be considered for selection of parents for hybridization program. Similarly, Sumathi *et al.* (2007), Kumar *et al.*(2022) also reported the importance of characters plant height, number of branches plant^{-1}, numberof capsules plant^{-1}, number of seeds capsule^{-1}.

When all the genetic parameters for eleven characters were considered, it was found that four characters seed yield plant^{-1}, number of branches plant^{-1}, capsule length and harvest index exhibited moderate to high GCV, high heritability and high genetic advance as percentage of mean. This indicates that there is lesser influence of environment and that these characters were governed by additive gene action and hence selection for such traits may be rewarding. When the correlation studies were considered out of the above three characters only number of branches plant^{-1} exhibited significant and positive correlation with seed yield plant^{-1}. However, capsule length and harvest index exhibited nonsignificant and negative and positive correlation respectively with seed yield plant^{-1}. The mean value of seed yield plant^{-1}of all the 35 germplasms when observed it was found that none of the germplasm exhibited significant superiority over the checks. The lower mean value for seed yield plant^{-1} may be due to the variations within the germplasms. Hence, it is suggested that selection of superior germplasm should be postponed in this generation and instead single plant showing high seed yield plant^{-1} within each of the 35 germplasm may be selected and raised in progeny row till homozygosity is attained. Based on these 17 individual plants from 9 germplasms were identified for raising in the progeny row in next generation.

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