

Research Article

Genotypic, phenotypic variability and evaluation of okra [*Abelmoschus esculentus* (L.) Moench] genotypes for yield components

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Abstract

Okra [*Abelmoschus esculentus* (L.) Moench] is India's major vegetable crop, accounting for 60% of exports. Comparatively, Tamil Nadu has a small area of cultivation and production. Hence, the present study involves the utilization of simple measure of variability and genetic variance to develop new varieties. The experiment was conducted with 60 genotypes of okra crop using 20 quantitative traits. The analysis of variance found that genotypes were significant (P 0.05 and P 0.01) for all of the traits tested. The fruit yield plant⁻¹ ranged from 176.40 to 438.40 g, with 347.42 g being the average. In all the traits studied, the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The closeness of PCV and GCV values suggested that the environment had little influence on manifestation of the characters under examination. GCV (1.89-13.98) and PCV (4.06-16.61) levels were found to be moderate (10-20) and low (<10), respectively, in the study. Heritability ranged from 21.73 (days to first fruit harvest) to 97.19 (plant height) percent. At 5% selection intensity, the genetic advance (GA)% mean ranged from 1.82 (days to first fruit harvest) to 27.38 (plant height). Plant height (13.68, 13.48), internodal length (16.61, 13.98), first fruiting node (13.00, 10.89), number of fruits plant⁻¹ (13.19, 11.91), number of marketable fruits plant⁻¹ (13.36, 11.97) and fruit yield plant⁻¹ (13.75, 12.29) showed high heritability and high GA% mean. Thus, the above-mentioned characteristics are additive genetic control and direct selection in okra has good potential for improvement in fruit yield.

Keywords: Genetic advance % mean, Genotypic coefficient of variation, Heritability, Okra, Phenotypic coefficient of variation

INTRODUCTION

Vegetables are critical components of Indian agriculture and food security because of their short growing season, high fruit production, nutritional value, economic viability, and potential to produce on- and off-farm jobs (Kumar, 2020). Okra or Bhendi [*Abelmoschus esculentus* (L.) Moench] is India's significant, nutritious vegetable crop within the Malvaceae family. Additionally, it is a dicotyledon, warm-season annual vegetable crop with a 90–100 day growing season that succeeds in tropical and subtropical regions of the world (Mohammed *et al.*, 2022; Melaku *et al.*, 2020; Reddy *et al.*, 2013) on sandy to clayey soil, mostly in Africa and Asia. (Oppong-Sekyere *et al.*, 2011, Tripathi *et al.*, 2011). Along with

other fresh veggies, okra accounts for 60% of Indian exports. In India, okra farming covers 528 (000 ha) with a production of 6146 (000 mt), whereas Tamil Nadu covers 12.78 (000 ha) with an output of 88.07 (000 mt). (Anonymous, 2017).

Detailed crop characterization is a critical initial stage in every crop breeding programme (Muluken *et al.*, 2016). Typical characterization gives information on crop collection diversity both within and across collections. Furthermore, information gained on genetic relatedness across crop plant genetic resources is valuable for both breeding and germplasm conservation (Aminu *et al.*, 2016). Characteristics of okra, such as growth, earliness, and yield, are related to being quantitative in nature. Polygenes regulate such traits, which are exten-

sively impacted by environmental changes (Saleem *et al.*, 2018; Reddy *et al.*, 2013). Okra fruit yield is a complex polygenic feature influenced by the interaction of various growth-related and physiological processes throughout the life cycle period (Adekoya *et al.*, 2014). The first fundamental step in any hybridization programme is to examine genetic diversity among available genotypes for desired traits (Rahman *et al.*, 2016). Plant breeders use heritability as a strategy to successfully separate the amount of genetic variation from overall phenotypic variation (Harshawardhan *et al.*, 2016). The finest selection opportunities are provided by strong genetic progress as well as high heritability (Mohammed *et al.*, 2022; Johnson *et al.*, 1955). Knowledge of genetic variability, heritability (bs), and other characteristics aids in the improvement of fruit production via the directed selection of component characteristics and their interaction with yield (Reddy *et al.*, 2013). Successful selection of genetically superior individuals requires considerable phenotypic diversity in the base population as well as strong heritability. As a result, the goal of this study was to measure morphological traits performance and to estimate genetic variability components in okra (*Abelmoschus esculentus* (L.) Moench) genotypes.

MATERIALS AND METHODS

Study area

The experimental study was performed in Sivapuri Village, Chidambaram, Cuddalore District, Tamil Nadu, India, in the summer of 2020–2021.

Experimental material and design

The experiment included 60 distinct genotypes (Table 1) of okra raised in a three-replication randomized complete block design (RCBD). Two to three seeds per hill were dibbled at 60 cm between rows and 30 cm among plants in a row. Thinning was performed on the tenth day, leaving one vigorous and robust seedling per hill. To ensure a healthy crop stand, standard cultural and agronomic practices were undertaken as recommended and need-based plant protection measures.

Observations recorded

Data on quantitative traits were recorded according to the International Plant Genetic Resources Institute (International Plant Genetic Resource Institute, 1991) descriptor list developed for okra. Observations were recorded from five randomly selected plants from each entry of genotype of replications and labelled for data collection, leaving the two plants grown as border plants at both ends of the row. Data for 20 morphological traits, included first flowering node, days to first flower, days to 50% flowering, days to first fruit harvest, fruiting period, plant height (cm), internodal length (cm),

peduncle length (cm), number of branches plant⁻¹, stem diameter (mm), number of nodes plant⁻¹, first fruiting node, fruit length (cm), fruit diameter (mm), number of locules plant⁻¹, number of fruits plant⁻¹, number of marketable fruits plant⁻¹, average fruit weight (g), number of pickings plant⁻¹, fruit yield plant⁻¹ (g).

Statistical analysis

The data obtained with respect to all the characters were subjected to ANOVA by Panse and Sukhatme (1952). As suggested by Robinson (1966), heritability values were calculated, whereas by using Hanson *et al.* (1956), the percentage was categorized as Low (0-30%), Moderate (30-60%), and High (> 60%). According to Johnson *et al.* (1955), genetic advance was measured in absolute units (GA) and as a percentage of the mean (GAM), implying selection of superiority of 5% of genotypes, and was classified as Low (0-10%), Moderate (10-20%), and High (> 20%). Burton (1952) formulas were used to calculate the PCV and GCV in percent, which were then classed as Low (0-10%), Moderate (10-20%), and High (> 20%). The data were computed by using R software (RStudio) and MS-Excel.

RESULTS AND DISCUSSION

Analysis of variance

The results of ANOVA for 20 characteristics of 60 okra genotypes are represented in Table 2. According to ANOVA, the mean sum of squares due to genotypes was highly significant ($P < 0.05$ and $P < 0.01$) for all traits, suggesting that the material under investigation possessed considerable genetic diversity. There was no significant variation in replication, demonstrating that environmental error (Genotype x environment) was less prevalent. These results indicated that significant variations exist across genotypes for all traits examined, which may give breeders an excellent opportunity to recognize high-performing accessions for desirable characteristics to improve crop breeding programs. Melaku *et al.* (2020) and Rambabu *et al.* (2019) both found significant variance among okra genotypes of the measured quantitative traits.

Mean performance

The mean values (Table 3.) indicated that the genotypes had early mean performance for days to first flower (38.32 days), days to 50% flowering (42.29 days), and days to first fruit harvest (48.03 days). The average mean performance was recorded for the following traits: first flowering node (5.30), plant height (87.88 cm), internodal length (6.21 cm), peduncle length (2.36 cm), number of branches per plant⁻¹ (3.77), first fruiting node (5.61), stem diameter (16.28 mm), number of locules per plant⁻¹ (5.22), and pickings per

plant⁻¹ (8.91). High mean performance was recorded for the following: fruiting period (58.59 days), No. of nodes plant⁻¹ (17.83), fruit length (14.21 cm), fruit diameter (16.33 mm), No. of fruits plant⁻¹ (26.18), No. of marketable fruits plant⁻¹ (23.97), average fruit weight (13.30 g) and fruit yield plant⁻¹ (347.42 g). These results are supported by Mohammed *et al.* (2022), who also reported a wide range of mean values for 23 quantitative traits in 36 okra genotypes, viz., peduncle length and No. of fruits plant⁻¹, also showed similar mean performances. The observed high No. of nodes plant⁻¹, fruit length and No. of fruits plant⁻¹ suggested a higher chance of improving the fruit yield of okra.

Estimates of variability components

The predictable genetic variability parameters viz. phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (bs), and genetic advance as a percentage of means (GA %) for 20 okra traits are shown in Table 3 and Fig 1.

Genotypic and phenotypic coefficients of variation

The occurrence of greater magnitudes of diversity in genotypes allows for crop improvement. A phenotypic (PCV) and genotypic (GCV) coefficient of variation was calculated for each of the 60 genotypes of the 20 attributes. As a result, by calculating the PCV and GCV, these parameters remained rendered unit-free. Because GCV captures the heritable genetic component of total variation, it is an excellent metric for comparing

the variability of various phenotypes. For all characteristics in this research, the PCV was greater than the GCV (Table 3 and Fig 1). This result is consistent with the findings of Reddy *et al.* (2012), Muluken *et al.* (2016), Sundaram *et al.* (2020), Temam *et al.* (2020) and Mohammed *et al.* (2022), who all reported that PCV was greater than GCV in their studies of okra crops. This indicates that the observed variance is caused not only by genotypes but also by the appropriate effect of the environment. This environmental influence might be attributed to soil fertility status, heterogeneity, and other uncontrollable variables.

Higher (>20) estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation were not found in any of the traits studied. According to Satesh *et al.* (2010), a high GCV and PCV indicates that environmental influences have less impact on the expression of such characteristics, so there is a greater opportunity to improve them via selective breeding.

The first flowering node, plant height, internodal length, first fruiting node, No. of fruits plant⁻¹, No. of marketable fruits per plant⁻¹, and fruit yield plant⁻¹ all had moderate (10-20) intensities of PCV and GCV. In addition, according to Reddy *et al.* (2012), the characters' moderate PCV and GCV values are more influenced by hereditary variables because environmental influences on phenotypic expression are minimal. As a result, these traits are accessible for further enhancement via selection. These results are similar in okra crops with the findings of Saryam (2012) for the first flowering node;

Table 1. List of okra genotypes

1	EC 305768	21	Hari Kranti	41	VRO - 22
2	EC 359637	22	Pusa A4	42	Ankur 41
3	IC 014026	23	MDU-1	43	AKO 102
4	Arka Anamika	24	VRO - 4	44	AKO 111
5	Arka Abhay	25	NRB 208	45	Maharani
6	Hisar Unnat	26	Kashi Pragati	46	Ankur 40
7	Pusa sawani	27	Gold 207	47	AKO 107
8	Pusa Makhmali	28	NOL 303+ (JULIE)	48	Mahyco 777
9	Punjab 8	29	GFS GOLD (V-4)	49	Lush green
10	P 7	30	NOL 1307 (SILKY)	50	Suguna A-51
11	Pusa 5	31	Dhanvi 66	51	Hyveg 155
12	Varsha uphar	32	Super champion 55	52	Super anamika
13	Punjab no.13	33	Ruchi	53	Super lady lock
14	Hina RCH	34	Ajeet-121	54	Hoshiarpur
15	Bhindi Selection 51	35	Anima	55	Madurai Local
16	Hari Pari	36	Harika	56	Chidambaram Local
17	MH 310	37	Sarala (LS-11)	57	Raja
18	Rani 792	38	Thakath (TS-102)	58	Kiran
19	Palam komal	39	Kashi Kranti	59	Bambeshwari
20	Salkeerthi	40	Hisar Naveen	60	Danteshwari

Table 2. Mean Sum of Squares from ANOVA for Fruit Yield and its components of 60 okra genotypes

Source	Replication	Treatment	Error	SEm	(CD) 5%	(CD) 1%	CV
DoF	2	59	118				
FFrN	0.383	1.25**	0.136	0.21	0.60	0.79	6.94
DFFr	7.772	6.09**	2.817	0.97	2.71	3.59	4.38
D50%Fr	7.406	10.498**	4.824	1.27	3.55	4.70	5.19
DFFrH	6.717	5.466**	2.982	1.00	2.79	3.69	3.6
FuP	16.706	29.191**	9.779	1.81	5.06	6.68	5.34
PtH (cm)	0.256	425.172**	4.065	1.16	3.26	4.31	2.29
InL (cm)	0.828	2.569**	0.31	0.32	0.90	1.19	8.97
PuL (cm)	0.018	0.137**	0.041	0.12	0.33	0.43	8.56
NB/Pt	0.151	0.614**	0.251	0.29	0.81	1.07	13.26
SeD (mm)	2.065	4.065**	1.092	0.60	1.69	2.23	6.42
NN/Pt	1.220	5.133**	0.627	0.46	1.28	1.69	4.44
FFuN	0.380	1.278**	0.158	0.23	0.64	0.85	7.1
FuL (cm)	0.367	6.169**	0.942	0.56	1.57	2.08	6.83
FuD (mm)	1.697	3.81**	0.951	0.56	1.58	2.09	5.97
NL/Fu	0.051	0.33**	0.019	0.08	0.22	0.29	2.63
NF/Pt	6.305	31.38**	2.194	0.86	2.39	3.17	5.66
NMF/Pt	1.474	26.735**	2.025	0.82	2.30	3.04	5.94
AFuW (g)	0.220	0.611**	0.109	0.19	0.53	0.71	2.48
NP/Pt	1.501	2.815**	0.545	0.43	1.19	1.58	8.29
FY/Pt (g)	1379.268	593.513**	458.918	12.37	34.64	45.79	6.17

**Significant at 5% and 1% probability levels; SEm: Mean of Standard Error; CD: Critical Difference; CV: Coefficient of Variation; DoF: Degree of Freedom; FFrN: First flowering node; DFFr: Days to first flower; D50%Fr: Days to 50% flowering; DFFrH: Days to first fruit harvest; FuP: Fruiting Period; PtH: Plant height (cm); InL: Internodal length (cm); PuL: Peduncle length (cm); NB/Pt: No. of branches plant⁻¹; SeD: Stem Diameter (mm); NN/Pt: No. of Nodes plant⁻¹; FFuN: First Fruiting Node; FuL: Fruit length (cm); FuD: Fruit Diameter (mm); NL/Fu: No. of Locules fruit⁻¹; NF/Pt: Number of Fruits plant⁻¹; NMF/Pt: No. of marketable fruits plant⁻¹; AFuW: Average Fruit Weight (g); NP/Pt: No. of pickings plant⁻¹; FY/Pt: Fruit yield plant⁻¹ (g)

Ranga *et al.* (2021) for plant height; Chetana *et al.* (2021) for internodal length and fruit yield plant⁻¹; Reddy *et al.* (2012) for the first fruiting node; Mohammed *et al.* (2022), Rambabu *et al.* (2019) and Kumari *et al.* (2017) for No. of fruits plant⁻¹.

Moderate PCV and low GCV were observed for the following traits: peduncle length, fruit length, number of branches plant⁻¹ and number of pickings plant⁻¹. Sundaram *et al.* (2020) reported moderate PCV and low GCV for No. of branches plant⁻¹; Muluken *et al.* (2016) reported moderate PCV for peduncle length; Rambabu *et al.* (2019) reported low GCV and PCV for fruiting period. Saryam (2012) reported moderate PCV for fruit length. Rambabu *et al.*, 2019 reported low GCV, and Temam *et al.* (2020) reported moderate PCV for No. of pickings plant⁻¹.

Low (<10) values of PCV and GCV were recorded for days to first flower, days to 50% flowering, days to first fruit harvest, fruiting period, stem diameter, No. of Nodes plant⁻¹, fruit diameter, No. of locules plant⁻¹ and average fruit weight. Similar results were reported by

Mohammed *et al.* (2022), Chetana *et al.* (2021) and Kumari *et al.* (2017) for days to first flower; by Sravanthi *et al.* (2021) and Saryam (2012) for days to 50% flowering and fruit diameter; by Sundaram *et al.* (2020) for days to first fruit harvest; by Rambabu *et al.* (2019) for fruiting period; and by Sibsankar *et al.* (2012) for No. of Nodes plant⁻¹. Low PCV and GCV values of characteristics indicate a greater impact of the environment on these traits, indicating that selection on a phenotypic basis would be ineffective for genetic improvement.

Heritability and Genetic advance

The degree of phenotypic variation induced by additive gene action is determined by heritability. Heritability is a useful indicator of the degree to which characteristics are passed on from parents to their progeny (Temam *et al.*, 2020). The amount of the heritable component of the variance determines the consistency of progeny performance in subsequent generations. Heritability is defined by Robinson (1966) as the potential and degree to which improvement may be achieved by selection,

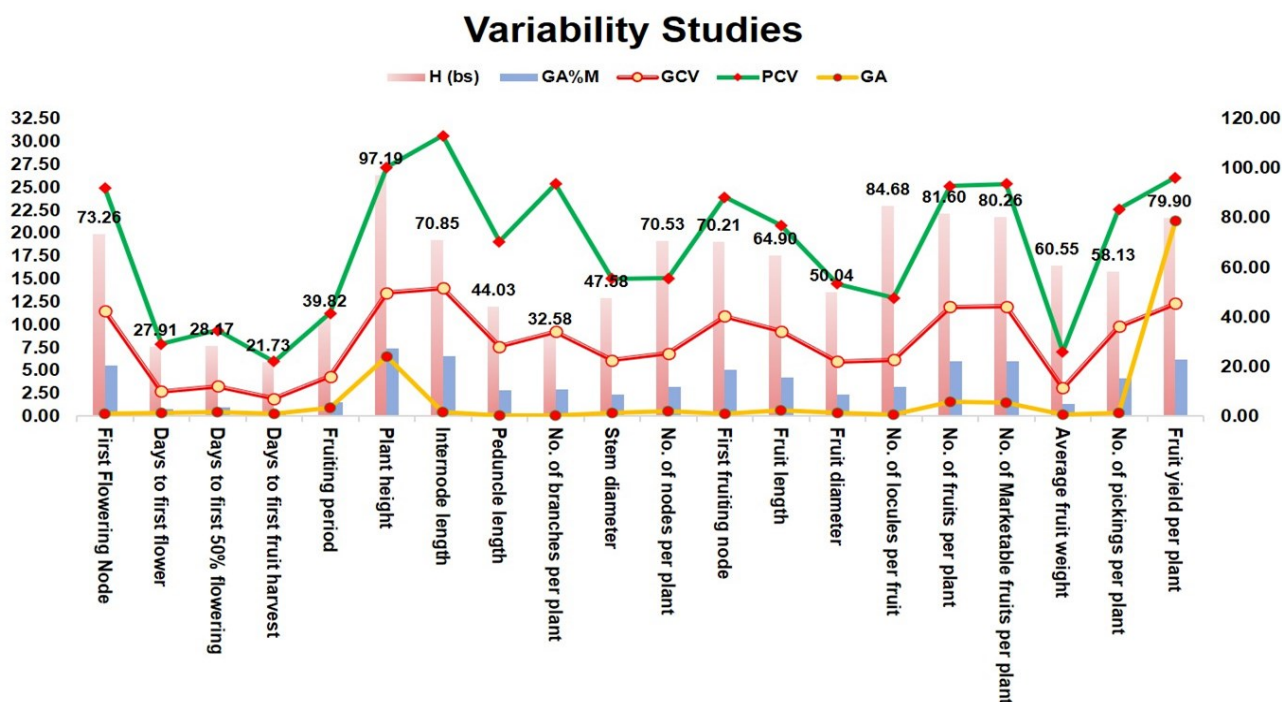


Fig. 1. Showing estimates of variability components in 60 okra genotypes (H (bs): heritability (broad sense); GA %M: genetic advance % mean; GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; GA: genetic advance)

and it can be used in both broad and limited contexts. To design genetic improvements, it is beneficial to understand how much improvement may be obtained by selection. The crop enhancement in the average genotypic value of the selected families over the total population over time is referred to as genetic advance (GA) under selection.

Estimates of the broadest sense of heritability and genetic advance as a percent of the mean (GA % M) at 5% selection intensity for 20 quantitative traits of 60 okra genotypes are presented in Table 3 and Fig. 1. The measured heritability ranged from 21.73% to 97.19% for the time from the first fruit harvest to plant height. High (>60) estimates of heritability were recorded for the traits first flowering node, plant height, internodal length, No. of nodes plant⁻¹, first fruiting node, fruit length, No. of locules plant⁻¹, No. of fruits plant⁻¹, No. of marketable fruits plant⁻¹, average fruit weight and fruit yield plant⁻¹, suggesting that, even if environmental factors least control the characteristics, selection for their improvement may be ineffectual, since heritability (bs) is assessed based on total genetic variation, which includes both total fixable (additive and AA type of epistasis) and nonfixable (dominance, AD and DD type of epistasis) variances (Singh and Narayan, 2017). The fruiting period, peduncle length, number of branches plant⁻¹, stem diameter, fruit diameter, and number of pickings plant⁻¹ have moderate heritability (30-60), showed that environmental variables have a considerable impact on these characteristics and that genetic

improvement via selection would be fairly challenging due to the environment's masking effects on genotypic effects (Reddy et al., 2012). Low (<30) heritability observed for the traits days to first flowering, days to 50% flowering, and days to first fruit harvest demonstrates the ineffectiveness of direct selection for trait development owing to heavily impacted environmental influences (Muluken et al., 2016). The strong heritability values suggest that programmes of okra development for characteristics such as fruit diameter, length, and fruit yield will be implemented in the future. Backcrossing is essential to concentrate these traits in genotypes since many traits seem to be governed by alleles with additive effects (Temam et al., 2020).

The genetic advance % of the mean observed range of 1.82-27.38 for a days to first fruit harvest to plant height. The first flowering node, plant height, internodal length, No. of fruits plant⁻¹, No. of marketable fruits plant⁻¹ and fruit yield plant⁻¹ exhibited high (>20) GA % of the mean, suggesting that additive genes control these parameters and that selection would be rewarding for the improvement of such parameters. This indicates that such characteristics may be developed by direct selection (Reddy et al., 2012). For peduncle length, No. of branches plant⁻¹, No. of nodes plant⁻¹, first fruiting node, fruit length, No. of locules plant⁻¹, and No. of pickings plant⁻¹ there was moderate (10-20) GA % of the mean. Days to first flower, days to 50% flowering, days to first fruit harvest, fruiting period, stem diameter, fruit diameter and average fruit weight, on the oth-

er hand, showed low (<10) GA % of the mean. This suggests that nonadditive genes control the traits, and thus heterosis breeding could be beneficial (Muluken *et al.*, 2016, Temam *et al.*, 2020).

Heritability (bs) is the only numerical measurement of the proportion of two variations, which may not lead to achievement if the choice is based only on heritability (bs) estimations. Johnson *et al.* (1955) proposed that heritability (bs) estimates, combined with GA % of the mean, stood more effective in estimating the impact of selecting the best accession. It contains more detailed information than each parameter alone, as well as a manifestation of additive gene activity, and is selectable (Akotkar *et al.*, 2010; Muluken *et al.*, 2016). The first flowering node, plant height, internodal length, No. of fruits plant⁻¹, No. of marketable fruits plant⁻¹, and fruit yield plant⁻¹ all had high heritability and high GA % of the mean. High heritability estimates, together with genetic advances, were more beneficial in estimating the impact of choosing the best genotype.

Similar findings of high heritability and GA % of the mean were reported by Ranga *et al.* (2021) for the first flowering node; by Mohammed *et al.* (2022) for plant height and No. of fruits plant⁻¹; by Temam *et al.* (2020) for internodal length, No. of marketable fruits plant⁻¹, and fruit yield plant⁻¹. The No. of nodes plant⁻¹, first fruiting node, fruit length, and No. of locules plant⁻¹ all the traits exhibited high heritability (bs) and moderate GA as % mean. Similar findings are reported by Das *et al.* (2012) for No. of nodes plant⁻¹ and by Chetana *et al.* (2021) for fruit length.

Moderate heritability with moderate GA % of the mean was observed for the trait peduncle length, number of branches plant⁻¹, and number of pickings plant⁻¹. Similar moderate heritability and GA % of the mean were reported by Muluken *et al.* (2016) for peduncle length, and this trait might be amenable for selection and improvement. Average fruit weight exhibited high heritability and a low genetic advance as a percent mean, while fruiting period, stem diameter, and fruit diameter

Table 3. Estimates of variability components for 20 quantitative traits of 60 okra genotypes

Quantitative traits	Range		Mean	Variance		Co-Variance		Heritability broad Sense (%)	Genetic Advance (GA)	GA % mean
	Min	Max		VG	VP	GCV	PCV			
FFrN	3.60	6.60	5.30	0.37	0.51	11.49	13.43	73.26	1.08	20.27
DFFr	35.00	41.00	38.32	1.09	3.91	2.73	5.16	27.91	1.14	2.97
D50%Fr	38.33	45.33	42.29	1.89	6.72	3.25	6.13	28.17	1.50	3.56
DFFrH	45.00	51.00	48.03	0.83	3.81	1.89	4.06	21.73	0.87	1.82
FuP	50.00	63.67	58.59	6.47	16.25	4.34	6.88	39.82	3.31	5.64
PtH (cm)	60.01	118.93	87.88	140.37	144.43	13.48	13.68	97.19	24.06	27.38
InL (cm)	4.41	8.72	6.21	0.75	1.06	13.98	16.61	70.85	1.51	24.25
PuL (cm)	1.99	3.05	2.36	0.03	0.07	7.59	11.44	44.03	0.24	10.38
NB/Pt	2.73	5.53	3.77	0.12	0.37	9.22	16.15	32.58	0.41	10.84
SeD (mm)	13.98	19.40	16.28	0.99	2.08	6.12	8.87	47.58	1.41	8.69
NN/Pt	13.80	20.73	17.83	1.50	2.13	6.87	8.18	70.53	2.12	11.89
FFuN	3.60	6.60	5.61	0.37	0.53	10.89	13.00	70.21	1.06	18.80
FuL (cm)	7.37	16.36	14.21	1.74	2.69	9.29	11.53	64.90	2.19	15.42
FuD (mm)	14.02	20.88	16.33	0.95	1.90	5.98	8.45	50.04	1.42	8.71
NL/Fu	5.00	7.40	5.22	0.10	0.12	6.18	6.71	84.68	0.61	11.71
NF/Pt	16.40	33.20	26.18	9.73	11.92	11.91	13.19	81.60	5.80	22.17
NMF/Pt	15.40	30.73	23.97	8.24	10.26	11.97	13.36	80.26	5.30	22.09
AFuW (g)	10.77	13.92	13.30	0.17	0.28	3.08	3.95	60.55	0.66	4.93
NP/Pt	6.07	11.13	8.91	0.76	1.30	9.77	12.81	58.13	1.37	15.34
FY/Pt (g)	176.40	438.40	347.42	1824.20	2283.12	12.29	13.75	79.90	78.65	22.64

FFrN: First flowering node; DFFr: Days to first flower; D50%Fr: Days to 50% flowering; DFFrH: Days to first fruit harvest; FuP: Fruiting period; PtH: Plant height (cm); InL: Internodal length (cm); PuL: Peduncle length (cm); NB/Pt: No. of branches plant⁻¹; SeD: Stem diameter (mm); NN/Pt: No. of nodes plant⁻¹; FFuN: First fruiting node; FuL: Fruit length (cm); FuD: Fruit diameter (mm); NL/Fu: Number of locules fruit⁻¹; NF/Pt: Number of fruits plant⁻¹; NMF/Pt: No. of marketable fruits plant⁻¹; AFuW: Average fruit weight (g); NP/Pt: Number of pickings plant⁻¹; FY/Pt: Fruit yield plant⁻¹ (g). VG: genotypic variance; VP: phenotypic variance; GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation.

had a moderate heritability and a low GA % mean. Days to first flowering, days to 50% flowering, and days to first fruit harvest had low estimates of both heritability and GA % of the mean; it is difficult to improve such traits. This might be because the environment seems to have a higher impact on the expression of the characteristics, limiting the potential for selective improvement due to the existence of nonadditive (dominant and/or epistatic) modes of gene action. Characters with low heritability associated with low GA % of the mean, i.e., hybridization or recurrent selection, should be followed with the trait of interest (Muluken et al., 2016). Similar low estimates were reported by Kumari et al. (2017) for days to first flowering, by Sundaram et al. (2020) for days to first fruit harvest in okra crops.

Conclusion

The mean sum of square (MSS) due to genotypes was highly significant ($P < 0.05$ and $P < 0.01$) for all traits under study, indicating that there was substantial genetic diversity among the material under examination, according to the analysis of variance. The fruit yield plant⁻¹ ranged from 176.40 to 438.40 g, with 347.42 g being the average. For all traits, the PCV was greater than the GCV. This indicates that the observed variance is caused not only by genotypes but also by the appropriate influence of the environment. The traits of first flowering node, plant height, internodal length, first fruiting node, No. of fruits plant⁻¹, No. of marketable fruits plant⁻¹, and fruit yield plant⁻¹ all had a moderate magnitude of GCV, PCV and high heritability (bs), and a high GA % of the mean stood more effective in estimating the impact of selecting the best accession. It contains more detailed information than each parameter alone, as well as a manifestation of additive gene activity and is selectable.

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