

GENETIC PARAMETERS AND THEIR IMPLICATIONS FOR YIELD IMPROVEMENT IN SESAME

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Abstract: The experimental material consists of Thirty four sesame germplasm lines including one check (Pragati). These genotypes were evaluated during *khariif* season 2016 in randomized block design with three replications at experimental farm of AICRP on safflower, Vasant Rao Naik Marathwada Krishi Vidyapeeth, Parbhani (Maharashtra). The observations were recorded on days to 50 per cent flowering, plant height, number of primary branches per plant, number of capsules per plant, days to maturity, seed yield per plant and seed yield (kg/ha). The variations among the genotypes were highly significant for all the characters studied. Phenotypic variance (V_p) values were more than the genotypic variance (V_g) in all the characters. High heritability values in broad sense coupled with high genetic advance was observed for seed yield per plant, plant height and days to 50% flowering. High heritability coupled with a high genetic advance expressed as per cent of mean offers the most effective condition for selection.

Keywords: Sesame, Genotype, Variability, Heritability and Genetic Advance.

Introduction: Sesame (*Sesamum indicum* L.) is a diploid species with $2n = 26$ chromosomes. It is a self pollinated crop and belongs to the family *pedaliaceae*. It is often called the 'queen of oilseed crops'. It is grown in tropical to the temperate zones from about $40^\circ N$ latitude to $40^\circ S$ latitude. It is grown in more than 50 countries in the world. In India during 2014-15, sesame is cultivated on an area of 17.46 mha with a production of 8.27 lakh tonnes and productivity of 474 kg per ha. (Ministry of Agriculture and Farmers welfare, Government of India, 2016, www.indiastat.com). It is widely cultivated in the states of Rajasthan, Uttar Pradesh, Madhya Pradesh, Gujrat, West Bengal, Tamil Nadu, Andhra Pradesh and Karnataka. In Maharashtra, the area under this crop is 0.21 mha, with 0.04 lakh metric tonnes production and average productivity of 190 kg per ha.

Success of any breeding programme depends on the magnitude of genetic variability present in a plant population. In crop plants segregation pattern of yield and related traits are continuous and their phenotypic expressions are highly vulnerable to environmental fluctuations. The effectiveness of selection for genetic improvement in yield and its contributing characters depends on genetic variability present in gene pool and extent of its heritability. The major function of heritability is to provide information on transmission of traits from parents to offspring.

Materials and Methods: The present investigation entitled "Genetic divergence studies in sesame (*Sesamum indicum* L.)" was conducted on experimental farm of AICRP on safflower, Vasant Rao Naik Marathwada Krishi Vidyapeeth, Parbhani (Maharashtra) during *khariif*, 2016. The material for the study comprised 35 germplasm collections of sesame received from Regional Rural Research Station, Jabalpur (Madhya Pradesh) representing diverse eco-geographical origin. The experiment was conducted at experimental farm of AICRP on safflower, Vasant Rao Naik Marathwada Krishi Vidyapeeth, Parbhani during *khariif*, 2016. The experimental material was evaluated in Randomized Block Design (R.B.D.) with three replications under rainfed condition. Sowing was carried out at the spacing of 30 cm and 15 cm between the rows and plants, respectively. The method of sowing was dibbling. Thinning was done 15 days after sowing. The recommended dose of fertilizer 50 kg N + 25 kg P_2O_5 per hectare was applied at the time of sowing. All other cultural practices were undertaken to maintain healthy crop. The observations were recorded on days to 50 per cent flowering, plant height (cm), number of primary

branches, number of capsules per plant, days to maturity, seed yield per plant (g), seed yield (kg per hectare).

Results and Discussion: The general analysis of variance was carried for each character to find out amount of variation for various characters. The variations among the genotypes were highly significant for all the characters studied (**Table 1**). Genetic variability is a pre-requisite in crop improvement programme. The breeder has to quantify the fixable and non-fixable components of variation for an effective selection programme. In the present study efforts are made to analyze the component of variability in the promising genotypes for future breeding work.

Range of Variability: In general a wide range of variability was observed for majority of the characters. Range of variability on the basis of mean values was more for the characters seed yield per hectare (353.00 to 485.67), plant height (47.60 to 116.60), number of capsules per plant (18.67 to 34.00) and days to maturity (78.33 to 96.33). Wide variation for different yield contributing characters in sesame have been reported by several workers including, Kumhar *et al* (2008), Jadhav and Mohrir (2012), Revathi *et al* (2012) and Ismaila and Usman (2014).

Genotypic and Phenotypic Variances: Phenotypic variance (V_p) values were more than the genotypic variance (V_g) in all the characters (**Table 2**). High genotypic and phenotypic variances were observed for the characters seed yield per hectare (G-966.71, P-1852.33) followed by plant height (G-294.98, P-303.22). The present findings are in close agreement with those of Abate *et al.*, (2015) for seed yield per hectare and plant height. The lowest genotypic and phenotypic variances were observed for character seed yield per plant (G-0.38, P-0.42). Abate and Mekbib (2015) reported similar findings for seed yield per plant. These results are in close agreement with Saxena and Bisen (2016) who reported the low genotypic and phenotypic variance. As genotypic and phenotypic variances are low for these characters, they can be improved by developing segregating population using diverse parents and selecting good transgressive segregants. Similar suggestions are given by Rathod (2014).

Genotypic and Phenotypic Coefficients of Variation: The selection under field condition may be strongly influenced by the environment factors affecting the progress in the improvement programme. In the present studies, the genotypic coefficient of variation for all the characters was lower than the phenotypic coefficient of variation. However the differences between them were of lower magnitude except few characters. This relationship indicated that there was small effect of environment on these characters and phenotypic selection for such characters may be effective. In the present study, high estimates of genotypic and phenotypic coefficient of variation were observed for seed yield per plant (GCV-48.86%, PCV-51.21%) and plant height (GCV-21.81%, PCV-22.12%). These results are in conformity with Narayanan and Murugan (2013). Higher values of phenotypic coefficient of variation than genotypic coefficient variation were also reported by Kumhar *et al.*, (2008), Jadhav and Mohrir (2012) and Revathi *et al.*, (2012). The low genotypic and phenotypic coefficient of variations were observed for days to 50% flowering and days to maturity. These results are in close agreement with those given by Saxena and Bisen (2016). The characters which have less influence of environment may be improved by simple selection method such as mass selection or by pure line selection.

Heritability and Genetic Advance: The heritability estimates along with expected genetic advance are more useful in predicting yield under phenotypic selection than heritability estimates alone (Johnson *et al.*, 1955). According to them heritability is categorized like, less than 30% as low, 30-60% as moderate and more than 60% as high heritability. In the present study, the highest broad sense heritability values were observed for the character plant height (97.30%), Seed yield per plant showed high heritability (91.02%), days to 50% flowering (90.01%) and days to maturity (75.58%). These results are in close agreement with findings of Suathi and Muralidharan (2010), Jadhav and Mohrir (2012), Bharathi *et al.*, (2014) and Azeez *et al.*, (2016). Moderate heritability was exhibited by seed yield per hectare (52.19%), and primary branches per plant (32.30%). Similar results were reported by Jhansi Rani and Ramakumar (2013) and Iqbal *et al.*, (2016). According to Johnson *et al.*, (1955) the expected genetic advance is categorized into less than 10% as low, 10-20% as moderate and more than 20% as high expected genetic advance. High heritability along with high genetic advance was observed for seed yield per plant and plant height. This finds support from the results furnished by Solanki and Gupta (2003), Gawali *et al.*, (2007), Parameshwarappa (2009), Tripathi *et al.*, (2013) and Bamrotiya *et al.*, (2016). High heritability along with medium genetic advance was exhibited by the character days to 50% flowering. Medium heritability with medium genetic advance was observed for seed yield per hectare. Similar findings were reported by Abate and Mekbib (2015). High heritability accompanied with low genetic advance was recorded for the character days to maturity. This result was in accordance with Meena Kumari and Ganesamurthy (2015).

The highest broad sense heritability (97.00%) was observed for plant height followed by days to 50% flowering (90.00%) and days to maturity (75.58%) while other characters had moderate to low heritability percentage. The highest genetic advance (96.02) was noticed for the character seed yield per plant followed by plant height (44.32), days to 50% flowering (16.23%), number of capsules per plant (15.52), number of primary branches per plant (12.36) and seed yield per hectare (11.48). Whereas, days to maturity (7.56) recorded medium genetic advance.

Thus, from the foregoing discussion, it is clear that the characters plant height, and seed yield (kg per hectare) recorded high heritability coupled with high expected genetic advance, indicating the presence of additive gene action and effectiveness of phenotypic selection. These results are in conformity with Abate and Mekbib (2015) who observed high heritability and high genetic advance for plant height and seed yield. Thus, while exploiting genetic variability a due weightage should be given to these characters.

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Table 1: Analysis of Variance of RBD for Various Traits in Sesame

Sr. No.	Source of variation	D.F.	Mean Sum of Square						
			Days to 50% flowering	Plant height (cm)	Number of Primary branches per plant	Number of capsules per plant	Days to maturity	Seed yield per plant (g)	Seed yield (kg per hectare)
1	Replications	02	0.1809	8.8887	0.5428	5.7428	2.9809	0.0315	577.37
2	Genotypes	34	23.1978**	893.18**	1.0577**	56.0056**	41.6538**	1.1939**	3785.752**
3	Errors	68	0.8280	8.2392	0.4350	21.2232	4.0496	0.038	885.6263

* and ** Indicates Significant at 5 % and at 1 %, Respectively.

Table 2: Genetic Variability Parameters for Yield and Yield Contributing Characters in Sesame Germplasm Lines

Sr. No	Characters	Range	General mean	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	GCV (%)	PCV (%)	Heritability (BS) (%)	Genetic advance	Genetic advance as % of mean 5%
1	Days to 50 % flowering (days)	30.00 - 42.67	32.87	7.46	8.28	8.31	8.76	90.01	5.34	16.23
2.	Plant height (cm)	47.60 - 116.60	78.74	294.98	303.22	21.81	22.12	97.28	34.90	44.32
3.	Number of Primary branches per plant	2.33 - 5.33	4.31	0.208	0.643	10.56	18.58	32.33	0.53	12.36
4.	Number of capsules per plant	18.67 - 34.00	26.85	11.59	32.88	12.68	21.33	35.33	4.17	15.52
5.	Capsule length (cm)	2.17 - 2.77	2.55	0.02	0.033	5.31	7.16	54.99	0.21	8.10
6.	Capsule breadth (cm)	0.60 - 0.73	0.66	0.001	0.0049	4.85	10.61	20.89	0.03	4.57
7.	Number of seeds per capsule	28.00 - 49.67	39.45	28.098	34.99	13.44	15.00	80.28	9.78	24.80
8.	1000 seed weight (g)	1.96 - 3.40	2.57	0.14	0.18	14.44	16.58	75.80	0.66	25.89
9.	Days to maturity	78.33 - 96.33	82.82	12.53	16.58	4.27	4.92	75.58	6.34	7.56
10.	Seed yield per plant (g)	0.36 - 3.06	1.27	0.38	0.42	48.86	51.21	91.02	1.22	96.02
11.	Seed yield (kg per hectare)	353.00 - 485.67	403.03	966.71	1852.33	7.71	10.68	52.19	46.27	11.48
12.	Oil content (%)	45.60 - 49.83	48.05	0.65	2.94	1.69	3.57	22.37	0.79	1.64

GCV = Genotypic Coefficient of Variation BS = Broad Sense
PCV = Phenotypic Coefficient of Variation
