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# Estimation of Genetic Parameters in Okra [Abelmoschus esculentus (L.) Moench] under Malwa region of Madhya Pradesh

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ABSTRACT: Sixteen okra genotypes were evaluated to estimate the genetic parameters of yield and its attributing traits. The genotypes were sown in randomized complete block design (RCBD) with 3 replications at the Research area, Department of Horticulture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, College of Agriculture, Indore, Madhya Pradesh. The differences were statistically significant among the genotypes for all the traits studied. Fruit and shoot borers and yellow vein mosaic virus (BYVMV) are major challenges in okra production. In the present study, High magnitude of the phenotypic coefficient of variance (PCV) than the genotypic coefficient of variance (GCV) was observed for all the traits. None of the characters reported higher PCV and GCV while, moderate PCV and GCV were observed for the number of branches per plant, number of nodes to 1<sup>st</sup> flowering, length of internodes and number of leaves per plant, fruit yield per plant, fruit yield per plot and fruit yield per hectare. High heritability coupled with high genetic advance as a percentage of mean (GAM) was observed for fruit yield per plant, fruit yield per hectare, number of nodes to 1<sup>st</sup> flowering and length of internodes, suggesting that direct selection of these traits for crop improvement will be rewarding due to predominance of additive variation.

Keywords: Variability, heritability, genetic advance, PCV and GCV, yield, Okra.

## **INTRODUCTION**

Okra [*Abelmoschus esculentus* (L.) Moench] belongs to the Malvaceae family and has chromosome 2n = 130. It is one of the most well-known vegetables. The world's most favoured fruit and vegetable is widely cultivated in tropical, subtropical, and warm regions like India, Africa, Turkey, and its neighbouring nations. In India, it occupies the fifth position, next to tomato in the area under vegetables in the country. It is grown throughout the country except in mountainous regions. India ranks 1<sup>st</sup> in the world with an area of 5.07 Million ha and production of 58.5 Million tonnes and productivity 11.5 tonnes per hectare. In Madhya Pradesh, okra is grown in a 2.8 Million ha area with a production of 32.8 Million tonnes and productivity of 11.7 tonnes (Anonymous, 2021).

It is an important fruit vegetable of high commercial and food value. Although its curry, soups, and young leaves are particularly popular, its tender immature green in fresh form is its main selling point. Characterization and quantification of genetic diversity and information on the genetic, for the effective use of plant genetic resources, variation within and among closely related crop varieties is crucial. When evaluating attributes, it is necessary to grow the plants to full maturity before identification because phenotypic and morphological diversity typically vary with environments. The amount of genetic parameters, heritable and non-heritable factors, and other factors have all been attempted to quantify such as genotypic and phenotypic coefficient of variation (GCV & PCV), heritability (bs) and genetic advance as a percentage of mean (GAM) in some of the quantitative traits of okra.

## MATERIALS AND METHODS

Sixteen germplasm lines of Okra [*Abelmoschus* esculentus (L.) Moench] were evaluated for yield and its contributing traits. List of genotypes used in the study is depicted in (Table 1). All the 16 genotypes of 14(4): 1024.1027(2022)

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okra were sown in a randomized complete block design (RCBD) with 3 replications at the Research Area of the Department of Horticulture, Rajmata Vijavaraje Scindia Krishi Vishwa Vidyalaya, College of Agriculture, Indore, Madhya Pradesh during Kharif, 2018. Recommended agronomic practices were carried out to attain the production potential of the okra crop. Randomly selected five plants from each genotype and for each replication, after observations their mean was calculated for fifteen morphological traits of okra. ANOVA for RCBD was worked out as per Panse and Sukhatme (1989). GCV and PCV was estimated as per the formula given by Comstock and Robinson (1952). The genetic advance (GA) was calculated according to Johnson et al. (1955). Heritability (bs) was calculated as per the formula given by Hanson et al. (1956).

 
 Table 1: List of sixteen Okra genotypes used for variability analysis.

Sr. No.	Genotypes	S. No.	Genotypes
1.	Parbhani Kranti	9.	Shaan
2.	Arka Anamica	10.	NS-7755
3.	No.55	11.	NS-862
4.	Sahiba	12.	Rasi-20
5.	Jhilmil	13.	NS-864
6.	NS-867	14.	Sonal
7.	Saarika	15.	Arya Mohini
8.	NS-801	16.	Shakti

#### **RESULTS AND DISCUSSION**

The prerequisite for any crop improvement program is genetic variability. In the present study, ANOVA revealed that the okra genotypes evaluated were highly significant for all the characters, indicating the presence of genetic variability among the genotypes. Analysis of the variance (ANOVA) of 15 characters is given in (Table 2). Shanthakumar and Salimath (2010); Senapati *et al.* (2011); Singh and Jain (2012); Shivaramegowda *et al.* (2016), Ravel *et al.* (2018); Ranga *et al.* (2021) also reported genetic variability in okra genotypes.

A higher magnitude of PCV than GCV was recorded for all the traits. Range, PCV, GCV, heritability and genetic advance as per cent age of mean (GAM) of 15 characters are given in Table 3. PCV ranged from 3.16% for days to 50% flowering to 18.14% for number of branches per plant at 60 DAS. None of the character reported higher PCV and GCV (>20%) while, moderate PCV and GCV (10-20%) were observed for the number of branches per plant at 60 DAS and 90 DAS (18.14, 16.71, 16.87, 14.98), number of nodes to 1<sup>st</sup> flowering (17.34, 14.58), length of internodes (16.84, 14.02), number of leaves per plant at 30 DAS, 60 DAS and 90 DAS (16.24, 13.98, 14.38, 11.65, 13.39, 10.98), fruit yield per plant (14.46, 14.03), fruit yield per plot (14.15, 13.68) and fruit yield per hectare (14.17, 13.69). All remaining characters reported low PCV and GCV. Sravanthi (2017) also reported moderate PCV and GCV for number of branches per plant and length of internodes. Kerure et al. (2017) reported moderate GCV and PCV for average fruit weight and number of nodes to 1<sup>st</sup> flowering.

More accurate and dependable methods of projecting improvement through selection are heritability estimates expressed as a percentage of the mean and genetic advancements (Johnson et al., 1955). In the present study, broad sense heritability estimates were high for all the characters (Table 3). High heritability coupled with high genetic advance as a percentage of mean (GAM) was observed for fruit yield per plant, fruit yield per plot, fruit yield per hectare, number of branches per plant at 60 DAS and 90 DAS, plant height at 60 DAS, number of leaves per plant at 30 DAS, number of nodes to 1<sup>st</sup> flowering and length of internodes. The results agree with Patel et al. (2014); Nagre et al. (2011) for fruit yield per plant. The present result is in agreement with the findings of Saifullah and Rabbani (2009); Das et al. (2012); Sharma and Prasad (2015). Since these traits are determined by additive gene actions, it also suggested a higher response for the selection of high-yielding genotypes.

Table 2: Analysis of variance for yield and its attributing characters of okra.

		Mean sum of square			
Characters (d.f.)		Genotype (15)	Replication (2)	Error (30)	
	30 DAS	5.110**	2.246	1.002	
Plant height (cm)	60 DAS	50.261**	7.107	3.649	
	90 DAS	48.998**	10.8	3.142	
No	60 DAS	0.326**	0.046	0.018	
Number of branches per plant	90 DAS	0.958**	0.398	0.078	
	30 DAS	2.593**	0.007	0.27	
Number of leaves per plant	60 DAS	10.235**	0.591	1.522	
* *	90 DAS	21.886**	0.527	3.059	
Number of nodes to 1 <sup>st</sup> flowering		2.540**	0.511	0.308	
Length of internodes (cm)		3.686**	1.355	0.475	
Days to 1 <sup>st</sup> flowering		5.001**	0.14	0.549	
Days to 50% flowering		4.723**	2.873	0.724	
Days to 1 <sup>st</sup> picking		14.491**	0.474	2.292	
Fruit length (cm)		5.229**	1.768	0.515	
Fruit width (cm)		0.020**	0.004	0.001	
Fruit weight (g)		6.076**	1.737	0.344	
Number of fruits per plant		17.469**	8.43	1.251	
Fruit yield per plant (g)		7750.400**	981.687	156.342	
Fruit yield per plot (	kg)	4.316**	0.207	0.098	
Fruit yield per hectare	e (q)	948.169**	39.775	22.003	

\*\* indicates 1% level of significance

Characters		Range	PCV	GCV	h <sup>2</sup> (bs)	GAM
	30 DAS	14.68 - 19.12	9.07	6.89	57.74	10.78
Plant height (cm)	60 DAS	24.84 - 38.83	13.59	12.23	80.98	22.67
_	90 DAS	72.74 - 86.76	5.34	4.86	82.95	9.12
Number of branches per	60 DAS	1.29 - 2.69	18.14	16.71	84.83	31.66
plant	90 DAS	2.87 - 4.68	16.87	14.98	78.83	27.36
	30 DAS	5.12 - 8.02	16.24	13.98	74.10	24.81
Number of leaves per plant	60 DAS	10.63 - 17.50	14.38	11.65	65.62	19.44
	90 DAS	17.64 - 27.35	13.39	10.98	67.23	18.54
Number of nodes to 1 <sup>st</sup> flowering		4.54 - 7.88	17.34	14.58	70.67	25.23
Length of internodes (cm)		5.73 - 9.03	16.84	14.02	69.26	24.03
Days to 1st flowering		40.25 - 44.36	3.41	2.91	72.97	5.12
Days to 50% flowering		43.76 - 47.87	3.16	2.54	64.77	4.21
Days to 1 <sup>st</sup> picking		45.76 - 53.31	5.20	4.15	63.95	6.84
Fruit length (cm)		12.09 - 16.26	10.12	8.79	75.31	15.70
Fruit width (cm)		1.59 - 1.89	5.19	4.75	83.69	8.96
Fruit weight (g)		12.50 - 17.35	10.13	9.32	84.72	17.67
Number of fruits per plant		20.05 - 28.38	10.64	9.59	81.20	17.81
Fruit yield per plant (g)		285.83 - 456.83	14.46	14.03	94.18	28.05
Fruit yield per plot (kg)		6.96 - 10.96	14.15	13.68	93.43	27.23
Fruit yield per hectare (q)		103.15 - 162.37	14.17	13.69	93.35	27.24

### CONCLUSION

The present study clearly indicated that greater variability was present among all the traits of selected okra genotypes. The magnitude of PCV was higher than GCV for all the traits. Moderate PCV and GCV were observed for the number of branches per plant at 60 DAS and 90 DAS, the number of nodes to 1st flowering, the length of internodes, the number of leaves per plant at 30 DAS, 60 DAS, and 90 DAS, the fruit yield per plant, the fruit yield per plot, and the fruit yield per hectare. High heritability coupled with high genetic advance as a percentage of mean (GAM) was observed for fruit yield per plant, fruit yield per plot, fruit yield per hectare, number of branches per plant at 60 DAS and 90 DAS, plant height at 60 DAS, number of leaves per plant at 30 DAS, number of nodes to 1st flowering, and length of internodes. It also indicated a higher response for the selection of high-yielding genotypes, as these characters are governed by additive gene actions. Based on estimations of genetic parameters, it is clear that the traits with high PCV, GCV, heritability, and genetic advance expressed as a percent mean were regarded as the most important traits, and selection of these traits will be more effective in increasing fruit production per plant.

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**Conflict of Interest.** Authors have declared that no competing interests exist.

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