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## Studies on genetic variability, heritability and genetic advance for yield and yield attributing characters in okra (*Abelmoschus esculentus* (L.) moench)

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**Abstract**

The present investigation was carried out at Horticulture Research Station, Dr. Y. S. R Horticultural University, Venkataramannagudem, West Godavari district during *kharif* season, 2018 to study genetic variability, heritability and genetic advance for yield and yield attributing characters in okra. Analysis of variance revealed that there were significant differences among genotypes for all the traits under study, indicating a large amount of genetic variability in the germplasm. Higher magnitude of PCV and GCV (> 20%) were observed for yellow vein mosaic virus infestation on plants, fruit and shoot borer infestation on plants and average fruit weight indicating the existence of wide range of genetic variability in the germplasm for these traits. High Heritability ( $h_b^2$ ) estimates (>60%) coupled with high estimates of genetic gain as percent of mean (>20%) were observed for average fruit weight and plant height indicating that these characters were least influenced by the environmental effect, since they were governed by additive genes and selection will be more rewarding if it was based on such traits.

**Keywords:** Okra, PCV, GCV, heritability, genetic advance

**Introduction**

Okra (*Abelmoschus esculentus* (L.) Moench) is an economically important vegetable crop grown in the tropical and subtropical parts of the world. It belongs to Malvaceae family having chromosome number  $2n=130$ . Okra is an important component of diet due to its high level of dietary fiber, low calories and rich source of minerals, like Ca, P, K and Mg. Fruit is a rich source of iodine, which is helpful in curing goitre, and leaves are used as remedy for dysentery. Okra mucilage has medicinal applications when used as a plasma replacement or blood volume expander (Maramag *et al.*, 2013) [10].

Fruit yield in okra depends on many yield components, since it is a polygenic character. Exploitation of variability is of great importance and prerequisite for the effective screening of superior genotypes. Knowledge of genetic parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful biometrical tools for understanding the extent of genetic variability in base population. According to Burton (1952) [4], GCV along with estimates of broad sense heritability ( $h^2$ ), genetic advance (GA) and genetic advance as per cent of mean (GAM) gives an idea about the nature of gene action governing a particular character which intern helps in effective genotype based selection making. Therefore, the present investigation was carried out to study the variability, heritability and genetic advance for seventeen quantitative traits in okra.

**Materials and methods**

The experimental material comprised of 29 hybrids of okra. These hybrids were evaluated by raising each entry in a plot of 2.5 m length and 2.5 m width, at a spacing of  $60 \times 45$  cm in a randomized block design with three replications at Horticulture Research Station, Venkataramannagudem during *kharif*, 2018. The observations were recorded on five randomly selected plants per plot in each replication for seventeen biometric characters *viz.*, plant height (cm), number of primary branches per plant, days to fifty per cent flowering, node at which first flower appears, internodal length of main stem (cm), number of nodes per plant, fruit length (cm), fruit girth (cm), average fruit weight (g), number of fruits per plant, number of seeds per fruit, fruit yield per plant (g), leaf chlorophyll content (SPAD Units), fruit moisture

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content (%), mucilage content (g/kg), fruit and shoot borer infestation (FSB) on fruits (%) and yellow vein mosaic virus infestation (YVMV) on plants (%).

Data was analysed by the methods outlined by Panse and Sukhatme (1985) [12] using the mean values of five random plants in each replication from all genotypes to find out the significance of genotypes effect. Genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated according to Burton and Devane (1953) [5]. Heritability in broad sense was estimated as per the formulae suggested by Allard (1960) [2]. Genetic advance (GA) was estimated as per the formula proposed by Lush (1940) [9]. The genetic advance as per cent of mean (GAM) was categorized as Low (0-10%), Moderate (11-20%) and High (21% and above) as suggested by Johnson *et al.* (1955) [8].

## Results and discussion

The analysis of variance (Table 1) showed highly significant differences ( $p < 0.05$ ) among the hybrids for all the traits. Morey *et al.* (2012) [11], Duggi *et al.* (2013) [7] and Akotkar *et al.* (2014) [1] also reported a wide variation among genotypes for different quantitative characters in okra.

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) of the important characters were analyzed to record the degree of variability in okra genotypes and presented in Table 2.

In the experiment, GCV was highest for yellow vein mosaic virus infestation on plants (25.68 %) and fruit and shoot borer infestation on plants (23.05 %), whereas moderate GCV was exhibited for average fruit weight (17.14 %), plant height (16.04 %) and internodal length of main stem (15.16 %). Low GCV was recorded for number of primary branches per plant (6.58 %), number of nodes per plant (5.87 %), days to 50 per cent flowering (2.26%), node at which the first flower appears (2.76%), fruit length (4.57 %), fruit girth (3.85 %), number of fruits per plant (9.62 %), number of seeds per fruit (3.56 %), fruit yield per plant (8.55 %), leaf chlorophyll content (3.06%), mucilage content (7.45%) and fruit moisture content (1.77%). The high GCV values indicated that maximum variability exists in these traits and there is enough scope for further improvement. Similar results were reported by Samim *et al.* (2018) [13].

High PCV was estimated for yellow vein mosaic virus infestation on plants (49.10 %), fruit and shoot borer infestation on plants (35.19 %) and average fruit weight (21.61%), whereas moderate PCV was recorded for mucilage content (17.04%), fruit yield per plant (17.19 %), number of fruits per plant (14.57 %), fruit length (10.18 %), plant height (20.33%), internodal length of main stem (19.98 %), number of primary branches per plant (10.42 %) and number of nodes per plant (13.45 %). Days to 50 per cent flowering (3.49 %), node at which the first flower appears (6.10 %), fruit girth (6.99 %), number of seeds per fruit (5.91 %), leaf chlorophyll

content (6.68 %) and fruit moisture content (3.44 %) recorded the lowest PCV. The PCV was higher than GCV for all the characters suggesting the environment had effect on the expression of the traits (Sharma and Prasad (2015) [14] and Chinatu *et al.*, 2017) [6].

The estimates of heritability in broad sense (%) of the seventeen quantitative characters were estimated and presented in Table 2. Estimates of heritability have been classified as high (>60%), moderate (30-60%) and low (30%). High estimates of heritability were observed for average fruit weight (63 %) and plant height (62%) whereas moderate estimates of heritability were observed for internodal length of main stem (58%), number of fruits per plant (44%), fruit and shoot borer infestation on fruits (43%), days to 50 per cent flowering (42%), number of primary branches per plant (40%), number of seeds per fruit (36%) and fruit girth (30%). This showed that large portions of exploitable variations are existing in these genotypes. Low estimates of heritability were recorded for YVMV infestation on plants (27%), fruit moisture content (27%), node at which the first flower appears (20%), fruit length (20%), fruit yield per plant (25%), leaf chlorophyll content (21%), mucilage content (19%) and number of nodes per plant (19%). These results are in accordance with the conclusions of Chinatu *et al.* (2017).

Genetic advance denotes the improvement in mean genotypic values of selected over base population and thus helps the breeder to select the progenies in the earlier generation itself (Singh and Narayanan, 1993) [15].

Genetic advance (percentage of mean) was observed to be high for FSB infestation on fruits (31.12%), average fruit weight (28.01%), YVMV infestation on plants (27.67%), plant height (26.09%) and internodal length of main stem (23.69%) whereas moderate genetic advance (percentage of mean) was observed for number of fruits per plant (13.09%) (Table 2). This implied that the large variations within these genotypes could be transferred to their progenies since these traits are expected to be under the control of additive gene action. These results are in agreement with the findings of Chinatu *et al.* (2017).

In the present experiment high heritability coupled with high genetic advance (percentage of mean) has been recorded for average fruit weight and plant height which indicates that these characteristics were less influenced by environment demonstrating either these were simply inherited characteristics governed by a few major genes or additive gene effect even if they were under polygenic control and therefore, selection of these characteristics would be more effective for yield improvement. These results are in agreement with the findings of Badiger *et al.* (2017) [3]. Moderate heritability coupled with high genetic advance (percentage of mean) has been reported in internodal length of main stem and fruit and shoot borer infestation on fruits as a result of environmental influence.

**Table 1:** Analysis of variance of okra hybrids

S. No	Characters	Mean sum of squares		
		Replications (df =2)	Treatments (df = 28)	Error (df = 56 )
01	Plant height (cm)	281.27	809.93***	136.00
02	Number of primary branches per plant	0.04	0.16***	0.05
03	Internodal length of main stem (cm)	3.95	4.33***	0.85
04	Number of nodes per plant	6.35	4.59*	2.69
05	Days to 50 per cent flowering	2.49	4.09***	1.29
06	Node at which the first flower appears (no.)	0.14	0.09*	0.05
07	Fruit length (cm)	0.60	2.49*	1.42
08	Fruit girth (cm)	0.20	0.37***	0.16

09	Average fruit weight (g)	11.90	39.87***	6.54
10	Number of fruits per plant	13.68	15.59***	4.69
11	Number of seeds per fruit	3.79	18.19***	6.71
12	Fruit yield per plant (g)	6541.13	3335.62*	1678.01
13	Leaf chlorophyll content (SPAD units)	15.11	13.21*	7.35
14	Mucilage content (g/kg)	3.94	2.49*	1.46
15	Fruit moisture content (%)	1.12	14.12***	6.76
16	YVMV infestation on plants (%)	14.95	33.42***	15.69
17	FSB infestation on fruits (%)	4.91	18.20***	5.59

\*, \*\*\* = significant at 5% and 1% level respectively. Values in parenthesis denote degrees of freedom

**Table 2:** Estimates of variability parameters in okra hybrids

Character	GCV	PCV	ECV	h <sup>2</sup>	GA	GAM (%)
Plant height (cm)	16.04	20.33	12.48	0.62	24.37	26.09
Number of primary branches per plant	6.58	10.42	8.08	0.40	0.25	8.57
Internodal length of main stem (cm)	15.16	19.98	13.01	0.58	1.68	23.69
Number of nodes per plant	5.87	13.45	12.10	0.19	0.72	5.29
Days to 50 % flowering	2.26	3.49	2.66	0.42	1.29	3.01
Node at which 1st flower appears (no.)	2.76	6.10	5.44	0.20	0.11	2.57
Fruit length (cm)	4.57	10.18	9.10	0.20	0.55	4.22
Fruit girth (cm)	3.85	6.99	5.83	0.30	0.30	4.36
Average fruit weight (g)	17.14	21.61	13.15	0.63	5.45	28.01
Number of fruits per plant	9.62	14.57	10.94	0.44	2.59	13.09
Number of seeds per fruit	3.56	5.91	4.72	0.36	2.43	4.42
Fruit yield per plant (g)	8.55	17.19	14.91	0.25	24.10	8.77
Leaf chlorophyll content (SPAD units)	3.06	6.68	5.94	0.21	1.32	2.89
Mucilage content (g/kg)	7.45	17.04	15.33	0.19	0.53	6.70
Fruit moisture content (%)	1.77	3.44	2.94	0.27	1.66	1.88
YVMV infestation on plants (%)	25.68	49.10	41.85	0.27	2.62	27.67
FSB infestation on fruits (%)	23.05	35.19	26.58	0.43	2.77	31.12

GCV-Genotypic Coefficients of Variation, PCV-Phenotypic Coefficients of Variation, ECV-Environmental Coefficients of Variation, h<sup>2</sup>-Heritability, GA-Genetic Advancement, GAM (%) - Genetic Advance Mean percentage.

## Conclusion

Analysis of variance revealed that there were significant differences among twenty nine entries for all the biometric characters indicating a large amount of genetic variability in the germplasm.

The estimates of phenotypic variance were higher than the corresponding

estimates of genotypic variance for all the traits, thereby indicating the influence of environment in the expression of these traits. Higher magnitude of PCV and GCV (> 20%) were observed for yellow vein mosaic virus infestation, fruit and shoot borer infestation and average fruit weight indicating the existence of wide range of genetic variability in the germplasm for these traits. High Heritability (h<sub>b</sub><sup>2</sup>) estimates (>60%) coupled with high estimates of genetic gain as percent of mean (>20%) were observed for average fruit weight and plant height indicating most likely that the heritability is due to additive gene effects.

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