Original Research Article

Deciphering the genetic variability for seed yield components in sesame (*Sesamum indicum* 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 Randomized Block 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. Among the traits studied, plant height exhibited the highest variability, while test weight had the least variability. 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. Notably, traits such as capsules per plant, seeds per capsule, biological yield per plant, and seed yield per plant showed both high heritability and high genetic gain. 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 [1], sesame holds a significant status as the "queen of oilseeds" [2]. 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 [3]. 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 [4]. Sesame seeds are rich source of energy, comprising approximately 50-60% oil, 18-25% protein and 13.5% carbohydrate [5]. 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 anti-pathogenic properties [6, 7]. 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 [8]. The effective and systematized exploration of genetic diversity is vital for the success of crop improvement programmes [9]. 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 [10]. It has been observed that, a genotype is influenced by environmental factors such as rainfall, day length, temperature etc. [11], 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, targeting various agro-morphological [12], seed yield [13, 14] and oil [15] traits using diverse germplasm panel. Moreover, genetic divergence in sesame employing molecular [16] as well as phenotypic diversity [17, 18] have also been studied. Despite the considerable efforts made by various researchers to improve the economic traits of sesame, organized research in this area still lags behind as compared to other oilseed crops [19, 20]. Therefore, present study has been planned with an objective of estimating genetic variability parameters for components traits of seed yield in sesame.

2. MATERIAL AND METHODS

2.1 Plant materials

The plant materials for present study consisted of twenty diverse genotypes of sesame *viz*., GT-10, RT- 372, RT- 125, RT- 46, RT- 383, RT- 103, RT-127, RT- 346, RT- 351, RT- 378, RMT- 486, PRAGATI, RT- 384, RT- 385, RMT- 425, TKG-22, RMT- 447, RMT- 479, RMT-505 and RMT-450, acquired from Agriculture University, Jodhpur, Rajasthan.

2.2 Design of experiment

The current study was conducted during the Kharif season of 2018 at the research farm of S.K.N. Agriculture University, Jobner, Rajasthan. Twenty sesame genotypes were evaluated in 3 replications with randomized block design. Each individual plot size was 4.0 x 0.6 m^2, containing two rows of each genotype 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.

2.4 Data analysis

The analysis of variance (ANOVA) was done as per Panse and Sukhatme [21]. Genotypic (σ^2_G) and phenotypic variance (σ^2_G) assessed as per Johnson et al. [22]:

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

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

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 was calculated as per Burton and de Vane [23]:

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

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

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. [24]:

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

Heritability values were categorized according to their percentage range: low (<30%), moderate (30-60%), and high (>60%) [25].

Prediction of expected genetic gain was elucidated as per Johnson et al. [22]:

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

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

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%) [25].

3. RESULTS AND DISCUSSION

3.1 Analysis of variance (ANOVA)

ANOVA represents the extant of variability among the genotypes [17]. It also partitions the total variation into different components. In the present investigation, genotypes have shown significant genotypic variation for all the traits *viz*., DFF, DM, PH, BPP, CPP, SPC, TW, BYPP, HI and SYPP (Table 1). This indicate 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, Anbanandan et al. [26] and Hika et al. [12] observed highly significant difference for different agro-morphological and seed traits.

Table 1. Analysis of variance showing mean squares for different genotypes in sesame

Sources of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Capsules per plant	Seeds per capsule	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)

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
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

3.2 Genetic variability parameters, heritability and genetic advance

The present study has been undertaken on 20 sesame genotypes for ten different seed yield traits. The mean performance 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, these traits have shown diverse range; the maximum range was recorded in case of plant height (83.13-108.40 cm), showing more divergence for plant height, whereas test weight had minimum range (3.00-3.51 g) indicating least divergence (Table 2). Similarly, 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 [25].

The estimates of phenotypic coefficient of variation (PCV) were of higher magnitude than estimates of genotypic coefficient of variation (GCV) for all the characters it 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 [27], 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 2). 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. [28], where high GCV and PCV was observed for plant height, branches per plant, capsules per plant and seed yield.

Heritability is an important genetic parameter, which determines the effectiveness of selection [22, 29]). 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 [25]. 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 2). 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 2). Therefore, selection for these traits will be more effective as major portion of genetic variation is exhibiting additive gene effects.

Table 2. Genetic variability parameters for yield and its contributing traits

Characters	**Mean**	**Range**	**h^2 (%)**	**σ^2_g**	**σ^2_e**	**σ^2_p**	**GCV (%)**	**PCV (%)**	**GA**	**GAM (%)**
Days to 50% flowering	44.37	40.67-51.00	49.25	3.61	3.72	7.33	4.28	6.10	2.75	6.20
Days to maturity	86.68	84.00-93.00	43.22	3.22	4.23	7.45	2.07	3.15	2.43	2.80

Plant height (cm)	92.66	83.13-108.40	61.84	53.2	32.83	86.03	7.87	10.01	11.81	12.75
Branches per plant	2.76	2.00-3.60	46.15	0.12	0.14	0.26	12.60	18.42	0.49	17.75
Capsules per plant	31.53	21.40-41.60	85.96	30.5	4.98	35.48	17.52	18.89	10.55	33.46
Seeds per capsule	50.15	42.20-65.67	64.18	41.87	23.37	65.24	12.90	16.11	10.68	21.29
Test weight (g)	3.24	3.00-3.51	50.00	0.01	0.01	0.02	3.04	4.33	0.14	4.39
Biological yield per plant (g)	17.00	10.60-21.90	63.68	7.33	4.18	11.51	15.93	19.96	4.45	26.19
Harvest index (%)	29.47	19.98-36.93	48.95	14.7	15.33	30.03	13.01	18.60	5.53	18.76
Seed yield per plant (g)	4.98	3.17-6.75	71.33	1.02	0.41	1.43	20.32	24.07	1.76	35.35

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%) [25]. 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 [30]. 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 2). Similar results were obtained by Bharathi et al. [28] 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 [14].

4. CONCLUSION

In the present investigation, efforts have been made to study genetic variability for twenty sesame genotypes. From this study, we conclude that genotypes have vast diversity among themselves, showing substantial variation for seed yield traits. Moreover, genetic variability studies are crucial for understanding variation within crop species and serve as a critical starting point for crop improvement programs. 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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