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RESEARCH ARTICLE

Comprehensive morpho-phenotypic characterisation and performance evaluation of okra genotypes

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Abstract

Although okra is an economically important vegetable crop, comprehensive studies on genetic variability, heritability and trait association under semi-arid conditions of North India are limited. Hence, the present field experiment was conducted to assess the genetic variability and performance of 30 okra (*Abelmoschus esculentus* (L.) Moench) genotypes during the kharif season of 2021 at Chaudhary Charan Singh Haryana Agricultural University, Hisar. The experiment was laid out in a randomised block design with three replications. The morphological characters evaluated included fruit colour, dentation of margin, colour between veins and surface between ridges, among others. The study aimed to assess key genetic variability parameters, namely genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance and heritability for yield and yield-contributing characters in okra genotypes. Significant variability was observed among genotypes for all qualitative and quantitative traits under study. High genotypic and phenotypic coefficients of variation were recorded for plant height and node of first fruiting, indicating substantial genetic variability. High heritability coupled with high genetic advance was observed for plant height, node of first fruiting, petiole length and fruit yield per plant, suggesting the predominance of additive gene action and the effectiveness of direct selection. Moderate heritability and genetic advance were recorded for the number of fruits per plant. Based on yield and yield-contributing traits, the genotypes HB-691-08, Hisar Unnat, Hisar Naveen, HBT-49-1 and HBTC-6-7-1 were identified as promising for use in future breeding programmes.

Keywords: genetic advance; genetic variability; genotypic coefficient of variation; heritability; okra; phenotypic coefficient of variation

Introduction

Okra (*Abelmoschus esculentus* (L.) Moench), an annual vegetable, is primarily grown for its soft, immature and tender fruits in tropical and sub-tropical regions of the world during the summer-spring and rainy seasons (1). Okra, commonly known as lady's finger, belongs to the Malvaceae family. It is a cost-effective crop and widely consumed because of its high nutritive value, marketability and medicinal value. Green fruits are also a rich source of iron and vitamin A, B_9 and C (2). The immature pods are consumed as a vegetable, while extracts from the harvested fruits are used in soups, sauces and various recipes. Crude fibre present in mature pods and stems is utilized by the paper industry. The dry fruit skin and fibres are used in the manufacture of paper, cardboard and fiber products. Due to the antioxidant, antidiabetic, antimicrobial and antitumor properties of okra mucilage, it has been widely used in the pharmaceutical industry. It also provides high-quality mucilage and oil from okra fruits (3). Okra fruits are useful against chronic dysentery and genitor urinary disorders (4). The stem and roots are used in clarifying cane juice during jaggery preparation. Okra is a heat- and drought-tolerant crop; however, it is sensitive to cold and cannot tolerate low temperatures (5).

Knowledge of genetic variability is fundamental in crop improvement (6). Information on genetic variability is crucial for enhancing production and other characteristics in okra and is necessary for the efficient screening of superior genotypes. Absolute variability in different characters alone cannot serve as a decisive criterion for identifying traits with high degree of variability. Relative values of phenotypic and genotypic coefficients of variation provide a more reliable estimate of magnitude of variability present in a population. Accordingly, it is essential to partition the total variation into genetic and non-genetic components and to standardise these estimates by calculating phenotypic and genotypic coefficients of variation. When determining the genetic variability of specific traits, the coefficient of variation is a useful parameter. Heritability does not indicate the percentage of diversity, rather it represents the proportion of phenotypic variance attributable to genetic factors, thereby assisting breeders in selecting superior genotypes for specific characters. It is necessary to partition the observed phenotypic variability into its heritable and non-heritable components using appropriate genetic parameters.

Therefore, selection based solely on yield is ineffective and emphasis should be placed on traits that are highly heritable and contribute substantially to yield. Genetic advance reflects the expected improvement in the mean genotypic values of the selected individuals over the base population, enabling breeders to select progenies even in early generations. Understanding of mean

performance of yield-related traits is essential for the effective selection of superior hybrids. This study was undertaken to improve productivity by assessing the magnitude and nature of genetic variability, which is essential for selecting and designing effective breeding programmes.

Materials and Methods

The experiment was conducted at the Research Farm of the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, during the kharif season of 2021. Thirty okra genotypes were evaluated in the field (Table 1). The experiment was laid out in a randomized block design (RBD) with 3 replications. The crop was shown by direct sowing method with a planting distance 60 cm × 30 cm (60 cm between rows and 30 cm plants within a row). Recommended agronomic practices were uniformly followed for all genotypes. Fertiliser was applied at 100:60:60 kg N:P_2O_5:K_2O ha^{-1}, with nitrogen applied in split doses. Irrigation was provided according to crop requirements and need-based plant protection measures were adopted to manage pests and diseases.

Observations for quantitative and qualitative characters were recorded on 5 randomly selected plants per replication for each genotype and the list of characters studied is presented in Table 1. The 30 genotypes included in the experimental study are listed in Table 2. The collected data were statistically analysed to determine genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as a percentage of the mean (GAM).

The recorded data were subjected to analysis of variance (ANOVA) using statistical software, following the procedure appropriate for a randomized block design (7). Genotypic and phenotypic coefficients of variation, heritability (in the broad sense), genetic advance, and genetic advance as percentage of mean (GAM) were estimated using standard biometrical formulae. Analysis of variance was performed (7). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated (8), and broad-sense heritability along with genetic advance were estimated (9, 10).

Variances: Genotypic and phenotypic variances were calculated as follows:

$$\sigma_g^2 = \frac{M_g - M_e}{r}$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Genotypic and phenotypic coefficient of variation: GCV and PCV were calculated by the formula given below:

Genotypic coefficient of variation (GCV) = $\sqrt{\frac{\sigma_g^2}{x}} \times 100$

Phenotypic coefficient of variation (PCV) $\sqrt{\frac{\sigma_p^2}{x}} \times 100$ =

Heritability (broad sense): Heritability in broad sense was calculated according to the formula as given below:

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Heritability was classified as low (< 50 %), moderate (50–80 %) and high (> 80 %).

Genetic advance: At 5 % selection intensity for each character, the expected genetic advance was calculated as follows:

Genetic advance = $h^2 \times K \times \sigma_p \times 100$

Results

Characterisation of okra genotypes for qualitative characters

The qualitative character includes colour between veins (light green or purple), foliage colour (light green, green or dark green), fruit colour (light green, green or dark green), dentation of margin (weak, medium or strong), petal base colour (pigmentation on one or both side), surface between ridges (concave, flat or convex), depth of lobbing (shallow, medium or deep) are presented in Table 3. Regarding colour between veins, the presence of green pigment between the veins was consistent across all 30 genotypes and there were no instances of sparsely pigmented coloration between the veins in any of the genotypes. There is variation in the foliage colour among the genotypes; 13 genotypes showed a dark green colour, 16 genotypes had a standard green foliage colour, while one

Table 1. Observations recorded during the experiment

A. Quantitative characters			B. Qualitative characters (DUS descriptors)		
(i) Growth and flowering traits			(i) Leaf and foliage characters		
Sl. No.	**Character**	**Unit**	**Sl. No.**	**Character**	**Descriptor states**
1	Plant height	cm	**14**	Colour between veins	Light green/green/dark green
2	Branches per plant	Number	**15**	Foliage colour	Light green/green/dark green
3	Inter-nodal length	cm	**16**	Dentation of margin	Weak/medium/strong
4	Petiole length	cm	**17**	Depth of lobbing	Deep/medium/shallow lobed
5	Days to 50 % flowering	Days			
6	First fruit node	Node number			
(ii) Yield and yield contributing traits			(ii) Flower characters		
Sl. No.	**Character**	**Unit**	**Sl. No.**	**Character**	**Descriptor states**
7	Fruit length	cm	**18**	Petal base colour	Pigmentation on one or both sides
8	Fruit diameter	cm			
9	Fruit weight	g			
10	Fruits per plant	Number			
11	Fruit yield per plant	g			
(iii) Seed traits			(iii) Fruit characters		
Sl. No.	**Character**	**Unit**	**Sl. No.**	**Character**	**Descriptor states**
12	Number of seeds per fruit	Number	**19**	Fruit colour	Light green/green/dark green
13	Test weight	g	**20**	Surface between ridges	Concave/flat/convex

Table 2. List of genotypes and their source

Sl. No.	Genotypes	Source	Origin	Sl. No.	Genotypes	Source	Origin
1.	HB-9-35	CCS HAU, Hisar	India	**16.**	Prabhani Kranti	MAU, Prabhani	India
2.	HB-9-37	CCS HAU, Hisar	India	**17.**	HBT-11-1	CCS HAU, Hisar	India
3.	HB-9-38	CCS HAU, Hisar	India	**18.**	HBT-42	CCS HAU, Hisar	India
4.	HB-9-43	CCS HAU, Hisar	India	**19.**	HBT-49-1	CCS HAU, Hisar	India
5.	HBT-1	CCS HAU, Hisar	India	**20.**	HBT-15	CCS HAU, Hisar	India
6.	Punjab-8	PAU, Ludhiana	India	**21.**	JNDOL-05	AAU, Gujrat	India
7.	Pusa Sawani	IARI, New Delhi	India	**22.**	HB-691-08	CCS HAU, Hisar	India
8.	Punjab Padmini	PAU, Ludhiana	India	**23.**	HBTC-6-7-1	CCS HAU, Hisar	India
9.	HB-9-29	CCS HAU, Hisar	India	**24.**	HBT-53	CCS HAU, Hisar	India
10.	HB-06-46-1-1	CCS HAU, Hisar	India	**25.**	Arka Abhay	IIHR, Bangalore	India
11.	HB-S-4	CCS HAU, Hisar	India	**26.**	Hisar Unnat	CCS HAU, Hisar	India
12.	HB-25-2-1	CCS HAU, Hisar	India	**27.**	Varsha Uphar	CCS HAU, Hisar	India
13.	HBBT-19	CCS HAU, Hisar	India	**28.**	Hisar Naveen	CCS HAU, Hisar	India
14.	HBT-48	CCS HAU, Hisar	India	**29.**	HB-9-27	CCS HAU, Hisar	India
15.	HB-08-3-1	CCS HAU, Hisar	India	**30.**	HBT-12-1	CCS HAU, Hisar	India

Table 3. Characterisation of okra genotypes for qualitative characters

Sl. No.	Specific qualitative morphological traits		Genotypes
1.	Foliage colour	Light green	HBT-15
		Green	HB-9-35, HB-9-37, HB-9-43, HBT-1, Punjab-8, Pusa Sawani, HB-9-29, HB-S-4, HB-25-2-1, HBT-48, Prabhani Kranti, HBT-11-1, HBT-42, Hisar Unnat, Varsha Uphar, Hisar Naveen
		Dark green	HB-9-38, Punjab Padmini, HB-46-1, HBBT-19, HB-08-3-1, HBT-49-1, JNDOL-05, HB-691-08, HBTC-6-7-1, HBT-53, Arka Abhay, HB-9-27, HBT-12-1
2.	Dentation of margin	Weak	HB-9-37, Punjab Padmini, HBT-42
		Medium	Nil
		Strong	HB-9-35, HB-9-38, HB-9-43, HBT-1, Punjab-8, Pusa Sawani, HB-9-29, HB-46-1, HB-S-4, HB-25-2-1, HBBT-19, HBT-48, HB-08-3-1, Prabhani Kranti, HBT-11-1, HBT-49-1, HBT-15, JNDOL-05, HB-691-08, HBTC-6-7-1, HBT-53, Arka Abhay, Hisar Unnat, Varsha Uphar, Hisar Naveen, HB-9-27, HBT-12-1
3.	Fruit colour	Light green	HBT-15
		Green	HB-9-35, HB-9-37, HB-9-43, HBT-1, Punjab-8, Pusa Sawani, HB-9-29, HB-S-4, HB-25-2-1, HBT-48, Prabhani Kranti, HBT-11-1, HBT-42, Hisar Unnat, Varsha Uphar, Hisar Naveen
		Dark green	HB-9-38, Punjab Padmini, HB-46-1, HBBT-19, HB-08-3-1, HBT-49-1, JNDOL-05, HB-691-08, HBTC-6-7-1, HBT-53, Arka Abhay, HB-9-27, HBT-12-1
4.	Surface between ridges	Concave	HB-9-35, Punjab-8, Pusa Sawani, HB-46-1, HB-S-4, HBT-42, HBT-49-1, JNDOL-05, HBTC-6-7-1, HBT-53, Arka Abhay, Hisar Naveen
		Flat	HB-9-37, HB-9-38, HB-9-43, HBT-1, Punjab Padmini, HB-9-29, HB-25-2-1, HBBT-19, HBT-48, HB-08-3-1, Prabhani Kranti, HBT-11-1, HBT-15, HB-691-08, Hisar Unnat, Varsha Uphar, HB-9-27, HBT-12-1
		Convex	Nil
5.	Petal base colour	Pigment one side	HB-9-29, HBBT-19, HBT-48, HB-08-3-1, HBT-11-1, HBT-49-1, HBT-15, HB-691-08, Hisar Unnat, HB-9-27, HBT-12-1
		Pigment both sides	HB-9-35, HB-9-37, HB-9-38, HB-9-43, HBT-1, Punjab-8, Pusa Sawani, Punjab Padmini, HB-46-1, HB-S-4, HB-25-2-1, Prabhani Kranti, HBT-42, JNDOL-05, HBTC-6-7-1, HBT-53, Arka Abhay
6.	Depth of lobbing	Deep	HB-9-35, HBT-1, Pusa Sawani, HB-S-4, HB-25-2-1, HBBT-19, Prabhani Kranti, HBT-42, HBT-49-1, HBT-15, JNDOL-05, HB-691-08, HBT-53, Arka Abhay, Varsha Uphar, Hisar Naveen, HB-9-27
		Medium	HB-9-37, HB-9-38, HB-9-43, Punjab Padmini, HBT-48, HB-08-3-1, HBTC-6-7-1, Hisar Unnat, HBT-12-1
		Shallow	Punjab-8, HB-9-29, HB-46-1, HBT-11-1
7.	Colour between veins	Light green	Nil
		Green	HB-9-35, HB-9-37, HB-9-38, HB-9-43, HBT-1, Punjab-8, Pusa Sawani, Punjab Padmini, HB-9-29, HB-46-1, HB-S-4, HB-25-2-1, HBBT-19, HBT-48, HB-08-3-1, Prabhani Kranti, HBT-11-1, HBT-42, HBT-49-1, HBT-15, JNDOL-05, HB-691-08, HBTC-6-7-1, HBT-53, Arka Abhay, Hisar Unnat, Varsha Uphar, Hisar Naveen, HB-9-27, HBT-12-1
		Dark green	Nil

genotype displayed a lighter shade of green.

Based on the observation of fruit colour in the 30 genotypes; 13 had fruits of dark green colour, 16 exhibited fruits of green colour and one genotype had fruits of light green colour. With respect to dentation of margin, the majority of the genotypes (27) had a strong dentation pattern along the margin and only a smaller subset of genotypes (3 out of 30) showed a weak dentation of the margin. The petal base colour in the 30 genotypes; 19 genotypes had a purple colour on both sides at the base of the petal and 11 genotypes exhibited a purple colour at the base of the petal inside only. Regarding surface between ridges, the majority of the genotypes (18) displayed a flat fruit surface, 12 genotypes showed a concave fruit surface and none of the genotypes exhibited a convex fruit surface between the ridges.

Analysis of variance and mean performance of okra genotypes for different characters

Analysis of variance and mean performance for yield and its component character in okra was presented in Table 4 & 5. The mean performance for plant height ranged between 106.3 cm to 42.7 cm (Table 5). The maximum plant height was recorded in HB-691-08 (106.3 cm), maximum number of branches per plant recorded in genotype HB-691-08 (3.5), highest petiole length recorded in genotype Arka Abhay (20.9 cm). The longest fruit length at marketable stage was recorded in Hisar Unnat (10.4 cm), highest

Table 4. Analysis of variance for yield and its component character in okra

Sl. No.	Characters	Mean sum of square			CV %	CD %
	Degree of freedom	Replications	Treatments	Error		
1.	**Plant height (cm)**	204.4	**107.77****	58.00	10.7	12.5
2.	**Branches per plant**	0.05	0.40**	0.11	12.1	0.6
3.	**Days to 50 % flowering**	1.01	46.22**	6.11	5.1	4.0
4.	**Petiole length (cm)**	2.03	17.31**	1.13	6.2	1.7
5.	**Inter-nodal length (cm)**	0.01	0.87**	0.21	9.0	0.7
6.	**First fruit node**	0.44	3.70**	0.19	8.4	0.7
7.	**Fruit length (cm)**	0.58	1.12**	0.23	5.4	0.8
8.	**Fruit diameter (cm)**	0.01	0.02**	0.05	5.5	0.1
9.	**Fruit weight (g)**	1.13	0.96**	0.30	6.0	0.8
10.	**Fruits per plant**	51.06	46.38**	18.76	12.9	7.0
11.	**Fruit yield per plant**	727.36	2873.9**	393.7	8.1	32.8

** Significant at 5 % level of probability ($p \leq 0.05$).

Table 5. Variability parameters for different traits in 30 okra genotypes

Characters	Mean	Range		GCV	PCV	Heritability	GA (%)
		Max.	Min.				
Plant height (cm)	70.9	106.3	42.7	25.2	27.3	84.6	47.7
Branches per plant	2.8	3.5	2.0	11.0	16.3	45.7	15.4
Days to 50 % flowering	48.2	54	40.3	7.5	9.1	68.6	12.9
Petiole length (cm)	17.2	22.3	13.4	13.4	14.8	82.5	25.1
Inter-nodal length (cm)	5.1	5.9	4.1	9.1	12.8	50.7	13.4
First fruit node	5.2	7.6	3.2	20.7	22.4	85.8	39.6
Fruit length (cm)	9.0	10.4	7.8	6.0	8.0	55.2	9.2
Fruit diameter (cm)	1.3	1.5	1.2	5.8	7.7	57.2	9.1
Fruit weight (g)	9.1	10.4	7.9	5.1	7.9	42.4	6.9
Fruits per plant	33.3	40.8	23.8	9.0	15.8	62.9	10.7
Yield per plant (g)	243.3	301.5	190.1	11.8	14.3	67.7	20.0

fruit diameter was observed in the genotype HBT-9-43 (1.8 cm). The maximum fruit weight was observed in genotype HBT-49-1 (11 g), highest number of fruits per plant was recorded in genotype HB-691 -08 (40.8) and highest fruit yield per plant was recorded in genotype HB-691-08 (301.5 g). The maximum number of seeds per fruit observed in genotype HBT-48 (56.7) and highest test weight was recorded in genotype Varsha Uphar (69.3 g). Minimum days to 50 % flowering were taken by the genotype Varsha Uphar (40 days) and shortest inter-nodal length was exhibited by genotype HB-691-08 (4.1 cm). The value of lowest first fruit node is 3, which was observed in the genotype Hisar Unnat.

Analysis for GCV, PCV, heritability and genetic advance

Variability parameters such as GCV, PCV, heritability and genetic advance for different traits given in Table 6. The estimates of genotypic coefficient of variation were found lower but close to phenotypic coefficient of variation, indicating that the influence of environment on these characters was found to be very negligible. The genotypic coefficient of variation value ranged from 5.1 to 25.2 %. The highest values of genotypic coefficient of variation were observed for plant height (25.2 %), first fruit node (20.7 %). Moderate values for yield per plant (11.8 %), branches per plant (11.0 %). The characters such as fruits per plant (9.0 %), days taken to 50 % flowering (7.5 %) exhibited the lowest values for GCV.

The estimates of phenotypic coefficient of variation varied from 27.3 to 7.7 %. The high values of PCV were observed for plant height (27.3 %), first fruit node (22.4 %). Moderate values for branches per plant (16.3 %), fruits per plant (15.8 %), yield per plant (14.3 %). The characters such as days taken to 50 % flowering (9.1 %), fruit length (8.0 %), fruit weight (7.9 %), fruit diameter (7.7 %) exhibited lower values for PCV.

Heritability in broad sense varied from 85.8 to 32.9 %. All characters under study exhibited high to moderate heritability for most of the characters. Maximum heritability was exhibited by the trait first fruit node (85.8 %), followed by plant height (84.6 %), petiole length (82.5 %). Moderate heritability exhibited by days taken to 50 % flowering (68.6 %), yield per plant (67.7 %), number of fruits per plant (63.9 %), fruit diameter (57.2 %), fruit length (55.2 %) and inter-nodal length (50.7 %). The lowest value for heritability was observed for characters such as branches per plant, inter-nodal length and fruit weight.

The genetic advance is defined as an increase in the mean genotypic value of selected plants over the parent population, which is primarily used to predict selection efficiency. Heritable variation can be studied effectively in conjunction with genetic progress. The highest and lowest estimates of genetic advance as percent of mean were 47.7 % and 6.9 %, respectively. The values for genetic advance were found high for the traits plant height (47.7 %) and first fruit node (39.6 %). Moderate value of genetic advance was found for traits such as yield per plant (20.0 %), branches per plant (15.4 %), inter-nodal length (13.4 %), days taken to 50 % flowering (12.9 %) and fruits per plant (10.7 %). The lowest values of genetic advance were found for fruit length (9.2 %), fruit diameter (9.1 %) and fruit weight (6.9 %).

Discussion

All the characters such as plant height, number of branches per plant, inter-nodal length, petiole length, fruit length, fruit diameter, fruit weight, number of fruits per plant, fruit yield per plant, test weight and number of seeds per fruit showed slightly higher PCV than GCV, which was in consistent with the results as given in the reference (11–14). High estimates of PCV and GCV were observed for traits such as plant height and first fruit node, which is in agreement with earlier findings (15–18), whereas similar results were observed in present experiment. Moderate GCV and PCV for yield per plant was also recorded previously (18, 19). High estimates of PCV and GCV along with high heritability and genetic advance as a

Table 6. Mean performance of okra genotypes for different morphological and seed traits in okra

Genotype	PH	BPP	DFF	PL	INL	FFN	FL	FD	FW	FPP	FYPP	NSPF	TW
HB-9-35	68.5	2.6	49.3	16.4	5.4	6.7	8.1	1.3	8.8	19.4	194.4	39.0	49.0
HB-9-37	73.5	2.9	51.3	16.7	5.9	5.5	8.5	1.4	9.3	19.0	228.7	39.6	46.2
HB-9-38	42.7	2.4	52.0	13.8	5.2	6.9	8.4	1.4	9.0	30.0	218.6	42.0	62.7
HB-9-43	62.5	3.0	52.0	16.9	5.5	5.4	9.1	1.8	8.8	28.6	235.5	31.0	48.2
HBT-1	46.7	2.7	54.0	14.7	5.6	4.9	9.3	1.6	9.7	32.9	222.1	41.0	65.2
Punjab-8	65.9	3.0	46.7	20.2	4.8	5.5	8.7	1.4	9.3	32.4	254.8	40.0	60.2
Pusa Sawani	80.7	3.1	45.7	17.5	4.6	5.0	9.7	1.5	9.5	29.3	252.3	42.6	65.3
Punjab Padmini	59.0	2.7	51.7	19.2	4.4	4.4	8.9	1.5	9.8	27.0	253.1	43.7	66.5
HB-9-29	45.1	2.8	48.6	14.1	5.8	5.5	8.7	1.4	10.3	29.7	215.8	52.4	69.3
HB-06-46-1-1	64.1	2.5	50.0	13.4	5.5	5.2	9	1.3	9.6	18.2	219.9	54.3	61.1
HB-S-4	56.8	2.9	49.3	19.1	4.5	5.1	9.6	1.6	9.2	36.4	246.2	30.0	44.0
HB-25-2-1	66.7	2.9	49.3	19.6	5.6	5.9	7.9	1.7	8.5	33.2	190.1	37.4	47.6
HBBT-19	62.0	2.7	50.3	14.8	5.8	4.8	9.0	1.3	8.7	28.1	230.8	39.0	44.8
HBT-48	85.8	2.5	47.0	14.2	5.5	6.9	8.9	1.3	8.9	29.0	241.1	43.0	57.8
HBT-08-3-1	46.6	2.3	53.7	16.5	5.0	5.4	8.7	1.8	8.6	18.8	217.3	45.6	59.1
Prabhani Kranti	77.6	2.6	47.6	20.4	4.7	6.4	9.7	1.8	9.4	36.4	249.0	45.0	63.8
HBT-11-1	43.2	2.0	51.6	16.6	5.7	5.2	8.9	1.5	8.3	19.6	282.4	47.6	65.1
HBT-42	75.2	2.4	50.3	17.3	5.0	4.3	9.2	1.4	9.0	33.6	211.9	49.7	61.0
HBT-49-1	101.0	3.5	41.6	19.6	4.5	3.8	9.9	1.5	11.0	37.7	293.8	53.3	57.4
HBT-15	80.1	2.5	49.0	14.5	4.9	5.7	8.4	1.8	8.7	26.2	226.0	47.3	65.2
JNDOL-05	75.1	3.1	50.6	17.5	5.6	7.6	9.5	1.3	7.9	28.7	251.4	38.0	47.8
HB-691-08	106.3	3.5	40.3	18.0	4.9	3.5	7.8	1.2	10.1	40.8	301.5	56.3	62.0
HBTC-6-7-1	98.9	2.9	45.6	20.4	4.2	3.9	10.0	1.6	9.5	38.7	280.5	50.3	62.5
HBT-53	85.1	3.3	47.3	17.6	4.8	4.4	8.6	1.3	9.0	35.6	238.5	52.0	65.0
Arka Abhay	104.5	3.3	45.6	20.9	4.1	4.2	9.7	1.5	8.7	36.7	270.7	55.7	66.4
Hisar Unnat	75.5	3.0	42	15.5	4.9	3.0	10.4	1.4	9.7	35.4	291.1	55.6	64.6
Varsha Uphar	93.7	3.2	40.6	19.7	4.8	3.6	9.0	1.3	8.5	37.5	250.0	48.0	69.3
Hisar Naveen	74.8	2.9	41	16.3	5.0	4.2	8.7	1.6	9.6	39.2	282.2	42.0	67.1
HB-9-27	64.2	2.2	51.3	15.6	5.7	5.0	8.6	1.3	8.3	28.4	196.9	40.6	48.5
HBT-12-1	48.4	2.8	51.6	16.3	5.0	7.0	8.3	1.2	10.4	29.5	200.0	29.6	49.9
SE (m)	4.4	0.2	1.4	0.6	0.2	0.25	0.2	0.04	0.31	2.5	11.4	2.2	1.6
CV %	10.7	12.1	5.1	6.2	9.0	8.4	5.4	5.5	6.0	12.9	8.1	7.6	4.4
CD %	12.5	0.6	4.0	1.7	0.7	0.7	0.8	0.1	0.8	7.0	32.5	6.2	4.6

PH-plant height, BPP- branches per plant, DFF- days to 50 % flowering, PL- petiole length, INL- inter-nodal length, FFN- first fruit node, FL- fruit length, FD- fruit diameter, FW- fruit weight, FPP- fruits per plant, FYPP- fruit yield per plant.

percentage of mean for the trait first fruit node, which is in agreement with the findings of the present investigation (20).

Heritability is the amount of phenotypic variation in a population that can be attributed to individual genetic differences, or it is a measure of how reliably a genotype can be identified by the expression of its phenotype. High heritability with high genetic advance was observed for plant height and first fruit node, which was similar to the results reported previously (21–24). Moderate heritability with moderate genetic advance was recorded for the character days taken to 50 % flowering, number of branches per plant and fruit diameter. Similar results for days to taken to 50 % flowering was observed as given in reference (25).

The close proximity between PCV and GCV values for most traits indicates minimal environmental influence and suggests that phenotypic selection would be effective. High variability coupled with high heritability and genetic advance for plant height and first fruit node indicates the predominance of additive gene action, making these traits reliable selection criteria in early generations. The moderate heritability and genetic advance observed for number of fruits per plant suggest the involvement of both genetic and environmental factors, indicating the need for selection in later generations. High variability in plant height may be attributed to differential growth vigour and inter-nodal elongation among genotypes, reflecting diverse genetic backgrounds.

Conclusion

The present investigation revealed considerable genetic variability among okra genotypes for yield and yield-associated traits. Traits such as plant height, first fruit node and fruit yield per plant exhibited high heritability coupled with high genetic advance, indicating their suitability for direct selection. Genotypes HB-691-08, HBT-49-1, Hisar Unnat, Hisar Naveen and HBTC-6-7-1 were identified as superior and can be utilized as potential parents in recombination breeding programmes aimed at yield improvement. Further evaluation across multi-location and seasons is recommended to confirm their stability and adaptability.

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Authors' contributions

Conceptualisation of the study was carried out by RF, SKD and DS. The original draft of the manuscript was prepared by RF, IA, AKR and N. The manuscript was reviewed and edited by RF, SKD, DS and TM. Visualisation and graphical components were developed by RF, IA, AKR, N and TM. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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