Original Research Article

Deciphering the genetic variability for seed yield components in sesame (*Sesamumindicum* L.)

ABSTRACT

The present study conducted an analysis of genetic variability for components traits of seed yield in 20 sesame (*Sesamum indicum* L.) genotypes at the Research Farm of S.K.N. College of Agriculture, Jobner. The experiment followed a randomizedblock design with three replications during *kharif*, 2018. The main objective of this study was to assess the genetic variability among the genotypes. The results of analysis of variance (ANOVA) showed significant genotypic variation for all traits, indicating their potential for breeding programs. In the present study, RT - 384, RMT - 447 and RMT - 486 were identified as high yielding genotypes with per plant seed yield of 6.75, 6.7 and 6.01 g, respectively. Among the traits studied, plant height exhibited the highest variabilitywith range of 83.13 to 108.40 cm, while test weight had the least variabilityhaving range of 3.00 -3.51 g. Furthermore, phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the traits, suggesting the influence of environmental factors on them. Among them, seed yield per plant had maximum value of GCV and PCV with magnitude of 20.32 and 24.07%, respectively; while, days to maturity had minimum value of GCV and PCV *i.e.,* 2.07 and 3.15%, respectively.Notably, traits such as capsules per plant, seeds per capsule, biological yield per plant and seed yield per plant exhibited high heritability with magnitudeof 85.96%, 64.18%, 63.68%, and 71.33%, respectively. Additionally, these traits displayed substantial genetic gains, with magnitudes of 33.46%, 21.29%, 26.19%, and 35.35%, respectively. This makes them promising for selection and eventually; these traits can be efficiently explored in different breeding programs for genetic improvement of sesame.

Keywords: Coefficient of variance, Genetic advance, Genetic variability, Heritability, Sesame

1. INTRODUCTION

Sesame (*Sesamum indicum* L.) is a diploid species (2n=2x=26) with an autogamous breeding system. It belongs to the family Pedaliaceae. It has been known by various names such as Gingelly, Til, Beniseed, and Nuvvulu in different regions of the country, sesame holds a significant status as the "queen of oilseeds". Ancient records point to Ethiopia (Africa) as the likely place of origin for sesame, and it was later introduced to India and China. Over a period of time, it became a staple food in Southern Asia and various other parts of the continent. The crop's widespread cultivation and utilization have made it an essential agricultural commodity with both culinary and economic significance. It is the 3rd major oilseed crop after groundnut and rapeseed-mustard. Sesame seeds are rich source of energy, comprising approximately 50-60% oil, 18-25% protein and 13.5% carbohydrate. Due to its cholesterol-free nature, sesame oil is often recommended for heart patients. Moreover, sesame seeds contain specific compounds that possess antioxidant as well as antipathogenic properties [1]. These health benefits make sesame a valuable addition to various culinary and medicinal applications.

Genetic variability has utmost importance in offering fundamental understanding of the nature and scope of variation existing within a crop species. Genetic variability serves as a pioneer step for any crop improvement program [2]. The effective and systematized exploration of genetic diversity is vital for the success of crop improvement programmes. Genetic variability assists in determining the level of parental diversity necessary to obtain superior genotypes in segregating populations. Moreover, it proves to be highly effective in predicting potential genetic gain [3]. It has been observed that, a genotype is influenced by environmental factors such as rainfall, day length, temperature etc., and these factors contribute to the non-heritable variations. Therefore, genetic variability studies play a key role to categorize the overall variation into heritable and non-heritable components. Moreover, heritability and genetic advance are the key factors determining effective trait selection during breeding programs. The knowledge of heritability and genetic advance assist a plant breeder to make correct decisions during the selection process, leading to more effective crop improvement programs and the development of superior cultivars with desirable traits.

Previously, various studies have been undertaken to study genetic variability in sesame.For instance, targeting various agro-morphologicaltraits such as days to 50% flowering, days to 95 % maturity, capsules filling period, primary branches per plant etc. using 64 diverse populations of sesame, genetic variability study has been performed[4]. Seed yield and its components were studiedfor genetic variability using thirty diverse mutant lines [5] and fifty-three diverse genotypes of sesame [6]. Thereafter, Pavani et al. [7] studied variability for oil content and identified low GCV and PCV using thirty sesame lines.Moreover, genetic divergence in sesame employing ten SSR markers among fifty sesame populations[8] as well as phenotypic diversity analysis employing D^2 analysis for various agro-morphological traits [9,10] has also been studied. Despite the considerable efforts made by various researchers,studiesthat utilize well established genotypes of a particular locality for sesame crop improvement are very limited. Therefore, present study has been planned using twenty improved genotypes of sesame inJaipur district of Rajasthan with an objective of estimating genetic variability parameters such as GCV, PCV, heritability and genetic advance for components traits of seed yield in sesame.

2. MATERIAL AND METHODS

Sesame is a short-day plant and exhibits sensitivity to factors such as photoperiod, temperature fluctuations, and unpredictable rainfall patterns. It is commonly cultivated as a rainfed crop and its sowing depends on onset of monsoon.The present investigation was carried out at the Research Farm of S.K.N. Agriculture University, Jobner, Rajasthan, situated at an elevation of 450 meters above the mean sea level, located at a north latitude of 26°05' and an east longitude of 75°28'. It falls within the agro climatic zone-III A (semi-arid eastern plain zone). This zone is known for its semi-arid climate, marked by significant temperature extremes in both the summer and winter seasons. Summer temperatures can soar to as high as 46°C, while winter temperatures can drop below freezing point. The average annual rainfall in this area is approximately 400mm, which is most probable during July to September.

2.1 Plant materials

The plant materials for present study consisted of twenty diverse genotypes of sesame(Table 1).Most of these genotypes includethe established varieties of Rajasthan. Therefore, to study important genetic variation among them, these varieties were included in the present investigation.

Table 1. Details of sesame genotypes used in the present investigation

S.N.	Genotypes	Releasing Institute	Releasing State	Acquired from
1.	RT - 46	Agricultural Research Station, Mandor, Jodhpur - 342304	Rajasthan	All the genotypes used in the present study were obtained from **AICRP Unit, Agricultural Research Station (Agriculture University Jodhpur) Mandor, Jodhpur-342304 (Rajasthan)**
2.	RT - 103	Agricultural Research Station, Mandor, Jodhpur - 342304	Rajasthan	
3.	RT - 125	Agricultural Research Station, Mandor, Jodhpur - 342304	Rajasthan	
4.	RT - 127	Agricultural Research Station, Mandor, Jodhpur - 342304	Rajasthan	
5.	RT - 346	Agricultural Research Station, Mandor, Jodhpur - 342304	Rajasthan	
6.	RT - 351	Agricultural Research Station, Mandor, Jodhpur - 342304	Rajasthan	
7.	RT - 372	Agricultural Research Station, Mandor, Jodhpur - 342304	Rajasthan	
8.	RT - 378	-	-	
9.	RT - 383	-	-	
10.	RT - 384	-	-	
11.	RT - 385	-	-	
12.	RMT - 425	-	-	
13.	RMT - 447	-	-	
14.	RMT - 450	-	-	
15.	RMT - 479	-	-	
16.	RMT - 486	-	-	
17.	RMT - 505	-	-	
18.	PRAGATI	Crop Research Station Mauranipur, Jhansi (CSAUA&T) - 284204	Uttar Pradesh	
19.	TKG - 22	Zonal Agricultural Research Station, Tikamgarh - 472001	Madhya Pradesh	
20.	GT - 10	Agricultural Research Station, (JAU), Amreli	Gujarat	

2.2 Design of experiment

During the *Kharif* season of 2018,twenty sesame genotypes were evaluated in 3 replications with randomized block design (Figure1). Pure seeds of each genotype were sown in individual plot of size4.0 mx 0.6 m. Each genotype contained two rows in each replication. The spacing between rows and plants was maintained at 30 cm and 10 cm, respectively. All other package and practices were carried out according to recommended standards.

2.3 Record of observations

In the current study, ten characters *viz*., days to 50 per cent flowering (DFF), days to maturity (DM), plant height (PH), branches per plant (BPP), capsules per plant (CPP), seeds per capsule (SPC), test weight (TW), biological yield per plant (BYPP), harvest index (HI) and seed yield per plant (SYPP) were studied and observations were recorded. To record observations for PH, BPP, CPP, SPC, TW, BYPP, HI and SYPP five plants were selected randomly from individual plot and their mean value was calculated, whereas in case of DFF and DM data was recorded on whole plot basis (Figure 1).

a. Plant Tagging

b. Recording of days to 50% flowering

c. Counting of capsules per plant

d. Measurement of plant height

Figure 1. Photographs showing different activities performed during field experiment

2.4 Data analysis

The analysis of variance (ANOVA) was done as per Panse and Sukhatme[11]. Genotypic (σ^2_g) and phenotypic variance (σ^2_p) assessed as per Johnson et al. [12]:

$$\sigma_g^2 = \frac{MSg - MSe}{r}$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where, r,MSg,MSe, σ_g^2, σ_p^2 and σ_e^2 denoting number of replications, mean sum of square due to genotypes, mean sum of square due to error, genotypic variance, phenotypic variance and environmental variance, respectively.

GCV and PCV were calculated as per Burton and de Vane [13]:

$$GCV = \frac{\sigma_g}{\bar{x}} \times 100$$

$$PCV = \frac{\sigma_p}{\bar{x}} \times 100$$

GCV, *PCV* and $\bar{x}$ denotes genotypic coefficients of variation, phenotypic coefficients of variation and overall mean, respectively.

Heritability (h^2) in broad sense was calculated as per Hanson et al. [14]:

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Heritability values were categorized according to their percentage range: low (<30%), moderate (30-60%), and high (>60%)[15].

Prediction of expected genetic gain was elucidated as per Johnson et al. [12]:

$$GA = i.h^2.\sigma_p$$

$$GAM = \frac{i.h^2.\sigma_p}{\bar{x}}$$

Where, i, h^2, σ_p, *GA* and *GAM* represent selection intensity, heritability, phenotypic standard deviation, genetic advance and genetic advance as percentage mean, respectively. Genetic advance was classified into three groups: low (0-10%), moderate (10-20%) and high (>20%)[15].

3. RESULTS AND DISCUSSION

3.1 Mean performance of sesame genotypes

The present study has been undertaken on 20 sesame genotypes for ten different seed yield traits. The overall mean of different traits *viz*., DFF, DM, PH, BPP, CPP, SPC, TW, BYPP, HI and SYPP were 44.37 days, 86.68 days, 92.66 cm, 2.76, 31.53, 50.15, 3.24 g, 17.00 g, 29.47% and 4.98 g, respectively (Table 2).Moreover, the mean performance of individual genotypes has been presented in the Table 2. These genotypes have shown diverse range for various traits. DFF exhibited a range spanning from 40.67 days (RT - 383) to 51 days (RMT - 479), while the DM demonstrated range between 84 days (RT - 383 and RT - 385) and 93 days (RMT - 479). PH revealed a significant diversity, ranging from 83.13 cm (RT - 372) to 108.4 cm (RT - 384). Notably, BPP values were ranging from 2 (RMT - 447) to 3.6 (RMT - 505). Similarly, CPP displayed a wide-range, extending from 21.4 (RMT - 505) to 41.6 (RMT - 447), while SPC ranged from 42.2 (RT - 46) to 65.67 (RMT - 505). TW was found to vary between 3 g (RMT - 425) and 3.51 g (RT - 127). BYPP demonstrated substantial variation ranging from 10.6 g (GT - 10) to 21.9 g (RMT - 450).HI was found torange from 19.98% (RMT - 479) to 36.93% (RT - 372), while SYPP encompassed values between 3.17 g (GT - 10) and 6.75 g (RT - 384).The maximum range was recorded in case of plant height (83.13-108.40 cm), showing more divergence, whereas test weight had minimum range (3.00-3.51 g) indicating least divergence (Table 2).In line with thepresent investigation,similar mean and range were observed by Ong'Injo andAyiecho et al. [5] for days to 50% flowering (mean 45days, range 42.8 days to 50.6 days) and plant height (mean 91.4 cm, range 71.0 cm to 100.1 cm) in the mutant lines of sesame.Moreover, similar results for test weight were reported by Saxena and Bisen [16] havingoverall mean of 3.32 g with range 2.96 g to 3.57 g.

Table 2. Mean performance of sesame genotypes for different seed yield and its components

SN	Genotypes	DFF	DM	PH	BPP	CPP	SPC	TW	BYPP	HI	SYPP
1	RT - 46	45.33	88.33	85.07	2.8	35	42.2	3.2	17.73	25.71	4.55
2	RT - 103	45	88.33	90.2	2.8	31	42.48	3.23	13.8	28.95	3.99
3	RT - 125	43.67	85.67	97.93	3	24.73	52.6	3.32	15.7	22.59	3.55

4	RT - 127	42	84.33	87	3	25	43.67	3.51	19.44	27.54	5.35
5	RT - 346	44.67	86.33	104.73	2.6	38.8	44.33	3.26	21.62	23.63	5.14
6	RT - 351	46	87	102.93	3.4	32	59.6	3.27	17.5	31.35	5.45
7	RT - 372	43.33	86	83.13	3	38.2	47.87	3.31	15.1	36.93	5.57
8	RT - 378	43.33	86.33	97.47	3	34.73	53.6	3.4	20.35	27.48	5.59
9	RT - 383	40.67	84	85.6	2.2	28.2	60.4	3.31	16.9	33.06	5.58
10	RT - 384	43.67	85	108.4	2.4	34.93	50.13	3.23	19.5	34.63	6.75
11	RT - 385	41	84	101.2	2.8	34.8	46.2	3.24	17.4	33.2	5.73
12	RMT - 425	44	86.67	101.2	3	35.4	49.93	3	14.5	31.54	4.5
13	RMT - 447	44.33	85.33	85.33	2	41.6	43.8	3.2	19.1	35.39	6.7
14	RMT - 450	44.67	86.67	88.8	2.4	34.8	45.67	3.23	21.9	26.38	5.76
15	RMT - 479	51	93	87.4	3	26.2	56.73	3.09	17.3	19.98	3.44
16	RMT - 486	45.33	87.67	97.73	2.6	34.2	44.27	3.1	18.5	32.48	6.01
17	RMT - 505	44.33	86.33	88.2	3.6	21.4	65.67	3.11	14.4	28.92	4.18
18	PRAGATI	43	84.67	92.6	2.2	24.73	48.2	3.18	15.9	32.08	5.1
19	TKG - 22	45	89.33	84.53	2.4	30.8	45.2	3.34	12.7	27.29	3.4
20	GT - 10	47	88.67	83.8	3	24	60.4	3.24	10.6	30.2	3.17
Overall Mean		**44.37**	**86.68**	**92.66**	**2.76**	**31.53**	**50.15**	**3.24**	**17**	**29.47**	**4.98**
Minimum		**40.67**	**84**	**83.13**	**2**	**21.4**	**42.2**	**3**	**10.6**	**19.98**	**3.17**
Maximum		**51**	**93**	**108.4**	**3.6**	**41.6**	**65.67**	**3.51**	**21.9**	**36.93**	**6.75**

3.2Analysis of variance (ANOVA)

ANOVA represents the extant of variability among the genotypes. It also partitions the total variation into different components. In the present investigation, genotypes were highly significant (at 1% level of significance) for all the traits *viz*., DFF, DM, PH, BPP, CPP, SPC, TW, BYPP, HI and SYPP at (Table 3). This indicates that all the studied genotypes have substantial variation for all the traits and these genotypes could be further utilized in different breeding programs. In support to the current findings,Hika et al. [4] observed highly significant difference ($p<0.01$)for days to 50 % flowering, branches per plant, plant height, capsules per plant, thousand seed weight, biological yield, harvest index and seed yield in different populations of sesame. While, Anbanandan et al. [17] observed significant variation for branches per plant, capsules per plant, seeds per capsules and seed yield per plant in different F_1 crosses.Error CV is used to define the efficiency of experimental design. In the present study, we observed low CV (<7%) for DFF, DM, PH and TW,as these traits are more stable against environmentanddo not show much variation among replications, ultimately resulting low experimental error. On the other hand, remaining traitsexhibited comparatively high error CV (>7%), indicating less stability against environment or experimental error(Table 3).

Table 3. Analysis of variance showing mean squares for different genotypes in sesame

Sources of variation	df	DFF	DM	PH	BPP	CPP	SPC	TW	BYPP	HI	SYPP
Replication	2	2.07	11.22	38.10	0.39	2.74	57.58	0.02	0.37	28.65	1.01

Genotypes	19	14.56**	13.88**	192.41**	0.50**	96.47**	148.97**	0.04**	26.17**	59.43**	3.48**
Error	38	3.72	4.23	32.83	0.14	4.98	23.37	0.01	4.18	15.33	0.41
Error CV		4.35	2.37	6.18	13.56	7.08	9.64	3.09	12.03	13.29	12.86
SEm ±		1.11	1.19	3.31	0.22	1.29	2.79	0.06	1.18	2.26	0.37
CD(α=5%)		3.18	3.41	9.48	0.63	3.69	7.99	0.17	3.38	6.47	1.06

*, ** = significant at 5% and 1% levels, respectively

3.3Genetic variability parameters, heritability and genetic advance

In the present investigation, genotypic and phenotypic variance were found to be maximum for plant height and minimum for test weight. Genotypic variance indicates the true variation present in a genotype, whereas phenotypic variance is cumulative effect of genotypic and environmental variance [15].The estimates of phenotypic coefficient of variation (PCV) were of higher magnitude than estimates of genotypic coefficient of variation (GCV) for all the characters.this showed that the apparent variation is not only due to genotypes but also due to the influence of environment. Similar observations were also made by Patil and Lokesha [18], while assessing the genetic variability among mutant lines of sesame. In the current study, we observed that SYPP had maximum value of GCV and PCV with magnitude of 20.32 and 24.07%, respectively; indicating greater variability among the genotypes for seed yield, whereas, DM had minimum value of GCV and PCV *i.e.,* 2.07 and 3.15%, respectively; indicating less variation for maturity among the genotypes (Table 4). Moreover, traits like DFF and TW had considerable low magnitude of variation, while remaining traits *viz*., PH, BPP, CPP, SPC, BYPP and HI had considerably high magnitude of variation. In line to this, similar results were observed by Bharathi et al.[19], where high GCV and PCV was observed for plant height, branches per plant, capsules per plant and seed yield.

Table 4. Genetic variability parameters for yield and its contributing traits

Characters	h^2 (%)	σ^2_g	σ^2_e	σ^2_p	GCV(%)	PCV(%)	GA	GAM (%)
DFF	49.25	3.61	3.72	7.33	4.28	6.10	2.75	6.20
DM	43.22	3.22	4.23	7.45	2.07	3.15	2.43	2.80
PH (cm)	61.84	53.2	32.83	86.03	7.87	10.01	11.81	12.75
BPP	46.15	0.12	0.14	0.26	12.60	18.42	0.49	17.75
CPP	85.96	30.5	4.98	35.48	17.52	18.89	10.55	33.46
SPC	64.18	41.87	23.37	65.24	12.90	16.11	10.68	21.29
TW (g)	50.00	0.01	0.01	0.02	3.04	4.33	0.14	4.39
BYPP (g)	63.68	7.33	4.18	11.51	15.93	19.96	4.45	26.19
HI (%)	48.95	14.7	15.33	30.03	13.01	18.60	5.53	18.76
SYPP (g)	71.33	1.02	0.41	1.43	20.32	24.07	1.76	35.35

Heritability is an important genetic parameter, which determines the effectiveness of selection [12, 20]. Based on the heritability, traits are characterized as follows, if h^2 is <30% it is low heritable, 30-60% it is moderately heritable and >60% considered as high heritable [15]. In present investigation, DFF, DM, BPP, TW and HI were recorded as moderately heritable with the percentage magnitude of 49.25, 43.22, 46.15, 50.00 and 48.95, respectively (Table 4). On the other hand, five traits *viz*., PH, CPP, SPC, BYPP and SYPP were categorized as highly heritable traits with 61.84, 85.96, 64.18, 63.68 and 71.33% heritability, respectively (Table 4). Therefore, selection for these traits will be more effective as major portion of genetic variation is exhibiting additive gene effects.

In addition, genetic advance is another important genetic parameter for selection of different characters. Genetic advance is categorized as low (<10%), moderate (10-20%), high (>20%) [15]. In the present study, PH, CPP and SCP have shown moderate genetic advance (>10%), whereas, remaining traits have shown low genetic advance (<10%). Genetic advance shows the expected amount of genetic gain in the progeny through selection [16]. Interestingly, when genetic advance was explained in terms percentage of trait mean (GAM), CPP, SPC, BYPP and SYPP shown high genetic advance, with percentage genetic gain of 33.46, 21.29, 26.19 and 35.35, respectively (Table 4). Similar results were obtained by Bharathi et al.[19] for capsules per plant, seeds per capsules and seed yield. High GAM indicates the effectiveness of selection and rapid genetic improvement of the traits under study in successive generations[6].

4. CONCLUSION

In the present investigation, efforts have been focusedto study genetic variability including GCV, PCV, heritability and genetic advance,for twenty sesame genotypes. From this study, we conclude that genotypes have vast diversity among themselves, showing significant variation for various components of seed yield. Moreover, genetic variability studies are crucial for understanding variation within crop species and serve as a critical starting point for crop improvement programs.RT - 384, RMT - 447 and RMT - 486identified as high yielding genotype withper plant seed yield of 6.75, 6.7 and 6.01 g, respectively.SYPP had maximum value of GCV and PCV with magnitude of 20.32 and 24.07%, respectively; indicating greater variability among the genotypes for seed yield, whereas, DM had minimum value of GCV and PCV i.e., 2.07 and 3.15%, respectively.Based on the different genetic parameters, it was found that the germplasm panel was more diverse for branches per plant, capsules per plant, seeds per capsule, biological yield per plant, harvest index, and seed yield per plant. It was also noted that traits such as capsules per plant, seeds per capsule, biological yield per plant and seed yield per plant, have shown high heritability as well as high genetic gain. Therefore, selection would be more rewarding for them and these traits can be efficiently explored in different breeding programs for genetic improvement of sesame.

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