

Original Research Article

<https://doi.org/10.20546/ijcmas.2018.706.187>

Assessment of Genetic Variability, Heritability and Genetic Gain in Advanced Mutant Breeding Lines of Sesame (*Sesamum indicum* L.)

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ABSTRACT

In present investigation, 133 genotypes comprised of advanced mutant breeding lines, germplasm lines, genotypes pertaining to Initial Varietal Trial, Advanced varietal Trial and Multi Location Trial, popular varieties national, zonal and local checks were evaluated for assessment of genetic variability at Regional Agricultural Research Station, Jagtial with Randomized Block design in 3 replications. Influence on breeding programmes is especially based on the extent to which variability occurs and the relative amount of variation in the different traits. It is measured by determining the genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV). Since heritability may be affected by environmental factors, information of predicted genetic gain will be more helpful in the selection process. Genetic advance (GA) on the other hand refers to the improvement of traits in genotypic value for the new population in comparison with the original population. From the above investigated material, the highest GCV and PCV was observed for traits seed yield per plant followed by number of capsules per plant, number of branches per plant and phyllody (% incidence). The heritability estimates were high for days to maturity followed by days to 50 % flowering, plant height, seed yield per plant, number of branches per plant, number of capsules per plant and phyllody (% incidence). High heritability coupled with high GAM indicates the presence of additive gene action for the characters and they are inherited through simple selection.

Keywords

PCV, GCV, heritability, GAM, mutant breeding lines, diseases

Article Info

Accepted:
18 May 2018
Available Online:
10 June 2018

Introduction

In the country oilseeds sector occupies an important position contributing to the Gross Domestic Product. In India, sesame is being grown over an area of 19.50 lakh hectares with production of 8.50 lakh tonnes and productivity of 436 kg/ha (www.indiastat.com, 2016). In Telangana, it is grown over an area of 0.14 lakh hectares with an annual production of 0.03 lakh tonnes and productivity of 214 kg/ha (www.indiasta.com, 2016). Major sesame growing states in India are West Bengal, Madhya Pradesh, Uttar Pradesh, Punjab and Gujarat.

In Telangana state, it is grown as *summer* crop in Jagtial, Nizamabad, Nirmal, Adilabad, Karimnagar, Khammam, Asifabad and Mahaboobnagar *etc.* It is called the “Queen of Oilseeds” and is also known as ‘benni seed’, ‘gingelly’, ‘simsim’, ‘til’ *etc.* and is the oldest and an ancient oil seed crop known to man. Africa is considered the primary centre of origin, while, India and Japan are considered as the two secondary centers of origin of this crop. India, China, Sudan, Mexico, Turkey, Burma and Pakistan are the important sesame producing countries. Sesame seed contains 50-60 % oil and 19-25 % protein with two lignans *i.e.*, sesamin and sesamol, which prevent rancidity and give sesame oil a long shelf life (Ashakumary *et al.*, 1999). Sesame has been given less attention by the farmers because of poor yield due to non-availability of cultivars to suit the diverse agro-climatic conditions.

Creation of newer variation for morphological, yield and yield attributing traits is possible through germplasm augmentation, hybridization and mutation breeding. Yield being a complex character, is collectively influenced by various component characters, which is polygenically inherited and subjected to environmental variation. Critical analysis of genetic variability present in the germplasm of

a crop and its estimation is a pre-requisite for initiating any crop improvement programme as well as adopting appropriate selection techniques and helps breeding of high yielding and good quality cultivars that will increase production. Heritability indicates the extent of transmissibility of a character into future generations. It is very difficult to judge whether observed variability is heritable or non-heritable. Hence, the knowledge of heritability is also essential for selection of component traits for yield improvement. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. In the light of above facts, this study was planned with objective of estimating genetic variability.

Materials and Methods

The present investigation for estimation of genetic variability was carried out with 133 genotypes including national check (TKG-22), Zonal check (Pragathi) and Local check (Swethatil) during *kharif*, 2017 at Regional Agricultural Research Station, Polasa, Jagtial. The characterization site is located at 18° 48' N latitude, 78° 56' E longitude and about 281m altitude of mean sea level. It has annual rainfall of 901 mm per year and average temperature 27.6°C. The material was grown at this site in 2 rows of 2 m long with inter-row spacing of 30 cm and intra-row spacing of 10 cm. The experiment was laid out in Randomized Block Design (RBD) with three replications during *kharif*, 2017. All the standard package of practices was followed during crop growth period. Observations were recorded on the basis of five random competitive plants selected from genotypes in every replication for seed yield and its attributing characters and disease parameters. WINDOSTAT statistical package was used for analysis. The genotypic, phenotypic variance, heritability and genetic advance as

per cent mean was calculated as per the formulae given by Burton and de Vane (1953) and Jonhson *et al.*, (1955).

Results and Discussion

Seed yield is a complex trait, polygenic and highly influenced by environmental conditions. A successful breeding programme depends upon the genetic variability present among the different genotypes. Phenotypic selection of parents for hybrids based only on their performance alone may not always be available procedure since phenotypically superior genotypes may yield inferior hybrids and/or poor recombinants in the segregating generations. It is therefore essential that parents are selected on the basis of their genetic worth, that is, heritability along with genetic advance are both important for selection (Hamouda *et al.*, 2016).

The mean sum of squares for yield and yield attributing traits *i.e.*, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, test weight, seed yield per plant along with the disease parameters *Alternaria* leaf spot, phyllody and *Cercospora* leaf spot were presented in Table 1. Among all the traits highest variance is observed for phyllody (1401.92) followed by plant height (898.37). This indicates 133 genotypes of sesame were studied to assess their genetic potential exhibited highest variability for phyllody followed by plant height.

The mean sum of squares was highly significant for days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, seed yield per plant, *Alternaria* PDI, phyllody (per cent incidence) and *Cercospora* PDI were highly significant. While for test weight it is non-significant. All the genotypes displayed considerable amount of differences

in their mean performance with respect to all the traits studied, which indicates that the genotypes under study were genetically diverse.

An assessment of heritable and non-heritable components in the total variability observed was indispensable in adopting suitable breeding procedure. The heritable portion of the overall observed variation can be ascertained by studying the components of variation such as coefficients of genotypic and phenotypic variability, heritability and predicted genetic advance. The range, mean, phenotypic and genotypic coefficients of variability, heritability estimates in broad sense and genetic advance as per cent of mean for the above parameters is presented in Table 2. The phenotypic and genotypic coefficient of variation was represented in Fig.1 whereas heritability and genetic advance as per cent of mean were represented in Fig.2. All the sesame genotypes exhibited a significant amount of variability (PCV and GCV) for all the yield and yield contributing characters and disease parameters *i.e.*, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, seed yield per plant, *Alternaria* PDI, phyllody (per cent incidence) and *Cercospora* PDI were evidenced significant by "F" test at p(0.01) level of significance. This type of wide range of variation provides ample scope of selection for desired genotypes and further improvement.

Days to 50 per cent flowering:

Overall mean for days to 50 per cent flowering was seen as 53.26 days with a wide variation between the earliest 38.33 days and late 69.33 days. 188 RK was earliest to flower while 50KRE8-1 was late followed by 30KRDS-1-2. This wide range of variation for days to 50 per cent flowering is in line with observations of earlier workers such as Jadhav and Mohrir

(2012). Genotypic and phenotypic coefficients of variation were moderate with 13.13 and 13.31 per cent respectively. These results were supported by Vanishree *et al.*, (2013). This wide range of variation provides shifting the seasonal timing of reproduction and produce novel varieties that are better adopted to local environment and change in climatic conditions. This character had high heritability (97.22 %) with genetic advance (14.20) and high genetic advance per cent of mean of 26.67% (Anitha and Manivannan, 2014) High heritability and GAM suggested that this character is predominantly controlled by complex gene interaction and this also indicated importance of additive genetic effects for control of this character.

Days to maturity

Maturity duration varied from 71.33 days to 113.33 days with mean of 85.22 days. Advanced breeding line 10KRE8-1, 188 RK and CPD local-2016 matured early while Rajeswari matured late. Low genotypic and phenotypic coefficients of variation were observed (9.01 and 9.11 % respectively) and also reported by Sumathi and Muralidharan (2010). Variation in days to maturity provides ample scope for selection of early and late maturing plants for further improvement. This trait has recorded high heritability (97.76 %) coupled with genetic advance (15.65). The per cent mean of genetic advance was moderate (18.36 %) similar to the results given by Monpara (2016). High heritability and moderate GAM of this trait indicated that environmental control of the character.

Plant height (cm)

Plant height varied from 47.20 to 132.70 cm with an overall mean of 94.68 cm. Among all the genotypes 30KRDS-1-14 (47.20) was dwarf, while AT-332(132.70) was the tallest. Genotypic and phenotypic coefficients of

variation were 17.80 and 19.18 per cent respectively which were moderate. Thirumala Rao *et al.*, (2013) also confirmed the same results. This trait exhibited high heritability (86.2 %) with expected genetic advance (32.24). The per cent mean of genetic advance was also high (34.05 %). This trait is having similar results given by Sandipan *et al.*, (2010). This trait is governed by complex gene interaction important for control of additive genetic effects for the control of this character which indicates response to selection.

Number of branches per plant

Number of branches varied from 1.66 to 8.00 with overall mean of 4.93 branches per plant. 82 RK, 162 RK were single branching type, while SDSN-15-16 is profuse branching type. High genotypic and phenotypic coefficients of variation 28.01 and 33.05 per cent respectively were recorded are collinear with results given by Gayatree *et al.*, (2011). Presence of high variability for genotypes evaluated facilitates genetic improvement. This trait recorded high heritability (71.8 %) with genetic advance (2.41). The per cent mean of genetic advance was high with 48.90% (Sandipan *et al.*, 2010). Results indicated possible scope for improvement through selection of this character and breeder may have reliable benefits in next generation with respect to this character.

Number of capsules per plant

Range of variation from 6.00 to 61.00 was observed for capsules per plant with an overall mean of 19.31 capsules per plant. II IBL Local (1), II IBL Local (7) and TKG-22(6) produced very less number of capsules, while SDSN-15-14 had more number of capsules (61) per plant. Genotypic and phenotypic coefficients of variation were high *i.e.*, 50.72 and 53.69 per cent respectively. Similar are given by Sumathi and Muralidharan, (2010).

Fig.1 Genotypic and phenotypic coefficients of variation for yield and yield attributing traits in sesame genotypes at RARS, Jagtial during *kharif*, 2017

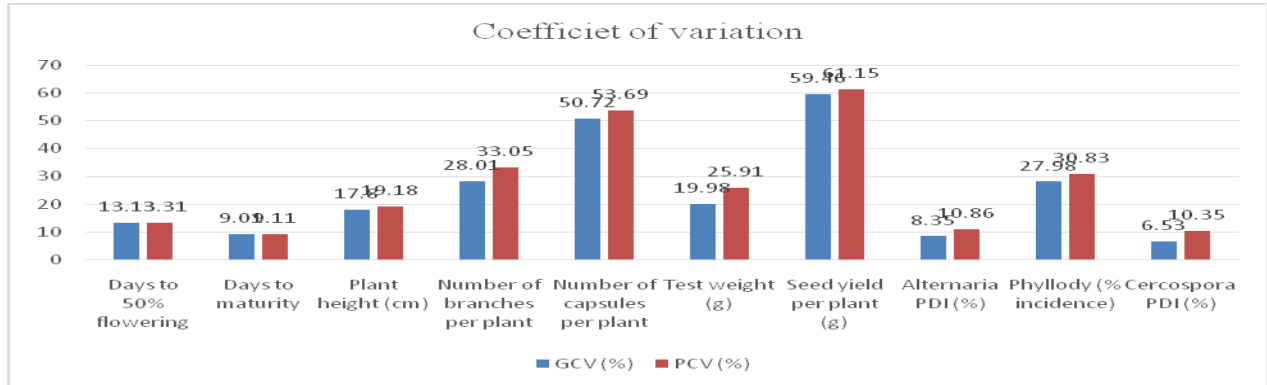


Fig.2 Heritability and Genetic advance as per cent of mean for yield and yield attributing traits in sesame genotypes at RARS, Jagtial during *kharif*, 2017

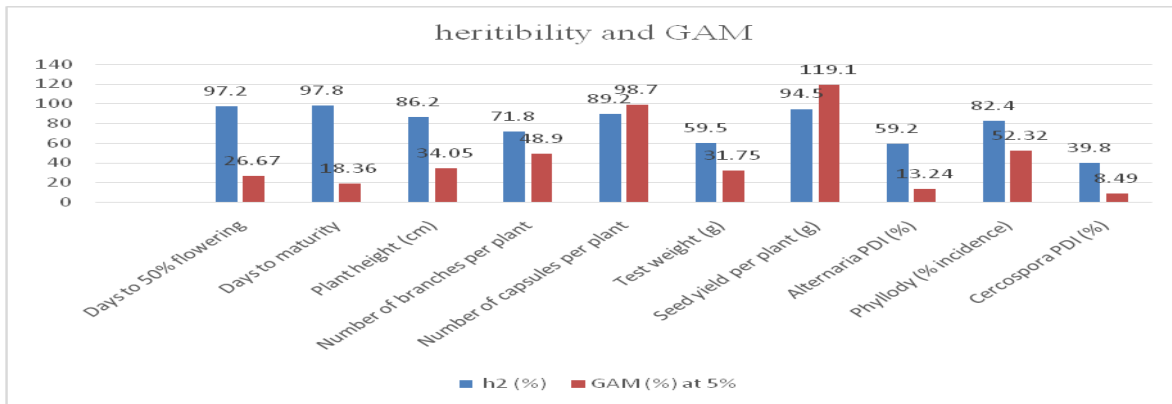


Table.1 Analysis of Variance for yield and yield attributing traits in sesame at RARS, Polasa, Jagtial during *kharif*, 2017

S. No.	Character	Mean Sum of Squares		
		Replications (df=2)	Genotypes (df=132)	Error (df=264)
1.	Days to 50% Flowering	1.10	148.15**	1.39
2.	Days to Maturity	1.31	178.38**	1.35
3.	Plant Height (cm)	52.36	178.38**	45.59
4.	Number of Branches per Plant	2.21	6.49**	0.75
5.	Number of Capsules per Plant	2.92	299.47**	11.57
6.	Test weight (g)	0.20	0.73	0.13
7.	Seed yield per Plant (g)	0.42	8.21**	0.15
8.	<i>Alternaria</i> leaf spot PDI (%)	8.72	204.24**	38.19
9.	Phyllody (% incidence)	276.68	1401.92**	93.21
10.	<i>Cercospora</i> leaf spot PDI (%)	145.46	170.13**	56.96

*. Significance level at 5% level of probability (1.43)

** Significance level at 1% level of probability (1.65)

Table.2 Genetic parameters for yield and yield attributing traits in sesame at RARS, Polasa, Jagtial during *kharif*, 2017

Trait	Range		Mean \pm SD	Variance		Coefficient of Variation		h^2 (%)	Genetic Advance (GA) at 5%	GAM (%) at 5%
	min	max		Genotypic	Phenotypic	GCV (%)	PCV (%)			
Days to 50 per cent flowering	38.33	69.33	53.26 \pm 0.68	48.92	50.31	13.13	13.31	97.22	14.20	26.67
Days to maturity	71.33	113.33	85.22 \pm 0.66	59.01	60.36	9.01	9.11	97.76	15.65	18.36
Plant height (cm)	47.20	132.70	94.68 \pm 3.88	284.26	329.85	17.80	19.18	86.18	32.24	34.05
Number of branches per plant	1.66	8.00	4.93 \pm 0.49	0.91	2.66	28.01	33.05	71.81	2.41	48.90
Number of capsules per plant	6.00	61.00	19.31 \pm 1.95	95.96	107.54	50.72	53.69	89.24	19.06	98.70
Test weight (g)	1.04	3.23	2.22 \pm 0.21	0.19	0.33	19.98	25.91	59.48	0.70	31.75
Seed yield per plant (g)	0.26	9.40	2.75 \pm 0.22	2.68	2.84	59.46	61.15	94.54	3.28	119.10
<i>Alternaria</i> leaf spot PDI (%)	56.66	100.00	89.03 \pm 3.55	55.35	93.54	8.35	10.86	59.17	11.79	13.24
Phyllody (% incidence)	6.33	100.00	74.63 \pm 5.55	436.23	259.45	27.98	30.83	82.39	39.05	52.32
<i>Cercospora</i> leaf spot PDI (%)	63.33	100.00	93.98 \pm 4.34	37.72	94.69	6.53	10.35	39.84	7.86	8.49

This trait recorded high heritability (89.24 %) with genetic advance of 19.06. The per cent mean of genetic advance was also high (98.70 %) (Bharathi *et al.*, 2014). Presence of high heritability and GAM for this trait reveals the additive gene effect and can be effectively used in selection procedure.

Test weight (g)

The average test weight was 2.22 g with a range varying from 1.04 to 3.23 g. 30KRDS-1-26 had lighter seeds (1.04g) while DS-46 had recorded heavier seed (3.23g). Moderate genotypic coefficient of variation (19.98 %) and high phenotypic coefficient of variation (25.91 %) were observed. The same results are recorded by Bharathi *et al.*, (2014). This trait recorded moderate heritability (59.5 %) with genetic advance (0.70) and the per cent mean of genetic advance was high (31.75 %). The results are similar with Rajani Bisen *et al.*, (2013). This trait is controlled by dominant genes and can be improved through heterosis breeding.

Seed yield per plant (g)

Seed yield per plant exhibited a wide amount of variation varying from 0.26 to 9.40 g per plant. The overall mean was 2.75g. II IBL Local (5) was poor seed yielder (0.26 g), while YLM-66 recorded maximum seed yield per plant (9.40 g). The genotypic and phenotypic coefficients of variation were 59.46 and 61.15 per cent which were moderate and high respectively (Abate *et al.*, 2015). The heritability was high (94.54 %) with genetic advance (3.28). The per cent mean of genetic advance was high (119.10%) (Tripathy *et al.*, 2016). Though seed yield was influenced by yield contributing characters high heritability and GAM indicates, this trait is controlled by additive gene effect and phenotypic selection of this character would fasten the varietal improvement period.

***Alternaria* PDI (Per cent Disease Index)**

The overall mean for the *Alternaria* disease is 89.03 %. The variation exhibited by the genotypes is between 56.66 and 100.00 percent. TKG-506 is recorded low (56.66) while, JCS-2698, Swethatil©, SDSN-15-14, Mall-1 is recorded highest (100.00). The genotypic and phenotypic coefficients of variation were low (8.35) and moderate (10.86) per cent respectively for *Alternaria* PDI. These results are in conformity by Shobha Rani and Ravi Kumar, (2002) in sunflower. The heritability was moderate (59.17 %) with genetic advance (11.79). The per cent mean of genetic advance was moderate (13.24%). The same results are recorded by Sujatha and Nadaf, (2013) in onion. This parameter is controlled both by additive and dominant gene effects which can be improved by recurrent selection.

Phyllody (% incidence)

For Phyllody (per cent incidence) overall mean observed was 74.63. The variation exhibited by the genotypes is between 6.33 and 100.00. SDSN-15-98 is recorded low (6.33) while II IBL Local (5) and SDSN-15-72 is recorded highest (100.00). The genotypic and phenotypic coefficients of variation were 27.98 and 30.83 per cent respectively which were high. The heritability (82.39 per cent) and the per cent mean of genetic advance were high (52.32 %). The genetic advance of the disease is 39.05. High heritability and GAM of this trait indicates that it is less controlled by environment and additive gene action plays important role which reveals response to selection is high.

***Cercospora* PDI (Per cent Disease Index)**

Cercospora disease is one of the important foliar diseases, the overall mean observed was 93.98 percent. The variation exhibited by the

genotypes is between 63.33 and 100.00 per cent. YLM-11 was recorded low (63.33 %) while 50 KRE8-1, 30 KRDS-1-6, 30 KRDS-1-18, 30 KRDS-1-71, 60 KRE8-1-4, 60 KRE8-1-5, RS Black, RS I Black, RS Black 108 and N-8 were recorded highest (100.00%) PDI. The genotypic and phenotypic coefficients of variation were low (6.53%) and moderate (10.35 %) respectively. Moderate GCV was reported by Kumari (2008) and Adama *et al.*, (2017) in ground nut. The heritability was moderate (39.84 %) coupled with the low per cent mean of genetic advance (8.49%). Moderate heritability coupled with low GAM emphasises that this parameter is highly influenced by environment and controlled by both additive and dominant gene effects. This parameter may be improved by heterosis breeding.

In the present study high PCV observed for all the parameters reveals the influence of environment on the manifestation of these parameters. Hence the difference between PCV and GCV was high for test weight (5.93) followed by number of branches per plant (5.04), number of capsules per plant (2.97), seed yield per plant (1.69) and plant height (1.38). This indicates test weight and number of branches per plant were influenced more by environment followed by seed yield per plant and plant height compared to other yield and yield contributing traits. This study also reveals days to 50 per cent flowering and days to maturity were least effected by environment.

An estimated heritability values alone is less reliable as these values are prone to alter with change in the environment and experimental material (Swarup and Chaugle., 1962). Hence, the use of high heritability coupled with high genetic advance is preferred and observed only for days to 50 per cent flowering, plant height, number of branches per plant, number of capsules per plant and seed yield. Thus,

these traits are most probably controlled by additive gene action which may respond to selection. Among disease parameters, high heritability coupled with high GAM was observed for phyllody and moderate was observed for *Alternaria* PDI and *Cercospora* PDI.

Wide range of variation is present among the genotypes which is high for characters number of branches per plant, number of capsules per plant, seed yield per plant and phyllody (% incidence). This magnitude of variation provides ample scope of selection for desired genotypes and further improvement. High heritability coupled with high genetic advance as per cent of mean was observed for days to 50% flowering, plant height, number of branches per plant, number of capsules per plant, seed yield per plant and phyllody (% incidence) suggesting that, these characters were controlled by additive gene action. These are inherent characters and could be improved by simple phenotypic selection. Moderate heritability associated with low GAM was observed for test weight which suggests the role of dominant gene action and can be improved using heterosis breeding.

Acknowledgment

Professor Jayashankar Telangana State Agriculture University for providing stipend during the study period.

Regional Agricultural Research Station, Polasa, Jagtial for providing site for conducting the experiment.

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How to cite this article:

Divya K., T. Shobha Rani, T. Kiran Babu and Padmaja, D. 2018. Assessment of Genetic Variability, Heritability and Genetic Gain in Advanced Mutant Breeding Lines of Sesame (*Sesamum indicum* L.). *Int.J.Curr.Microbiol.App.Sci.* 7(06): 1565-1574.
doi: <https://doi.org/10.20546/ijcmas.2018.706.187>