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Estimating genetic variability, heritability and genetic advance for yield and yield contributing traits in okra (*Abelmoschus esculentus* (L.) Moench) genotype

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Abstract

The present investigation was carried out to evaluate genetic variability, heritability, and genetic advance in thirty-six diverse genotypes of okra for yield and yield-contributing characters at the experimental research farm of the Breeder Seed Production Unit, VNMKV, Parbhani (M.S.) during *kharif* 2022. The analysis of variance shows a significant amount of variability among genotypes of okra for all characters studied. Genetic variability analysis revealed a high magnitude of genetic variability for the traits, viz., plant height and pod yield per plant. As genetic variability in any crop is pre-requisite for the selection of superior genotypes over the existing cultivars, it is effective for the selection of an appropriate breeding strategy for evolving superior varieties. A high percent of genotypic co-efficient of variation (>20%) was observed for the number of ridges per fruit, yield per plant and percent of incidences of YVMV. The estimates of heritability in a broad sense range from 13.3% for fruit diameter to 99.9% for the number of ridges per fruit. While high heritability accompanied by high genetic advance was recorded for the characters plant height, internodal length, number of ridges per fruit, fruit weight, fruit length, leaf area, number of seeds per fruit, 100 seed weight, percent pod borer infestation, percent incidence of YVMV and yield per plant, it indicated the prevalence of additive gene effects, and thus selection for these characters in genetically diverse material would be effective for desired genetic improvement.

Keywords: Okra, co-efficient of variation, genetic variability, heritability, genetic advance

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench], an herbaceous, hairy annual plant, is predominantly grown in tropical, subtropical, and temperate zones across the world. India is also considered its native place, as ancestral wild forms have been found here. India leads the globe in okra production, contributing 72 percent of world production and producing okra on an area of 546 thousand ha with a production of 6700 thousand metric tonnes and a productivity of 12.27 metric tonnes/ha. As per FAO estimates, around 75 percent of the okra market is in India, and 12 percent is in Nigeria. The top 5 trading partners of India are Singapore, United Kingdom, United Arab Emirates, Qatar, and Canada. In fact, almost 84% of India's total okra exports come from this source. Middle East countries like Kuwait, Bahrain, and Oman are emerging as potential markets for okra exports (APEDA, 2021).

The cultivated species *Abelmoschus esculentus* is an amphidiploid (29T + 36Y) with 2n = 130 chromosomes and a genome size range of 3897 Mb to 17321 Mb. Eight *Abelmoschus* species occur in India; out of those four, *A. esculentus* and *A. caillei* (West African okra) are grown for their fruits (used as vegetables), *A. manihot* (aibika) as a leaf vegetable, and *A. moschatus* (ambrette, musk mallow) for its aromatic seeds and other uses for ornamental purposes (Hinsley, 2022) [1]. The mature dried seed of okra is roasted, grounded, and used as a caffeine-free substitute for coffee in Turkey (Calisir *et al.*, 2005) [7]. The okra bast fibre isolated values are 67.5% a-cellulose, 15.4% hemicellulose, 7.1% lignin, 3.4% pectin, 3.9% fatty and waxy matter, and 2.7% aqueous extract (Alam and Khan, 2007) [2]. It is bright, shiny, and sufficiently strong to be spun into yarn and is also used in the paper industry. The Okra Enation Leaf Curl Virus is emerging as a serious threat, and can inflict a yield penalty of about 30–100% in okra. Therefore, crop improvement programmes are needed to develop okra varieties with high yield potential, dwarfness, earliness, good nutritional quality, and multiple resistances or tolerances against viral diseases and pests, which may fit in an intensive cropping system for boosting okra production.

Genetic improvement of any crop mainly depends on the amount of genetic variability present in the population, and the germplasm serves as a crucial source of the base population and

provides scope for wide variability. Heritability is the heritable portion of phenotypic variance. It offers an evaluation of a character's transmission from parent to offspring. A higher heritable variance means a greater probability of character enhancement through selection. Heritable variation can be effectively used with a greater degree of accuracy when heritability is studied in conjunction with genetic advancement (Johnson *et al.* 1955) [12]. The extent of variability present in the crop becomes a prerequisite as it provides the basis for effective selection of desirable genotypes, which are needed for further planning and execution of crop improvement initiatives to obtain high-yielding varieties. The coefficient of variation is relevant in the assessment of the degree of genetic variability for a specific trait in a base population. It is essential to differentiate the overall variation into genetic and non-genetic components and to standardize this by determining the coefficients of phenotypic and genotypic variability. Heritability denotes the proportion of phenotypic variation due to genotypes, which helps the breeders select the elite variety for a character. However, it fails short of revealing the anticipated genetic gain in a single selection cycle. Genetic advance denotes the improvement in the mean genotypic values of selected families over the base population and thus helps breeders select the progenies in the earlier generation itself.

The foremost goal of every crop improvement effort is to

enhance economic yield, which is a complex and dependent trait that is mostly inherited quantitatively and is governed by a number of yield-contributing characteristics that are greatly influenced by environmental variables. In order to assess the potential of genetically distinct lines and cultivars, breeders need to look for a variety of yield-influencing features. The genotype-environment interaction complicates the accurate assessment of these traits. Therefore, the present investigation was undertaken to discover potential okra genotypes based on morphological traits.

Materials and Methods

The workflow of the present research, entitled "heterosis and combining ability studies for yield and yield contributing characters in okra [*Abelmoschus esculentus* (L.) moench]" was conducted on the experimental field of Breeder Seed Production Unit, VNMKV, Parbhani during *kharif* 2022.

Experimental Material: The experimental material for this proposed research work comprised 10 parents among which 6 promising lines and 4 testers (Table-1) were obtained from NBPGR, New Delhi and their 24 F₁ hybrids along with 2 standard checks (Mahyco Bhindi No-10 and Pusa Sawani). Each 10-parent cross among each other in line x tester mating fashion, to derive 24 F₁ hybrids. A total 36 genotypes were evaluated at the Breeder Seed Production Unit, VNMKV, Parbhani during *kharif* 2022.

Table 1: List of germplasm

Sr. No.	Genotype	Source
1	EC-305612	NBPGR, New Delhi
2	EC-305609	NBPGR, New Delhi
3	EC-305653	NBPGR, New Delhi
4	IC-9856C	NBPGR, New Delhi
5	IC-3340C	NBPGR, New Delhi
6	IC-3769A	NBPGR, New Delhi
7	Parbhani Kranti	V.N.M.K.V. Parbhani
8	IC-3302	NBPGR, New Delhi
9	IC-4328	NBPGR, New Delhi
10	IC-4507	NBPGR, New Delhi

Experimental site and Climate: The experimental research field is located at the main campus of Vasant Rao Naik Marathwada Krishi Vidyapeeth, in Parbhani district of Marathwada region of East-central Maharashtra. The site of experiment is located at 19° 23' North of latitude, 76° 80' East of longitude and 409 meter above the mean sea level. It falls under a sub-tropical climate with extreme summers and medium winters. During the winter season, especially in the months of December and January, temperatures fall as low as 8–10 °C. The temperature rises to 46–48 °C in the months of April and May of the summer season. The mean relative humidity of this area is 75 percent, with an average annual rainfall of 950 mm.

Experimental design and Layout: The experiment was set up in a Randomized Block Design with two replications. Each plot is consisted of two rows of each genotype in each replication with a plant population of 10 in each row at spacing of 30 cm x 60 cm. All the prescribed cultural and plant protection practises were undertaken to raise a healthy crop. The observation were recorded on five competitive

plants of each genotypes in each replication for sixteen quantitative traits: plant height (cm), number of branches per plant, number of nodes per plant, internodal length (cm), number of ridges per fruit, days to 50% flowering, number of fruit per plant, fruit weight (g), fruit length (cm), fruit diameter (mm), leaf area (cm²), number of seeds per fruit, 100 seeds weight (g), pod borer infestation (%), incidence of yellow vein mosaic (%) and yield per plant (g). The analysis of variance (ANOVA) were carried out as suggested by Panse and Sukhatme (1961) [14].

Estimation of variability: The extent of variability present among the genotypes for distinct quantitative traits was measured in terms of range, mean, variances and co-efficient of variation. The genotypic variance, phenotypic variance, environmental variance according to (Lush, 1940). While, magnitude of phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV) and environmental co-efficient of variation (ECV) existing in a particular character was computed by the formula given by (Cockerham, 1963) [10].

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

$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + MSe$$

$$\text{Environmental variance } (\sigma^2e) = MSe$$

Where, r = number of replications, MSg = mean square due to genotype, MSe = mean square due of error

$$\text{GCV}\% = \frac{\sqrt{\sigma^2g}}{\bar{x}}$$

$$\text{PCV}\% = \frac{\sqrt{\sigma^2p}}{\bar{x}}$$

Where, \bar{x} = general mean for the character under consideration. The GCV and PCV estimates were categorized as low (< 10%), moderate (< 10-20%) and high (>20%) Sivasubramaniam and Madhavamanon (1973) [21].

Estimation of heritability: Heritability in broad sense for each trait was calculated according to (Burton and Devane, 1953) [6].

$$h^2(\text{bs}) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

$$h^2(\text{ns}) = \frac{\sigma^2A}{\sigma^2p} \times 100$$

$h^2(\text{bs})$ = Heritability in broad sense, $h^2(\text{ns})$ = heritability in narrow sense, σ^2g = Genotypic variance, σ^2p = Phenotypic variance, σ^2A = Additive genetic variance.

The estimation of broad sense heritability were classified as low (< 50%), moderate (50-70%) and high (>70%) as suggested by Robinson (1966) [20].

Estimation of Genetic advance: Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection. It is calculated with the method suggested by Allard (1960) [3] as.

$$\text{Genetic advance} = K \cdot \sigma p \cdot h^2$$

Where, K = Constant value of 2.06 at 5% selection intensity, σp = Phenotypic standard deviation of the character, h^2 = Heritability of the character

$$\text{GA as percentage of mean} = \frac{GA}{\bar{x}} \times 100$$

Where, GA = Genetic advance, \bar{x} = general mean.

The magnitude of genetic advance as percentage of mean was classified as low (< 10%), moderate (< 10-20%) and high (>20%).

Results and Discussion

Analysis of variance

Analysis of variance revealed that mean sum of squares due to

genotypes was found to be highly significant at 1% and 5% level of significance (Table-2) for all the sixteen quantitative characters *viz.*, plant height (393.829 **), number of branches per plant (0.058 **), number of nodes per plant (1.387 **), internodal length (1.408 **), number of ridges per fruit (4.118 **), days to 50% flowering (8.039 **), number of fruits per plant (5.021 **), fruit weight (8.008 **), fruit length (4.982 **), fruit diameter (0.028 **), leaf area (142.752 **), number of seeds per fruit (269.205 **), 100 seed weight (2.317 **), percent pod borer infestation (16.216 **), percent incidences of YVMV (2.535 **) and yield per plant (5766.640 **) indicating the existence of sufficient amount of variability among genotypes and there are ample scope for improvement via effective selection. The similar findings were previously reported for fruit yield and other yield attributing traits in okra by Awasthi *et al.* (2022) [5], Sravanthi *et al.* (2021) [23], Alam *et al.* (2020) [1] and Verma *et al.* (2018) [26].

Table 2: Analysis of variance (ANOVA)

Sr. No.	Characters	Mean Sum of Squares		
		Replication	Genotypes	Error
	Degree of freedom	1	35	35
1	Plant height (cm)	1.742	393.829 **	8.806
2	Number of branches per plant	0.008	0.058 **	0.032
3	Number of nodes per plants	0.268	1.387 **	0.692
4	Internodal length (cm)	0.045	1.408 **	0.122
5	Number of ridges per fruit	0.000	4.118 **	0.000
6	Days to 50% flowering	13.347	8.039 **	4.404
7	Number of fruits per plant	0.005	5.021 **	0.970
8	Fruit weight (g)	0.055	8.008 **	0.622
9	Fruit length (cm)	1.445	4.982 **	0.358
10	Fruit diameter (mm)	0.007	0.028 **	0.015
11	Leaf area (cm ²)	6.540	142.752 **	4.966
12	Number of seeds per fruit	0.642	269.205 **	5.463
13	100 seed weight (g)	0.142	2.317 **	0.194
14	Pod borer infestation (%)	0.320	16.216 **	0.822
15	Incidence of YVMV (%)	0.045	2.535 **	0.361
16	Yield per plant (g)	0.802	5766.640 **	18.554

** Significant at 1 percent level of probability or level of significance

Mean performance of the genotypes

The values for simple measures of variability like mean and range of all the genotypes for yield and its contributing characters are presented in (Table-3). The range of mean values could present a rough estimate about the variation in the magnitude of variability present among genotypes. The characters showing high range of variation have more scope for improvement. The parent EC-305609 (134.0) and cross combinations EC-305612 x IC-3302 (133.9), EC-305612 x Parbhani Kranti (132.5) was recorded significantly high plant height. The parent EC-305609 (2.0) and cross EC-305609 x Parbhani Kranti (2.1), EC-305609 x IC-4507 (2.0) and EC-305612 x Parbhani Kranti (1.9) produces significantly a greater number of branches per plant. The parent EC-305609 (16.3) and cross EC-305609 x IC-4507 (16.8) recorded significantly maximum number of nodes per plant. The parent EC-305612 (8.5), cross combinations EC-305612 x IC-3302 (8.6), EC-305609 x IC-4328 (8.6) and EC-305609 x IC-3302 (8.5) showed maximum internodal length. The parent IC-3340C (10.5) and cross combinations IC-3340C x IC-3302 (9.0) and IC-3340C x IC-4328 (8.0) was recorded significantly maximum number of ridges per fruit. The parent EC-305609 (43.5 days) and cross EC-305609 x Parbhani

Kranti (43.0 days), followed by EC-305609 x IC-4507 (43.5 days), was found to be the earliest for 50% flowering. Among parents EC-305609 (17.3) recorded maximum number of fruits per plant, Among the cross combinations, EC-305609 x Parbhani Kranti (17.2), followed by EC-305609 x IC-4507 (17.1), and EC-305612 x IC-4507 (16.7) produced maximum number of fruits. The parent EC-305609 (19.2 g) showed maximum weight while among the hybrids, the cross EC-305609 x Parbhani Kranti (19.8 g) and EC-305609 x IC-4507 (19.6 g) produces significantly maximum weight. Among the parents EC-305609 (17.0 cm), recorded maximum length of fruit, cross EC-305609 x Parbhani Kranti (17.8 cm) recorded significantly maximum length of fruit. Among the parents IC-3340C (2.05 mm) recorded recorded maximum diameter of fruit, cross IC-3340C x Parbhani Kranti (2.05 mm), followed by IC-9856C x IC-4328 (2.00 mm), recorded significantly maximum diameter of fruit. The parent IC-9856C (68.8), recorded for maximum leaf area, cross EC-305653 x Parbhani Kranti (71.4) recorded significantly maximum leaf area. The parent EC-305609 (80.1) was observed comparatively maximum number of seed per fruit, cross EC-305609 x

Parbhani Kranti (89.0) and EC-305609 x IC-4507 (86.0) produces significantly a greater number of seed per fruit. Among the parents EC-305609 (7.6 g), recorded for significantly maximum 100 seed weight, cross EC-305609 x Parbhani Kranti (8.1 g) recorded maximum 100 seed weight. The parent EC-305609 (15.2%) recorded significantly minimum of pod borer infestation, among the hybrids EC-305609 x Parbhani Kranti (13.0%) recorded significantly lowest incidence of pod borer infestation. The parent EC-305609 (4.8%) recorded significantly minimum percent incidence of yellow vein mosaic virus than the rest of the parents, Among the hybrids, EC-305609 x Parbhani Kranti (3.7%) recorded significantly minimum incidence of yellow vein mosaic virus than the rest of crosses. Parent EC-305609 (332.8 g) was produced significantly higher yield per plant, The cross-combination EC-305609 x Parbhani Kranti (343.0 g) followed by EC-305609 x IC-4507 (334.2 g) were recorded for the significantly higher fruit yield per plant. These finding agree with previous report of Awasthi *et al.* (2022) [5], Vani *et al.* (2021) [25], Priyanka *et al.* (2018) [16].

Table 3: The mean performance of parents and hybrids for sixteen yield and yield contributing traits in Okra

S. N.	Genotypes	Plant height (cm)	Number of branches per plant	Number of nodes per plants	Internodal length (cm)	Number of ridges per fruit	Days to 50% flowering	Number of fruits per plant	Fruit weight (g)
1	EC-305612	121.5	1.8	14.3	8.5	5.0	44.5	16.4	18.6
2	EC-305609	134.0	2.0	16.3	8.3	5.0	43.5	17.3	19.2
3	EC-305653	116.3	1.6	16.2	7.2	5.0	46.0	15.4	17.4
4	IC-9856C	98.4	1.5	14.8	6.5	8.0	48.0	14.0	14.2
5	IC-3340C	89.5	1.4	15.2	5.7	10.5	48.5	11.9	13.2
6	IC-3769A	125.5	1.7	15.3	8.0	5.0	45.0	16.7	18.0
7	Parbhani Kranti	106.4	1.6	14.3	7.2	5.0	47.0	13.8	15.6
8	IC-3302	102.8	1.5	15.7	6.4	5.0	47.5	13.2	15.0
9	IC-4328	94.5	1.4	13.6	6.8	5.0	51.0	10.8	13.1
10	IC-4507	110.3	1.6	14.6	7.4	5.0	46.5	15.0	16.8
11	EC-305612 x PrabhaniKranti	132.5	1.9	15.4	8.5	5.0	45.5	15.6	17.6
12	EC-305609 x Prabhani Kranti	125.4	2.1	15.9	7.9	5.0	43.0	17.2	19.8
13	EC-305653 x Parbhani Kranti	123.3	1.7	16.4	7.5	5.0	47.0	15.4	16.5
14	IC-9856C x Parbhani Kranti	115.6	1.7	15.4	7.4	8.0	47.0	14.0	15.2
15	IC-3340C x Parbhani Kranti	112.4	1.6	15.9	7.0	7.0	47.5	13.1	15.0
16	IC-3769A x Parbhani Kranti	129.8	1.8	15.8	8.1	5.0	45.5	16.4	18.6
17	EC-305612 x IC-3302	133.9	1.7	15.4	8.6	5.0	46.0	15.5	17.0
18	EC-305609 x IC-3302	130.8	1.8	15.3	8.5	5.0	45.0	16.5	18.7
19	EC-305653 x IC-3302	98.4	1.6	14.9	6.6	5.0	45.5	14.6	16.8
20	IC-9856C x IC-3302	93.9	1.7	15.9	5.8	8.0	47.0	13.8	14.8
21	IC-3340C x IC-3302	103.8	1.6	15.4	6.7	9.0	48.0	13.2	14.4
22	IC-3769A x IC-3302	106.5	1.7	16.1	6.5	5.0	46.5	15.2	17.8
23	EC-305612 x IC-4328	95.5	1.6	13.7	6.9	5.0	47.0	14.2	16.8
24	EC-305609 x IC-4328	127.6	1.7	14.8	8.6	5.0	46.5	15.1	16.5
25	EC-305653 x IC-4328	102.2	1.6	15.1	6.7	5.0	48.0	14.0	15.8
26	IC-9856C x IC-4328	97.7	1.5	16.1	6.0	7.0	51.0	12.6	14.0
27	IC-3340C x IC-4328	101.6	1.5	14.4	7.0	8.0	51.5	12.1	13.4
28	IC-3769A x IC-4328	92.6	1.7	15.9	5.8	5.0	49.5	14.4	16.5
29	EC-305612 x IC-4507	123.3	2.0	16.4	7.5	5.0	44.0	16.7	18.8
30	EC-305609 x IC-4507	131.5	2.0	16.8	7.8	5.0	43.5	17.1	19.6
31	EC-305653 x IC-4507	109.3	1.8	14.7	7.4	5.0	46.0	15.6	17.2
32	IC-9856C x IC-4507	101.4	1.7	14.8	6.8	6.0	47.0	14.7	16.2
33	IC-3340C x IC-4507	98.5	1.6	15.2	6.5	7.0	47.0	13.6	16.0
34	IC-3769A x IC-4507	127.0	1.9	16.4	7.7	5.0	45.0	16.0	19.4
35	Mahyco Bhindi No -10 (hybrid)	113.3	1.9	16.9	6.6	6.0	48.0	15.6	19.3
36	Pusa Sawani	99.2	1.7	14.3	6.8	5.0	46.5	15.0	13.1
	Grand Mean	112.1	1.6	15.3	7.2	5.8	46.6	14.7	16.5
	SE± (m)	2.08	0.12	0.60	0.24	0.01	1.46	0.69	0.56
	CD @ 5%	6.02	0.37	1.70	0.70	0.05	4.21	2.00	1.63
	CD @ 1%	8.10	0.49	2.30	0.94	0.06	5.66	2.69	2.19

SN	Genotypes	Fruit length (cm)	Fruit diameter (mm)	Leaf area (cm ²)	Number of seeds per fruit	100 seed weight (g)	Pod borer infestation (%)	Incidence of YVMV (%)	Yield per plant (g)
1	EC-305612	16.2	1.70	64.9	69.0	6.6	17.0	5.1	305.0
2	EC-305609	17.0	1.80	67.4	80.1	7.6	15.2	4.8	332.8
3	EC-305653	15.8	1.70	62.7	61.0	5.6	18.8	6.0	268.2
4	IC-9856C	13.0	1.90	68.8	55.0	4.8	22.1	7.2	198.4
5	IC-3340C	11.6	2.05	48.5	52.0	4.1	25.4	8.5	157.8
6	IC-3769A	16.6	1.60	49.1	73.0	6.9	18.0	5.9	301.4
7	Parbhani Kranti	13.8	1.70	47.5	56.0	5.8	14.2	4.4	215.2
8	IC-3302	13.2	1.80	43.5	51.0	5.2	21.6	6.7	201.0
9	IC-4328	11.2	1.80	42.5	46.0	3.9	23.8	7.8	140.2
10	IC-4507	15.0	1.70	48.8	59.0	6.4	19.5	6.4	252.3
11	EC-305612 x Parbhani Kranti	16.3	1.75	65.5	65.0	7.2	15.5	4.4	274.1
12	EC-305609 x Parbhani Kranti	17.8	1.90	64.9	89.0	8.1	13.0	3.7	343.0
13	EC-305653 x Parbhani Kranti	15.4	1.75	71.4	63.0	7.0	16.1	4.8	256.2
14	IC-9856C x Parbhani Kranti	14.6	1.90	65.8	57.0	5.9	18.0	5.8	212.8
15	IC-3340C x Parbhani Kranti	13.4	2.05	53.5	55.0	5.6	19.1	6.2	196.5
16	IC-3769A x Parbhani Kranti	16.2	1.80	56.1	78.0	7.4	15.3	4.3	304.0
17	EC-305612 x IC-3302	14.9	1.80	57.0	67.0	7.1	15.9	4.6	264.0
18	EC-305609 x IC-3302	16.7	1.80	60.5	81.0	7.6	15.0	4.2	308.4
19	EC-305653 x IC-3302	15.0	1.85	56.0	60.0	6.7	16.9	5.2	246.6
20	IC-9856C x IC-3302	14.0	2.05	71.0	56.0	5.6	18.4	6.1	204.3
21	IC-3340C x IC-3302	13.6	1.95	49.3	53.0	5.1	19.8	6.4	190.4
22	IC-3769A x IC-3302	15.6	1.85	53.8	76.0	7.2	15.9	4.6	266.2
23	EC-305612 x IC-4328	15.8	1.75	55.9	59.0	6.5	17.5	5.7	238.0
24	EC-305609 x IC-4328	15.2	1.90	58.0	61.0	6.9	16.4	5.0	250.4
25	EC-305653 x IC-4328	14.3	1.75	54.6	54.0	6.3	17.8	5.6	221.2
26	IC-9856C x IC-4328	12.8	2.00	67.6	52.0	5.2	20.2	6.5	178.3
27	IC-3340C x IC-4328	13.4	1.90	47.6	51.0	4.8	21.4	6.7	162.4
28	IC-3769A x IC-4328	14.8	1.75	52.0	60.0	6.7	17.2	5.4	238.8
29	EC-305612 x IC-4507	16.8	1.90	70.0	83.0	7.8	14.0	4.1	314.6
30	EC-305609 x IC-4507	17.4	1.90	70.6	86.0	8.0	13.4	3.9	334.2
31	EC-305653 x IC-4507	16.0	1.75	59.1	69.0	7.2	15.7	4.5	270.2
32	IC-9856C x IC-4507	15.7	1.90	65.3	58.0	6.5	17.5	5.5	238.4
33	IC-3340C x IC-4507	13.8	1.85	53.1	56.0	6.1	17.9	5.7	219.0
34	IC-3769A x IC-4507	16.5	1.85	62.2	80.0	7.6	14.6	4.1	310.8
35	Mahyco bhindi No -10 (hybrid)	14.2	1.90	69.0	78.0	5.7	15.8	4.5	301.1
36	Pusa Sawani	14.3	1.60	61.8	57.0	6.5	19.0	5.5	200.2
	Grand Mean	14.9	1.83	58.3	63.8	6.3	17.5	5.46	247.5
	SE± (m)	0.42	0.09	1.60	1.65	0.31	0.64	0.42	3.04
	CD @ 5%	1.23	0.25	4.52	4.74	0.89	1.84	1.22	8.74
	CD @ 1%	1.65	0.34	6.12	6.39	1.20	2.48	1.64	11.78

GCV and PCV

The genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in a broad sense, and genetic advance are depicted in (Table-4) respectively. The coefficient of variation (CV) unveiled significant genetic variation in various agro-economic traits. The measure of coefficient of variation is an essential tool in the comparison of variation in a set of data with multiple units. Moreover, a high CV implies dispersion in the variable.

In the present investigation, the high estimates of phenotypic co-efficient of variation (>20%) were observed for number of ridges per fruit (25.19), percent incidences of YVMV (22.42) and yield per plant (21.80). While, moderate PCV values (< 10-20%) were observed for plant height (12.86), number of branches per plant (12.70), internodal length (12.28), number of fruits per plant (11.99), fruit weight (12.03), fruit length (11.15), leaf area (14.80), number of seeds per fruit (18.37), 100 seed weight (17.93) and percent pod borer infestation (16.93). Furthermore, low PCV values (< 10%) were observed for number of nodes per plant (6.49), days to 50% flowering (5.40) and fruit diameter (7.89). The phenotypic co-efficient of variation (PCV) was higher than the associated

genotypic co-efficient of variation (GCV) for each character studied. The high percent of genotypic coefficient of variation (>20%) were observed for number of ridges per fruit (25.18), percent incidences of YVMV (19.47) and yield per plant (21.73). While, moderate GCV values (< 10-20%) were observed for plant height (12.59), internodal length (11.32), fruit weight (11.01), fruit length (10.39), leaf area (14.28), number of seeds per fruit (18.05), 100 seed weight (16.57) and percent pod borer infestation (16.09). However, low GCV values (< 10%) were observed for number of branches per plant (6.73), number of nodes per plant (3.34), days to 50% flowering (3.07), number of fruits per plant (9.96) and fruit diameter (2.88). The report showed a negligible difference between PCV and GCV for almost all the traits. The relatively small variation between PCV and GCV indicated that there was less environmental impact on character expression, and they had a higher chance of developing these characteristics through direct selection based on phenotypic performance. These similar results were reported by Pundir *et al.* (2022) [17], Vani *et al.* (2021) [25], Rambabu *et al.* (2019) [18], Priyanka *et al.* (2018) [16], Khalid Syfullah *et al.* (2018) [24], Chandramouli *et al.* (2016) [8].

Table 4: Estimates of mean, range, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability (bs)

Sr. No.	Characters	Grand Mean	Range (Min-Max)	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Co-efficient of variation		Heritability in broad sense (h^2_{bs})	Genetic advance	Genetic advance as % of mean
						GCV%	PCV%			
1	Plant height (cm)	112.16	89.5-134.0	199.43	208.22	12.59	12.86	95.7	28.47	25.38
2	Number of branches per plant	1.69	1.4-2.1	0.01	0.04	6.73	12.70	28.1	0.12	7.35
3	Number of nodes per plants	15.36	13.6-16.9	0.26	0.99	3.34	6.49	26.5	0.54	3.55
4	Internodal length (cm)	7.22	5.7-8.6	0.67	0.78	11.32	12.28	84.9	1.55	21.51
5	Number of ridges per fruit	5.83	5.0-10.5	2.16	2.17	25.18	25.19	99.9	3.02	51.87
6	Days to 50% flowering	46.67	43.00-51.5	2.06	6.35	3.07	5.40	32.4	1.68	3.60
7	Number of fruits per plant	14.73	10.8-17.3	2.15	3.12	9.96	11.99	68.9	2.51	17.04
8	Fruit weight (g)	16.57	13.1-19.8	3.33	3.97	11.01	12.03	83.7	3.44	20.76
9	Fruit length (cm)	14.9	11.2-17.4	2.42	2.79	10.39	11.15	86.8	2.99	19.96
10	Fruit diameter (mm)	1.83	1.60-2.05	0.00	0.02	2.88	7.89	13.3	0.03	2.16
11	Leaf area (cm ²)	58.37	42.5-71.4	69.50	74.66	14.28	14.80	93.0	16.57	28.38
12	Number of seeds per fruit	63.85	46.0-89.0	132.96	137.67	18.05	18.37	96.5	23.34	36.55
13	100 seed weight (g)	6.38	3.9-8.1	1.11	1.31	16.57	17.93	85.4	2.01	31.55
14	Pod borer infestation (%)	17.59	13.0-25.4	8.01	8.87	16.09	16.93	90.31	5.54	31.50
15	Incidence of YVMV (%)	5.46	4.4-8.5	1.13	1.50	19.47	22.42	75.43	1.90	34.83
16	Yield per plant (g)	247.50	343.0-140.2	2893.51	2912.97	21.73	21.80	99.3	110.43	44.62

Heritability and Genetic advance

The effectiveness of selection for any character depends not only on the extent of genetic variability but also on the extent to which it will be transferred from one generation to the next. The genotypic and phenotypic coefficients of variation alone do not show the proportion of total heritable variation. Heritability and genetic advance as percent of mean estimates are better indicators in this respect. The data revealed that estimates of heritability in broad sense range from (13.3) for fruit diameter to (99.9) for number of ridges per fruit. High heritability (>70%) were recorded for plant height (95.7), internodal length (84.9), number of ridges per fruit (99.9), fruit weight (83.7), fruit length (86.8), leaf area (93.0), number of seeds per fruit (96.5), 100 seed weight (85.4), percent pod borer infestation (90.31), percent incidences of YVMV (75.43) and yield per plant (99.3). While, moderate heritability (50-70%) were observed number of fruits per plant (68.9). Furthermore, low heritability were obtained for number of branches per plant (28.1), number of nodes per plant (26.5), days to 50% flowering (32.4) and fruit diameter (13.3) denotes high proportion of additive genetic components in the inheritance of these characters. These results are in accordance with the studies of Pundir *et al.* (2022) [17], Ranga *et al.* (2021) [19], Singh *et al.* (2020) [1], Rambabu *et al.* (2019) [18], Phanikrishna *et al.* (2015) [15].

The heritability accompanied with genetic advance as percent mean is more effective in predicting the gain under phenotypic selection than heritability estimates alone. The traits plant height, internodal length, number of ridges per fruit, fruit weight, fruit length, leaf area, number of seeds per fruit, 100 seed weight, percent pod borer infestation, percent incidence of YVMV and yield per plant shows high estimates of heritability accompanied with high genetic advance as percent mean indicating additive gene effect and thus selection for these characters in genetically diverse material would be effective for desired genetic improvement. Similar results were reported by Chetana *et al.* (2021) [9], Walling *et al.* (2020) [27], Rambabu *et al.* (2019) [18], Khalid Syfullah *et al.* (2018) [24], Chandramouli *et al.* (2016) [8], Phanikrishna *et al.* (2015) [15] for genetic advance as percent of mean. The characters number of fruits per plant shows moderate heritability accompanied with moderate genetic advance as

percent mean. While, the number of branches per plant, number of nodes per plants, days to 50% flowering and fruit diameter exhibited low heritability accompanied with low genetic advance as percent mean, it implies that the expression of characters is highly influenced by environmental effects and selection is quite ineffective.

Conclusion

The present investigation revealed that the analysis of variance validated the significance of differences among different genotypes. The traits, *viz.*, plant height, internodal length, number of ridges per fruit, fruit weight, fruit length, leaf area, number of seeds per fruit, 100 seed weight, percent pod borer infestation, percent incidence of YVMV, and yield per plant, which have high heritability coupled with high genetic gain, could be considered effective tools for selection in okra as such traits indicate dominance of additive gene effect. The low-to-high range of heritability, GCV, PCV, and genetic advance as a percent of the mean was recorded for most of the characters. The traits that have the desired value of variability parameters and mean performance can be utilised in further crop improvement initiatives. This study implies that there was significant genetic variability among the okra genotypes studied for different yield and yield-contributing characters.

References

1. Alam K, Singh MK, Kumar M, Singh A, Kumar V, Ahmad M, *et al.* Genetic variability, heritability and genetic advance for selection parameters of genotypes in okra (*Abelmoschus esculentus* (L.) Moench). International Journal of Chemical Studies. 2020;8(6):1016-1022.
2. Alam MS, Khan GA. Chemical analysis of okra bast fiber (*Abelmoschus esculentus*) and its physico-chemical properties. Journal of textile and apparel technology and management. 2007, 5(4).
3. Allard RW. Principles of plant breeding. John Wiley and Sons, New York, U.S.A.; c1960.
4. APEDA. Agricultural and Processed Food Products Export Development Authority. Ministry of Commerce and Industry, New Delhi, India; c2021.

<https://www.apeda.gov.in/>

5. Awasthi S, Singh DP, Lal B, Singh P, Upadhyay A, Singh PK, *et al.* Assessment of Genetic Variability, Heritability and Genetic Advance of Okra Genotypes (*Abelmoschus esculentus* L. Moench). Assessment. 2022;53(04):7501-7512.
6. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy journal. 1953;45(10):478-81.
7. Çalışır S, Özcan M, Haciseferoğulları H, Yıldız MU. A study on some physico-chemical properties of Turkey okra (*Hibiscus esculenta* L.) seeds. Journal of Food Engineering. 2005;68(1), 73-78.
8. Chandramouli B, Shrihari D, Rao AV, Rao MP. Studies on genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench) genotypes. Plant Archives. 2016;16(2):679-82.
9. Chetana MP, Deshmukh JD. Genetic variability, heritability and genetic advance in Okra (*Abelmoschus esculentus* (L.) Moench). The Pharma Innovation Journal. 2021;10(12): 2687-2690.
10. Cockerham CC. Estimation of genetic variances. Statistical genetics and plant breeding. 1963;982:53-94.
11. Hinsley SR. Malvaceae info: *Abelmoschus* notes; c2022.
12. Johnson HW, Robinson HE, Comstock RE. Genotypic and Phenotypic correlation in soybean and their implications Selection. Agron. J. 1955;47(7):477- 485.
13. Lush JL. Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. Journal of animal science. 1940;33(1):293-301.
14. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers, 1st edition, Indian Council of Agricultural Research, New Delhi; c1961.
15. PhaniKrishna M, Hameedunnisa B, Rao AM, Kumar NS. Estimation of heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench.]. Plant archives. 2015;15(1):489-491.
16. Priyanka VM, Reddy T, Begum H, Sunil N, Jayaprada M. Studies on genetic variability, heritability and genetic advance in genotypes of okra [*Abelmoschus esculentus* (L.) moench]. International Journal of Current Microbiology and Applied Sciences. 2018;7(5):401-11.
17. Pundir S, Singh MK, Alam K, Ahmad M. To assess the genetic variability, heritability and genetic advance as percent of mean for selection parameters in Okra [*Abelmoschus esculentus* (L.) Moench]. 2022;11(5):1963-1968
18. Rambabu B, Waskar DP, Khandare VS. Genetic variability, heritability and genetic advance in okra. International Journal of Pure and Applied Bioscience. 2019;7(1):374-82.
19. Ranga AD, Kumar S, Darvhankar MS. Variability among different yield and yield contributing traits of Okra (*Abelmoschus esculentus* L. Moench) genotypes. Electronic Journal of Plant Breeding. 2021;12(1):74-81.
20. Robinson HF. Quantitative genetics in relation to breeding on centennial of Mendelism. The Indian Journal of Genetics and Plant Breeding. 1966;26:171-187.
21. Singh AK, Singh DK, Singh NK, Kushwaha ML, Maurya SK. Genetic analysis in okra under tarai region of Uttarakhand. International Journal of Chemical Studies 2020; 8(1): 2767-2770.
22. Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. The Madras Agricultural Journal.1973;60(9-13):1093-1096.
23. Sravanthi U, Prabhakar BN, Saidaiah P, Rao AM, Narayana DL, Sathish G, *et al.* Studies on genetic variability in okra (*Abelmoschus esculentus* (L.) Moench). The Pharma Innovation Journal. 2021;10(11):151-155.
24. Syfullah K, Sani MN, Nasif SO, Parvin S, Rony MM, Islam MS, *et al.* Genetic variability, heritability, character association and morphological diversity in okra (*Abelmoschus esculentus* L. Moench). International Journal of Plant & Soil Science. 2018;25(6):1-11.
25. Vani VM, Singh BK, Raju SV, Singh AK. Studies on genetic variability, heritability and genetic advance for various quantitative traits in okra [*Abelmoschus esculentus* (L.) Monech] genotypes under north Gangetic plains of Uttar Pradesh. Journal of Pharmacognosy and Phytochemistry. 2021;10(3):272-4.
26. Verma V, Singh B, Singh MK, Singh SK. Studies on genetic variability, heritability and genetic advance in Okra [*Abelmoschus esculentus* (L.) Moench.]. Journal of Pharmacognosy and Phytochemistry. 2018;7(4):1114-1115.
27. Walling N, Kanaujia SP, Alila P, Sharma MB, Ozukum C. Genetic Variability and correlation studies in okra [*Abelmoschus esculentus* (L.) Moench] Genotypes under foothill conditions of Nagaland. International Journal of Recent Scientific Research. 2020;11(2):37651-37654.