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**MA Kharat**  
M.Sc. (Horti.) Scholar,  
Department of Horticulture,  
College of Agriculture Parbhani,  
VNMKV, Parbhani,  
Maharashtra, India

**DK Zate**  
Assistant Professor, Department  
of Agricultural Botany college of  
Agriculture Parbhani, VNMKV  
Parbhani, Maharashtra, India

**RV Bhalerao**  
Assistant Professor, Department  
of Horticulture College of  
Agriculture Parbhani, VNMKV,  
Parbhani, Maharashtra, India

**DR Bhise**  
M.Sc.(Horti) Scholar department  
of horticulture college of  
Agriculture Parbhani, VNMKV,  
Parbhani, Maharashtra, India

**Corresponding Author:**  
**MA Kharat**  
M.Sc. (Horti.) scholar,  
Department of Horticulture,  
College of Agriculture Parbhani,  
VNMKV, Parbhani,  
Maharashtra, India

## Genetic variability, heritability, and genetic advance for selection parameters of okra (*Abelmoschus esculentus* (L.) Moench) genotype

MA Kharat, DK Zate, RV Bhalerao and DR Bhise

### Abstract

Present investigation was carried out at the department of Horticulture college of Agriculture, VNMKV, Parbhani. Analysis of variance show significant variability among the traits of okra for all character's studied. Heritability estimates varied from 41.00 percentage for number of days to first harvest to 92.00 percent for plant height. Number of primary branches showed high (>25%) GCV. Moderate heritability (bs) estimates were recorded in number of nodes per plant (82%), node at which 1st flowering (79%), weight of fruit (73%), internodal length (72%), length of fruit (71%) and days to 50% flowering (64%). The highest heritability (bs) estimates were obtained in the characters like number of ridges per fruit (100%), yield per plant (99%), incidence of yellow vein mosaic virus (96%), number of branches per plant (95%), diameter of fruit (94%), incidence of yellow vein mosaic virus (94%), plant height (92%), Number of fruits per plant (91%), number of seed per fruit (91%), weight of 100 seed (87%). The genetic advancement as percent of mean (>20%) was found to be highest for yield per plant, number of fruits per plant, number of seed per fruit, number of branches per plant, while the moderate genetic advance more than (10%) was observed for weight of 100 seed, number of nodes at which 1st flowering appeared, number of fruits per plant, number of ridges per fruit, plant height.

**Keywords:** Heritability, genetic variability, okra, *Abelmoschus esculentus*

### Introduction

Okra (*Abelmoschus esculentus* L. (Moench)), is an economically important vegetable crop grown in tropical and sub-tropical parts of the world. This crop is suitable for cultivation as a garden crop as well as on large commercial farms. It is grown commercially in India, Turkey, Iran, Western Africa, Yugoslavia, Bangladesh, Afghanistan, Pakistan, Burma, Japan, Malaysia, Brazil, Ghana, Ethiopia, Cyprus and the Southern United States. In India, Okra is cultivated in an area of 0.51 million hectare with 6.18 million tonnes of produce with an average productivity of 12.04 tonnes per hectare and in Maharashtra it occupies an area of 13.98 thousand hectare with an annual production of 139.40 thousand tonnes and productivity of 9.97 tonnes per hectare (Anonymous, 2018). The states which are majorly involved in okra production are west Bengal, Gujarat, Orissa, Bihar and Andhra Pradesh. Heritability is the portion of genotypic variance to phenotypic variance, which indicates the relative success of selection. It is useful in selection of elite genotype from diverse genetic population. Heritability is that portion of variation transmitted from parent to offspring. Higher the heritable variation greater will be the possibility of fixing the characters by selection. Hence, studies on heritability are of more important to be analyzed, whether the observed variation for a trait is heritable or not. Planning and execution of a breeding program for the improvement of quantitative attributes depends, to a great extent, upon the genetic magnitude of genetic variability. The genotypic and phenotypic coefficient variation are helpful in exploring the nature of variability in the breeding population whereas, the estimate of heritability provides index of transmissibility of characters. Heritability and genetic advance estimates help the breeder to apply appropriate breeding methodology in the crop improvement programme. Thrust of any crop improvement programme is to enhance economic yield which is a complex dependent character, mostly inherited quantitatively and is determined by a number of yield components, greatly affected by environmental factors. In determining the potential of genetically different lines and cultivars, breeders have to observe various traits that influence yield. Accurate evaluation of these characters is made more difficult by the genotype by environment interaction.

## Material and Method

The investigation on heterosis studies in okra was carried out at the Department of horticulture, College of Agriculture, VNMKV, Parbhani Dist. Parbhani, Maharashtra. The Experimental material comprised 12 parents among which 10 line and 2 testers (Table-1) were collected from NBPGR, New Delhi and their 20 F1s hybrid with 3 standard checks (Mahyco bhindi No-10, Pusa Sawani, Parbhani Kranti). Each 12-parent cross among each other in line x tester mating design crosses to derive 20 F1 hybrid. The experiment was laid out in randomized block design with two replications. Each treatment or genotype in each replication was represented by one row each according to 20 plants at a spacing row to row spacing of 60 cm and 30 cm from plant to plant. Five plants were randomly selected for each genotype from each replication and evaluated for the quantitative characters of parents and hybrid. Estimation of Variability: Different parameters such as mean, coefficient of variation etc. were used to estimate to the diversity present among the genotypes for different quantitative traits and genotypic variances and coefficient of variation using formula suggested by Burton as:

$$\text{Genotypic variance } (\sigma^2g) = \frac{\text{MSg} - \text{Mse}}{r}$$

Where, r is numbers of replications, MSg is mean square due to genotypes, MSe is mean square of error (Environmental variance), Environmental variance ( $\sigma^2 e$ ) is error mean square, Phenotypic variance ( $\sigma^2p$ ) is  $\sigma^2g + \text{MSe}$  where,  $\sigma^2g$  is genotypic variance and phenotypic coefficient variation (PCV) estimated as the following formula:

$$\text{PCV} = \frac{\sqrt{\sigma^2p}}{\text{GM}} \times 100$$

Where, GM is an overall mean of character and  $\sigma^2p$  is  $\sigma^2g + \text{MSe}$

$$\text{GCV} = \frac{\sqrt{\sigma^2g}}{\text{GM}} \times 100$$

Where, GM is an overall mean of character and  $\sigma^2g$  is  $\text{MSg} + \text{MSe} / \text{Replications}$

$$\text{H (Broad scene)} = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where  $\sigma^2g$  = Genotypic variance  $\sigma^2p$  = phenotypic variation (Variance genotypic + variance environmental)

## Estimation of Heritability

Heritability in narrow sense was calculated following Falconer (1960) [2].

$$h^2(\text{us}) = \frac{\sigma^2A}{\sigma^2A + \sigma^2D + \sigma^2e}$$

Were,

$\sigma^2A$  - Additive genetic variance  $\sigma^2D$  - Dominance variance  $\sigma^2e$  - Environmental variance

Further heritability was calculated classified as high (30-60%), medium (IC low (5-10%) following Robinson's (1966) method of heritability classification.

Estimation of Genetic Advance: it is the improvements in the mean genotypic value of the selected families over the base population. Genetic advance was calculated in percent of mean according to Johnson *et al.*, (1955) [3].

$$\text{GA (\% of mean)} = \frac{\sigma^2g \times (K)}{(\sigma^2\rho) \times \text{mean}} \times 100$$

Were

K, Selection differential at 5% selection intensity (K = 2.06)

$\sigma^2g$  = Genotypic variance

$\sigma^2\rho$  = Phenotypic stand and deviation of the character

## Result and Discussion

### Variability Parameters

The analysis of variance revealed a significant variance (Table 2) among the genotype for all the character *viz.*, Days to 50% flowering (3.85\*\*), Number of days to 1st harvest (3.88\*\*), Number of node at which 1st flower appeared (0.23\*\*), Number of fruit per plant (0.31\*\*), Weight of fruit (1.80\*\*), Length of fruit (0.58\*\*), Diameter of fruit (0.02\*\*), Number of ridges per fruit (0.21\*\*), Number of node per plant (0.49\*\*), Plant Height (98.44\*\*), Number of branches per plant (0.07\*\*), Internodal length (0.56\*\*), Number of seed per fruit (89.59\*\*), weight of 100 seed (0.97\*\*), yield per plant (1638.88\*\*), Pod borer infestation (10.49\*\*), Incidences of YVMV (9.24\*\*) showed that presence of wide spectrum of variability among the genotype. The mean value of all character present in (Table-3) and Genetic variability parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as percent of mean at 5% are mentioned in (Table-4) respectively. Estimation of mean for all the characters studied where, a wide range was observed the parent EC-305689 and cross IC-293590 X EC-305652, Punjab 8 X EC-305675, Punjab 8 X EC-305613, Punjab 8 X EC-305741, Punjab 8 X EC-305714 (43.5) recorded minimum days required to 50% flowering while parent EC-305741 recorded maximum days required to 50% flowering. The parent EC-305714 and cross IC-293590 X EC-305652 recorded significantly minimum days for first harvest of fruit while among the EC-305741 (55.00), Punjab-8 x EC-305653 (52.0) required comparatively maximum days for first fruit of harvest. The parent EC-305672 (2.8) observed significantly earliest for node at which first flower appeared, cross combination IC-293590 X EC-305672 (3.5) reported significant earliness in node at which first flower appeared. Among parents EC-305653 (17.5) recorded maximum number of fruits per plant, Among the cross combinations, Punjab-8 X EC-305613 (17.8) produced maximum number of fruits. Among the parents EC-305652 (11.5g) recorded maximum weight of fruit, cross Punjab-8 X EC-305664 recorded significantly maximum weight of fruit. The tester Punjab-8 (11.1 cm) was found significantly maximum length of fruit, cross combinations Punjab-8 X EC-305664 (11.8 cm) was recorded significantly maximum length of fruit. Among the parents EC-305652, EC-305689, EC-305653 & IC-293590 (1.8 cm) recorded maximum diameter of fruit, the cross combinations IC-293590 X EC-305652 (2 cm) was

recorded significantly maximum diameter of fruit. The parent EC-395689 and EC-305741 (6.0) was found significantly maximum number of ridges per fruit, cross combinations IC-293590 x EC-305664 and Punjab-8 x EC-305652 (6.0) was recorded significantly maximum number of ridges per fruit. Among parents EC-305613 (11.2) recorded maximum number of nodes per plant. Among the cross combinations, IC-293590 X EC-305675 (11.8) produced maximum number of nodes. The parent EC-305689 (113.0) was recorded comparatively high plant height, cross combinations Punjab-8 X EC-305612 (122.5 cm) was recorded significantly high plant height. The parent EC-305664, EC-305741 & EC-305714 (1.5) was observed comparatively maximum number of branches per plant, The cross Punjab-8 X EC-305653 (2) produces significantly a greater number of branches per plant. The parent EC-305689 & Punjab-8 (10.1 cm) showed maximum internodal length, The parent EC-305689 & Punjab-8 (10.1 cm) showed maximum internodal length. The parent EC-305741 (50.4) was observed comparatively maximum number of seed per fruit, cross Punjab-8 X EC-305741 (58.4) produces significantly a greater number of seed per fruit. The parent EC-305653 8.1(g) showed maximum weight, Among the hybrids, the cross IC-293590 X EC-305652 & IC-293590 X EC-305653 7.3(g) produces significantly maximum weight. Parent EC-305652 (191.0 g) was produced significantly higher yield per plant, The cross-combination IC-293590 X EC-305652 (193.7 g) and followed by Punjab-8 X EC-305652 (191.7 g) were recorded for the significantly higher fruit yield per plant. The parent EC-305675 (2.9%) recorded significantly minimum of pod borer infestation, among the hybrids, IC-293590 x EC-305689 (3.8%) recorded significantly lowest incidence of pod borer infestation. The parent EC-305664 (4.4%) recorded significantly minimum per cent incidence of yellow vein mosaic virus than the rest of the parents, Among the hybrids, Punjab-8 x EC-305641 (2.6%) recorded significantly minimum incidence of yellow vein mosaic virus than the rest of crosses. Similar result was found by Phanikrishna *et al.*, 2015, Mudhalvan *et al.*, 2018 and Kumar *et al.*, 2019<sup>[7, 6, 4, 5]</sup>. Analysis of GCV, PCV, heritability and genetic advance as percent of mean was observed for days to 50% flowering GCV (2.71), PCV (3.39), Heritability (64), genetic advance as percent of mean (4.47). Number of days to 1st harvest showed GCV (2.08), PCV (3.27), Heritability (41), Genetic advance as percent mean (2.73). number of node at which 1st flowering showed GCV (8.67), PCV (9.74), Heritability (79), genetic advance as percent of mean (15.91). Number of fruits per plant showed GCV (14.82), PCV (15.50), Heritability (91), genetic advance as percent of mean (29.20). Weight of fruit showed GCV (8.57), PCV (10.00), Heritability (73), genetic advance as percent of mean (15.11). Length of fruit showed GCV (4.65), PCV (5.51), Heritability (71), genetic advance as percent of mean (8.08). Diameter of fruit showed GCV (4.86), PCV (5.02), Heritability (94), genetic advance as percent of mean (9.70). Number of ridges per fruit showed GCV (6.31), PCV (6.31), Heritability (100), genetic advance as percent of mean (13.00). Number of nodes per plant showed GCV (4.39), PCV (4.84), Heritability (82), genetic advance as percent of mean (8.21). Plant height showed GCV (6.49), PCV (6.75), Heritability (92), genetic advance as percent of mean (12.86). Number of branches per plant showed GCV (12.95), PCV (13.30), Heritability (95), genetic advance as percent of mean (25.97). Internodal length showed

GCV (4.89), PCV (5.78), Heritability (72), genetic advance as percent of mean (8.52). Number of seed per fruit showed GCV (14.79), PCV (15.52), Heritability (91), genetic advance as percent of mean (29.05). Weight of 100 seed showed GCV (10.17), PCV (10.88), Heritability (87), genetic advance as percent of mean (19.60). Yield per plant showed GCV (18.77), PCV (18.85), Heritability (99), genetic advance as percent of mean (38.52). Pod borer infestation showed GCV (32.35), PCV (33.45), Heritability (94), genetic advance as percent of mean (64.46). Incidence of yellow vein mosaic virus showed GCV (29.73), PCV (30.39), Heritability (96), genetic advance as percent of mean (59.90).

The estimates of phenotypic coefficient of variation (PCV) for different characters. The phenotypic coefficient of variation (>25%) was observed for pod borer infestation percentage (33.45) and incidence of yellow vein mosaic virus (30.39). The moderate phenotypic coefficient of variation (10-25%) was observed for yield per plant (18.85) number of seeds per fruit (15.52), number of fruits per plant (15.50), number of branches per plant (13.30), weight of 100 seed (10.88), Length of fruit (10.00), However, low phenotypic coefficient variation (<10%) was observed for number of days to first harvest(3.27), days to 50%flowering (3.39), plant height (6.75), internodal length (5.78), Length of fruit (5.51), diameter of fruit (5.02), number of ridges per fruit (6.31), number of node per plant (4.84). The genotypic coefficient of variation (GCV) was found to be less than phenotypic coefficient of variation (PCV) for all traits studied, which indicated that these traits were having interaction with environment to some extent. The high percentage of genotypic coefficient of variation (>25%) was observed pod borer infestation percentage (32.35). The moderate genotypic coefficient of variation (10-25%) was observed for number of fruits per plant (14.82), Number of branches per plant (12.95), number of seed per fruit (14.79), weight of 100 seed (10.17), yield per plant (18.77). However, low genotypic coefficient of variation (<10%) was observed for days to 50%flowering (2.71), number of days to 1st harvest (2.08), number of nodes at which 1st flowering (8.67), weight of fruit (8.57), length of fruit (4.65), diameter of fruit (4.86), number of ridges per fruit (6.31), number of nodes per plant (4.39), plant height (6.49), internodal length (4.89). The present report revealed that estimates of PCV were generally higher than their corresponding GCV for all the characters studied, indicated that the influence of environment in expressing the variability with traits. (Thulasiram *et al.*, 2017, Syfullah *et al.*, 2018 and Kumari *et al.*, 2019)<sup>[10, 9, 4, 5]</sup>.

The data revealed that the heritability in broad sense ranged from (41.00) for number of days to 1st harvest to (100) for plant height. High heritability (>60%) was obtained for number of ridges per fruit (100.00), yield per plant (99.00), incidence of yellow vein mosaic virus (96.00), number of branches per plant (95.00), diameter of fruit (94.00), pod borer infestation (94.00), plant height (92.00), number of fruits per plant (91.00), number of seed per fruit (91.00), weight of 100 seed (87.00), number of nodes at 1st flowering (79.00), (weight of fruit (73.00), internodal length (72.00), length of fruit (71.00). The moderate heritability (<60%) was observed for number of days to 1<sup>st</sup> harvest (41.00) denotes high proportion of additive genetic components in the inheritance of these attributes. (Sravanthi *et al.*, 2017, Verma *et al.*, 2018 and Kumari *et al.*, 2019)<sup>[4, 5]</sup>.



The data showed that the genetic advance expressed as percentage of mean was high (>20%) for yield per plant (58.63) While the moderate genetic advance (<20 to 10%) was observed for plant height (13.62), number of seed per fruit (12.83). low genetic advance (<10%) for days to 50% flowering (2.02), number of days to 1st harvest (1.39), number of node at 1st flowering (0.58), number of fruit per

plant (4.37), wight of fruit (1.54), length of fruit (0.86), diameter of fruit (0.17), number of ridges per fruit (0.67), number of node per plant (0.87), number of branches per plant (0.38), internodal length (0.85), weight of 100 seed (1.30), pod borer infestation percentage (4.49), incidence of yellow vein mosaic virus (4.28) similar result found by (Syfullah *et al.*, 2018 and Rambabu *et al.*, 2019)<sup>[8]</sup>.

**Table 1:** List of germplasm

Sr. No	Genotype	Source
1	EC-305613	NBPGR, New Delhi
2	EC-305652	NBPGR, New Delhi
3	EC-305689	NBPGR, New Delhi
4	EC-305672	NBPGR, New Delhi
5	EC-305675	NBPGR, New Delhi
6	EC-305664	NBPGR, New Delhi
7	EC-305653	NBPGR, New Delhi
8	EC-305612	NBPGR, New Delhi
9	EC-305741	NBPGR, New Delhi
10	EC-305714	NBPGR, New Delhi
11	Punjab-8	NBPGR, New Delhi
12	IC-293590	NBPGR, New Delhi

**Table 2:** Analysis of variances

Source of Variation	Days to 50% Flowering	No days to 1st Harvest	No. of node at 1st flowering	Number of Fruits / Plant	Fruit Weight (g)	Fruit Length (cm)	Fruit Diameter (cm)	No of Ridges / fruit	No of Nodes / plant
Replication	1.73	1.73	0.32	0.15	0.04	0.04	0.01	0.00	0.20
Genotypes	3.85**	3.88**	0.23**	0.31**	1.80**	0.58**	0.02**	0.21**	0.49**
Error	0.85	1.64	0.03	0.46	0.28	0.10	0.00	0.00	0.05

Source of Variation	Plant Height (cm)	No of Branches / plant	Inter nodal Length (cm)	No of Seeds / Fruit	100 Seed wt (g)	Yield/Plant (g)	Pod Borer Infestation (%)	Incidence of YVMV
Replication	3.75	0.01	0.00	114.94	0.34	6.90	0.05	2.46
Genotypes	98.44**	0.07**	0.56**	89.59**	0.97**	1638.88**	10.49**	9.24**
Error	3.85	0.00	0.09	4.28	0.06	6.37	0.35	0.20

**Table 3:** Mean performance of parents and hybrid for yield and yield attributing traits

S.N	Genotypes	Days to 50% Flowering	No days to 1st Harvest	No. of node at 1st flowering	Number of Fruits / Plant	Fruit Weight (g)	Fruit Length (cm)	Fruit Diameter (cm)	No of Ridges / fruit	No of Nodes / plant
1	EC305613	44.5	51.5	3.0	13.5	8.5	10.3	1.5	5.0	11.2
2	EC305652	45.0	50.0	3.0	16.5	11.5	10.2	1.8	5.0	11.1
3	EC305689	43.5	49.5	3.5	13.5	8.7	10.4	1.8	6.0	10.3
4	EC305672	46.0	53.0	2.8	14.5	9.8	10.1	1.7	5.0	9.9
5	EC305675	44.5	51.0	3.4	17.4	10.4	10.0	1.7	5.0	10.5
6	EC305664	47.0	53.0	3.5	13.8	11.3	10.3	1.7	5.0	11.0
7	EC305653	44.5	49.5	3.7	17.5	10.3	10.1	1.8	5.0	10.5
8	EC305612	47.0	53.0	3.4	17.1	10.2	10.9	1.6	5.0	10.2
9	EC305741	49.5	55.0	3.5	10.0	10.9	9.3	1.7	6.0	10.2
10	EC305714	44.0	48.5	3.4	11.3	10.3	9.4	1.6	5.0	9.9
11	Punjab-8	44.0	50.0	3.9	16.1	10.8	11.1	1.7	5.0	10.9
12	IC-293590	46.0	52.0	3.8	17.1	10.4	10.6	1.8	5.0	10.3
13	IC293590 X EC305714	46.5	51.0	3.7	12.5	10.3	10.5	1.8	5.0	10.5
14	IC293590 X EC305652	43.5	48.5	3.6	17.3	11.4	10.8	2.0	5.0	11.6
15	IC293590 X EC305689	45.5	51.0	4.0	13.5	9.1	10.9	1.8	5.0	10.9
16	IC293590 X EC305612	46.0	51.5	4.1	16.4	11.2	11.3	1.8	5.0	10.3
17	IC293590 X EC305672	45.5	51.0	3.5	16.5	9.3	10.6	1.8	5.0	10.2
18	IC293590 X EC305653	44.0	50.0	4.0	17.5	10.7	10.5	1.8	5.0	10.4
19	IC293590 X EC305613	46.5	51.5	3.6	14.0	8.9	10.8	1.8	5.0	10.8
20	IC293590 X EC305664	45.5	51.0	3.7	14.9	11.0	10.6	1.9	6.0	10.2
21	IC293590 X EC305741	45.0	50.0	4.0	11.5	10.4	10.9	1.9	5.0	11.3
22	IC293590 X EC305675	45.5	50.5	3.8	17.4	10.8	10.2	1.9	5.0	11.8
23	Punjab 8 x EC305675	43.5	49.5	3.6	17.0	10.9	10.8	1.8	5.0	10.4

S.N	Genotypes	Days to 50% Flowering	No days to 1st Harvest	No. of node at 1st flowering	Number of Fruits / Plant	Fruit Weight (g)	Fruit Length (cm)	Fruit Diameter (cm)	No of Ridges / fruit	No of Nodes / plant
24	Punjab 8 x EC305652	45.5	51.5	3.6	16.8	11.4	11.1	1.8	6.0	11.3
25	Punjab 8 x EC305672	44.5	50.5	3.6	16.4	9.2	10.7	1.8	5.0	10.6
26	Punjab 8 x EC305653	45.5	52.0	4.4	17.8	10.2	10.7	1.8	5.0	10.7
27	Punjab 8 x EC305689	47.5	51.5	4.3	13.5	9.5	11.1	1.8	5.0	11.2
28	Punjab 8 x EC305612	44.5	50.5	4.0	15.9	11.1	11.7	1.9	5.0	11.3
29	Punjab 8 x EC305664	44.5	51.5	3.7	14.8	11.6	11.8	1.9	5.0	10.9
30	Punjab 8 x EC305613	43.5	49.5	3.7	13.0	9.9	10.9	1.8	5.0	11.1
31	Punjab 8 x EC305741	43.5	49.5	3.6	10.2	11.0	10.3	1.8	5.0	10.2
32	Punjab 8 x EC305714	43.5	49.0	3.6	11.5	9.9	11.1	1.9	5.0	10.2
33	Mahyco bhindi No -10 (hybrid)	43.5	49.5	3.9	15.2	9.0	9.8	1.9	5.0	10.9
34	Pusa sawani	45.5	51.5	3.8	16.1	8.0	10.4	1.8	5.0	10.6
35	Parbhani Kranti	46.5	51.5	4.2	16.5	9.3	10.8	1.8	5.0	10.2
	Grand Mean	45.2	50.8	3.7	15.0	10.2	10.6	1.8	5.1	10.7
	SE $\pm$	0.65	0.91	0.12	0.48	0.37	0.22	0.02	0	0.15
	CD @ 5%	1.87	2.6	0.33	1.38	1.07	0.64	0.05	0	0.44
	Cd @ 1%	2.51	3.49	0.44	1.85	1.44	0.85	0.06	0	0.59

S.N	Genotypes	Plant Height (cm)	No of Branches / plant	Inter nodal Length (cm)	No of Seeds / Fruit	100 Seed wt (g)	Yield / Plant (g)	Pod Borer Infestation (%)	Incidence OF YVMV
1	EC305613	102.5	1.3	9.0	37.6	7.1	112.5	5.2	9.5
2	EC305652	104.0	1.2	9.5	49.8	7.5	191.0	6.7	8.5
3	EC305689	113.0	1.3	10.1	35.7	6.2	115.0	7.7	8.6
4	EC305672	95.7	1.2	9.7	38.5	7.2	142.8	9.4	8.6
5	EC305675	101.5	1.1	9.7	45.3	7.3	181.4	2.9	9.4
6	EC305664	96.9	1.5	8.9	48.3	7.2	153.9	5.0	4.4
7	EC305653	99.0	1.2	9.4	43.5	8.1	180.1	5.1	5.8
8	EC305612	99.0	1.3	9.8	36.4	7.2	171.3	6.0	6.6
9	EC305741	99.5	1.5	9.9	50.4	7.2	106.5	8.4	7.6
10	EC305714	94.5	1.5	9.5	32.5	5.4	117.5	4.6	9.5
11	Punjab-8	109.3	1.4	10.1	35.8	6.4	176.6	8.3	4.6
12	IC-293590	97.0	1.1	9.5	44.6	6.4	172.7	5.8	5.5
13	IC293590 X EC305714	98.0	1.6	9.3	42.8	6.1	128.0	7.3	5.6
14	IC293590 X EC305652	117.8	1.6	10.1	51.3	7.3	193.7	4.9	7.5
15	IC293590 X EC305689	108.5	1.5	9.9	35.3	7.2	122.0	3.8	8.7
16	IC293590 X EC305612	102.6	1.5	9.9	43.7	5.3	177.0	7.1	4.1
17	IC293590 X EC305672	101.5	1.6	9.9	48.3	6.8	149.5	11.0	6.1
18	IC293590 X EC305653	106.0	1.4	10.2	45.5	7.3	186.1	10.8	7.0
19	IC293590 X EC305613	108.0	1.4	9.9	49.8	5.3	122.2	9.7	7.5
20	IC293590 X EC305664	99.0	1.5	9.8	35.1	6.2	160.7	5.9	8.9
21	IC293590 X EC305741	103.3	1.7	9.2	49.1	6.4	120.5	10.0	5.6
22	IC293590 X EC305675	106.6	1.7	9.0	48.3	5.5	185.8	4.4	9.2
23	Punjab 8 x EC305675	114.5	1.3	11.1	34.4	6.4	184.4	5.8	8.6
24	Punjab 8 x EC305652	113.5	1.7	10.1	41.9	6.2	191.7	6.3	7.2
25	Punjab 8 x EC305672	109.0	1.5	10.3	32.7	6.4	147.6	7.4	7.8
26	Punjab 8 x EC305653	113.0	2.0	10.6	45.8	7.1	182.7	4.4	9.5
27	Punjab 8 x EC305689	119.0	1.7	10.7	41.8	6.3	125.0	4.5	8.6
28	Punjab 8 x EC305612	122.5	1.4	10.9	52.9	7.0	175.6	6.7	5.8
29	Punjab 8 x EC305664	112.0	1.5	10.3	55.9	6.8	167.0	4.9	6.4
30	Punjab 8 x EC305613	112.0	1.5	10.2	45.4	7.2	122.1	9.3	4.2
31	Punjab 8 x EC305741	105.2	1.7	10.5	58.4	5.4	113.5	10.1	2.6
32	Punjab 8 x EC305714	104.0	1.5	10.3	44.4	6.6	123.5	11.7	4.3
33	Mahyco bhindi No -10 (hybrid)	106.2	1.4	10.3	50.7	6.8	146.5	9.6	6.7
34	Pusa sawani	110.7	1.6	10.5	45.9	7.2	128.1	6.6	13.5
35	Parbhani Kranti	103.5	1.7	9.9	47.4	6.6	152.0	6.5	7.0
	Grand Mean	105.9	1.5	9.9	44.1	6.6	152.2	7.0	7.2
	SE $\pm$	1.39	0.03	0.22	1.46	0.18	1.78	0.42	0.32
	CD @ 5%	3.99	0.09	0.62	4.2	0.52	5.13	1.2	0.92
	Cd @ 1%	5.35	0.12	0.84	5.64	0.71	6.89	1.61	1.23

**Table 4:** Estimates of genetic variability

Characters	Grand Mean	Genotypic Variance	Phenotypic Variance	Genotypic Coefficient of Variance	Phenotypic Coefficient of Variance	Heritability (bs)	Genetic Advance	Genetic Advance as Percent of Mean
Days to 50% Flowering	45.2	1.50	2.35	2.71	3.39	64.00	2.02	4.47
No days to 1st Harvest	50.8	1.12	2.76	2.08	3.27	41.00	1.39	2.73
No. of node at 1st flowering	3.7	0.10	0.13	8.67	9.74	79.00	0.58	15.91
Number of Fruits / Plant	15.0	4.93	5.38	14.82	15.50	91.00	4.37	29.20
Fruit Weight (g)	10.2	0.76	1.04	8.57	10.00	73.00	1.54	15.11
Fruit Length (cm)	10.6	0.24	0.34	4.65	5.51	71.00	0.86	8.08
Fruit Diameter (cm)	1.8	0.01	0.01	4.86	5.02	94.00	0.17	9.70
No of Ridges / fruit	5.1	0.10	0.10	6.31	6.31	100.00	0.67	13.00
No of Nodes / plant	10.7	0.22	0.27	4.39	4.84	82.00	0.87	8.21
Plant Height (cm)	105.9	47.30	51.14	6.49	6.75	92.00	13.62	12.86
No of Branches / plant	1.5	0.04	0.04	12.95	13.30	95.00	0.38	25.97
Inter nodal Length (cm)	9.9	0.24	0.33	4.89	5.78	72.00	0.85	8.52
No of Seeds / Fruit	44.1	42.66	46.93	14.79	15.52	91.00	12.83	29.05
100 Seed wt (g)	6.6	0.45	0.52	10.17	10.88	87.00	1.30	19.60
Yield/Plant (g)	152.2	816.25	822.62	18.77	18.85	99.00	58.63	38.52
Pod Borer Infestation(%)	7.0	5.07	5.42	32.35	33.45	94.00	4.49	64.46
Incidence Of YVMV	7.2	4.52	4.72	29.73	30.39	96.00	4.28	59.90

### Conclusion

Generally, significant genetic variability in the considered character in okra genotypes was observed and this shall be used as important input for the future crop improvement. It is revealed that from these results new okra genotypes can be developed to increase the production and productivity.

### References

- Burton GW. Quantitative inheritance in grasses. Proc. 6<sup>th</sup> Int. Grassland Cong. 1952;1:227-283.
- Falconer DS. Introduction to Quantitative Genetics. 2nd edition. Longman Inc. New York; c1960. p. 1-340.
- Johnson HW, Robinson HF, Comstock RI. Estimates of Genetic and environmental variability in soybean, Agronomy Journal. 1955a;47(2):314-318.
- Kumar A, Kumar M, Sharma VR, Singh MK, Singh B, Chand P. Genetic Variability, Heritability and Genetic Advance studies in Genotypes of Okra [*Abelmoschus esculentus* (L.) Moench]. Journal of Pharmacognosy and Phytochemistry. 2019;8(1):1285-1290.
- Kumari A, Singh VK, Kumari M, Kumar A. Genetic Variability, Correlation and Path coefficient analysis for Yield and Quality traits in Okra [*Abelmoschus esculentus* (L.) Moench]. International Journal Current Microbiology Applied Sci. 2019;8(6):918-926
- Mudhalvan S, Kumar NS. Studies on genetic divergence for fruit yield and Its component traits in Okra [*Abelmoschus esculentus* (L.) Moench] genotypes under coastal eco- system. Plant Archives. 2018;18(2):1598-1602.
- PhaniKrishna MP, Begum H, Rao AM, Kumar NS. Estimation of heritability and genetic advance in Okra [*Abelmoschus esculentus* (L.) Moench.]. Plant Archives. 2015;15(1):489-491.
- Rambabu B, Waskar DP, Khandare VS. Genetic Variability, Heritability and Genetic Advance in Okra. International Journal Pure Applied Bioscience. 2019;7(1):374-382.
- Syfullah K, Sani MNH, Nasif SO, Parvin S, Rony MMH, Islam MS *et al.* Genetic Variability, Heritability, Character Association and Morphological Diversity in Okra (*Abelmoschus esculentus* L. Moench). International Journal of Plant and Soil Science. 2018;25(6):1-11.
- Thulasiram LB, Bhople SR, Srikanth M, Nayak BR. Genetic variability and heritability studies in Okra (*Abelmoschus esculentus* (L.) Moench). Plant Archives. 2017;17(2):907-910.
- Ivanov S, Burnaev E. Anonymous walk embeddings. In International conference on machine learning. 2018 Jul 3;2186-2195. PMLR.