PLANT SCIENCE TODAY
Vol 12(sp3): 01–08
https://doi.org/10.14719/pst.8767

eISSN 2348-1900

RESEARCH ARTICLE

Genetic variability, correlation and path analysis for fruit yield and its attributes in F_2 generation in selected crosses of okra (*Abelmoschus esculentus* (L.) Moench.)

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Received: 09 April 2025; Accepted: 11 September 2025; Available online: Version 1.0: 08 December 2025

Cite this article: Elangaimannan R, Sathishkumar M, Venkatesan M, Dhanasekaran D, Arunkumar V, Suganthi S. Genetic variability, correlation and path analysis for fruit yield and its attributes in F_2 generation in selected crosses of okra (*Abelmoschus esculentus* (L.) Moench.). Plant Science Today. 2025;12(sp3):01–08. https://doi.org/10.14719/pst.8767

Abstract

Studies were conducted to know the genetic variability and character association and path co-efficient for nine quantitative characters in F_2 generation of three crosses in okra. The results indicated that the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were moderate to high for yield per plant, number of fruits per plant, plant height in cross-1. High broad sense heritability coupled with high genetic advance as mean percent was recorded for plant height, internodal length, fruit length, fruit grith, fruit weight, number of nodes per plant, number of fruits per plant and fruit yield per plant for all the three crosses which indicated lower environmental influence on these traits and the prevalence of additive genes. Simple and early selection schemes would be effective for the improvement of these traits. In all the three crosses, fruit yield was positively and significantly correlated with number of fruits per plant, fruit grith, number of nodes per plant and fruit weight. This indicated that the fruit yield could be improved through indirect selection of these traits. The higher frequency of total desirable transgressive segregants was recovered in cross-3. Overall, cross-2 combines high genetic variability, strong heritability and high direct effects on yield-related traits, making it the most promising for selection and improvement in okra breeding.

Keywords: correlation; genetic advance; genetic variability; heritability

Introduction

Okra is an important vegetable crop grown in India and many parts of the world. Okra breeding strategy involves assembling or generating variable germplasm and selection of superior genotypes for utilizing them in hybridization program to develop a superior variety. The success of any crop improvement program depends on the extent of genetic variability existing in the population or germplasm. Variability results due to difference in the genetic constitution of the individuals of a population or in the environment in which they are grown. The GCV % does not reflect the amount of heritable variation. The knowledge of heritability of a character helps the plant breeders in predicting the genetic advance for any quantitative characters and aids in exercising necessary selection procedure. Heritability estimates show the amount of heritable and non-heritable components of variation exhibited by the individual trait. The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because selection on any particular trait may bring about undesirable changes in associated characters.

Materials and Methods

The present study was carried out in okra involving second generation progenies of three crosses and their respective parents. Field evaluation of okra crosses was carried out at the experimental farm of Department of Genetics and Plant breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar during March 2024. The study comprises of five parents namely, IC330087, IC33175, IC29359, EC169344 and EC169336 with three F_2 crosses such as, IC33087 × EC169336 (cross-1), IC33175 × IC29359 (cross-2) and IC33175 × EC169344 (cross-3).

Three crosses that were developed by half-diallel method and their parental lines were obtained from seed bank of Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University for this study. The cross combinates were

IC33087 × EC169336, IC33175 × IC29359, IC33175 × EC169344 and the five parents namely IC330087, IC33175, IC29359, EC169344 and EC169336. The parents were evaluated following a randomized block design with three replications by maintaining ten plants in a row per replication and the F_2 population sown without replication following single plot design at Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar.

The experimental material consists of three F_2 segregating population and the five parents associated with them. The parents were sown in a randomized block design with three replications. Each parent was grown in a single row with a spacing of 30 cm × 15 cm by maintaining ten plants. The biometrical characters were recorded for the three crosses, such as 184 plants in cross-1, 218 plants in cross-2 and 196 plants in the cross-3, respectively. Five competitive plants per parent were randomly selected from each replication and tagged. The mean of these five plants was considered for statistical analysis.

With respect to F_2, observations were recorded in all the plants of each cross for nine economic characters such as days to 50 % flowering and days to flowering, plant height (cm), mean internodal length (cm), fruit length (cm), fruit diameter (cm), fruit weight (g), number of nodes per plant, number of fruits per plant and fruit yield per plant (g) were recorded.

Statistical analysis was estimated for genotypic and phenotypic co-efficient of variation (GCV and PCV) were calculated (1). The heritability in broad sense was calculated and expressed in percentage. The genetic advance (GA) for a particular character was estimated (2). The GA as percent of mean (3). The direct and indirect effects on seed yield were calculated through path coefficient analysis (4, 5). Analysis of variance, genetic variability and heritability was analysed by the statistical tool RStudio. Transgressive segregation in F_2 segregating generation of three cross the mean performance of the individual progenies' population was compared with the parental mean and the superior progenies were identified.

Results and Discussion

The magnitude of genetic variability can determine the pace and quantum of genetic improvement through selection or hybridization program followed by selection. Phenotypic variance measures the magnitude of variation arising out of differences in phenotypic values, while the genotypic variance measures the magnitude of variation arising out due to difference within the genotypic values. Thus, study of genetic variability along with heritability is the first step to succeed in selection and utilization of genotypes in breeding programs. The experimental findings of the present investigation have been discussed here under.

Variability studies

Selection is also useful when there is genetic variability among the individuals in a population. Hence, insight into the magnitude of genetic variability present in a population is important to a plant breeder for starting a judicious breeding program. The better index for measuring genetic variation is the GCV for comparing the genetic variability present in different traits (6). A close relationship between GCV and PCV was observed for all the characters in the present study. The better index for measuring genetic variation is the GCV to compare the variability present in different characters (6).

In the present investigation, the magnitude of the PCV was slightly greater than the GCV, revealing very little influence of environmental variation for their expression. This indicated that phenotypic variability may be considered a reliable measure of genotypic variability. The characters fruit girth registered low PCV and GCV in all the three crosses and fruit length in cross-1 and cross-2. These findings are in accordance with the results for fruit girth (7). Greater magnitude of PCV and GCV was observed for yield per plant, number of fruits per plant, plant height in cross-1 and cross-2; for internodal length in cross-2 and cross-3 and for fruit weight and fruit length in cross-3 (Table 1). Similar findings were reported for fruit yield per plant, number of fruits per plant and plant heigh; for fruit yield per plant and plant height; for fruit weight and for internodal length (8-11). The greater magnitude of PCV was observed for fruit weight (cross-1) and fruit yield (cross-2 and cross-3). High GCV was recorded for fruit number (cross-1) and fruit yield (cross-2 and cross-3). High heritability was registered for fruit number for all three crosses. As these traits are highly heritable, selecting them will likely result in substantial genetic gain and improvement in desired characteristics. Therefore, these traits could be considered prime candidates for direct selection to enhance crop performance and yield.

Moderate PCV and low GCV were observed for fruit weight in cross-1 and cross-2, plant height and number of fruits per plant in cross-3. Similar findings were reported for fruit weight (12, 13). It indicates that the variability due to genetic factors alone is low. This suggests that the trait is relatively stable genetically, with less scope for further improvement through selection. High PCV and moderate GCV were observed for internodal length in cross-1, for fruit yield per plant in cross-3. Similar findings were reported for fruit yield per plant and for internodal length (14, 15). High PCV indicates significant overall variability in the trait, while moderate GCV suggests that a considerable portion of this variability is genetically inherited, but there is also a substantial environmental influence. Moderate PCV and moderate GCV were observed for number of nodes per plant and days to first flowering in all the three crosses (Table 1). Similar findings were reported and for number of nodes per plant and for days to first flowering (16, 17). Moderate PCV and GCV values suggest that while there is still considerable genetic variability, environmental factors also play a significant role. This implies that selection for these traits might be less straightforward, requiring more refined and careful selection methods.

Comparison of variability for different traits across three crosses

Fruit length and fruit weight showed low amount of variability both at phenotypic and genotypic level in all the three crosses and yield per plant, number of fruits per plant recorded high variability in cross -1 and cross-2 but moderate in cross-3. Days to flowering, nodes per plant reported moderate variability in all the three crosses. For the next generation, prioritize selecting high-yielding genotypes from cross-1 and cross-2. Hence, focus should give more on traits with high variability, like yield per plant and number of fruits, for significant improvement and a balanced selection to moderate variability traits like days to flowering and nodes per plant.

Heritability and genetic advance as percent of mean

During the present investigation, high heritability was exhibited by fruit length, fruit girth, fruit weight, number of nodes per plant, number of fruits per plant and fruit yield per plant in F_2 populations of all the three crosses, while high heritability had been noticed for

Table 1. genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean for various traits

Sr. No.	characters	Cross-1				Cross-2				Cross-3			
		(PCV %)	(GCV %)	(h^2bs) (%)	(GAM)	(PCV %)	(GCV %)	(h^2bs) (%)	(GAM)	(PCV %)	(GCV %)	(h^2bs) (%)	(GAM)
1	**Days to first flowering**	12.25	12.19	26.68	15.93	11.48	11.34	55.25	25.78	11.27	11.17	38.23	16.25
2	**Plant height at final harvest (cm)**	23.39	21.96	57.26	21.72	17.62	15.79	80.24	29.13	15.72	14.38	58.26	30.15
3	**Internodal length (cm)**	20.63	16.44	63.50	26.99	19.20	13.94	52.71	20.84	21.47	21.09	96.46	42.67
4	**Fruit length (cm)**	15.38	13.38	75.62	23.96	16.41	14.17	74.51	25.19	16.80	15.20	81.87	28.34
5	**Fruit girth (cm)**	22.21	20.02	81.25	37.17	28.69	24.10	70.59	41.72	25.11	21.65	74.36	38.46
6	**Fruit weight (g)**	28.99	14.97	99.05	25.00	20.57	18.01	76.61	32.47	20.63	12.75	98.28	22.81
7	**No. of nodes/plant**	18.42	13.94	88.14	42.47	22.65	16.83	97.60	23.08	25.12	19.17	83.74	27.12
8	**No. of fruits/plant**	22.55	22.50	99.98	46.44	18.25	18.24	99.88	37.55	19.69	19.68	99.96	40.54
9	**Fruit yield/plant (g)**	23.47	22.25	89.95	43.48	35.73	34.83	94.99	69.92	32.70	31.71	94.04	63.35

internodal length in cross-1 and cross-3, for plant height in cross-2 (Table 1). These traits are largely governed by genetic factors, making them suitable candidates for selection in breeding programs. Similar reports were observed for fruit weight, fruit length and plant height at final harvest; number of fruits per plant and fruit yield per plant (10, 18-20). Moderate estimates of heritability were recorded for plant height in cross-1 and cross-3, for days to first flowering in cross-2 and cross-3. Which indicated that selection based on phenotypic performance would be rewarding on partitioning of environmental variances. These findings are in accordance with plant height and for days to first flowering (19, 21).

High genetic advance as percent of mean in F_2 populations of all the three crosses was exhibited by plant height at final harvest, internodal length, fruit length, fruit girth, number of nodes per plant, fruit weight and number of fruits per plant and fruit yield per plant, reinforcing the potential for substantial genetic improvement through selection. The high genetic advance suggests that these traits not only have high heritability but also respond well to selection, offering promising avenues for enhancing yield and other agronomic traits. Similar results were reported for number of fruits per plant; fruit yield per plant; internodal length and plant height at final harvest (22-24). However, the moderate genetic advance as percent of mean was observed in F_2 populations of all the three crosses for days to first flowering, revealed comparatively less response to selection.

High heritability coupled with high genetic advance as per cent of mean was recorded in F_2 populations of all the three crosses for characters like; plant height at final harvest, internodal length, fruit length, fruit girth, fruit weight, number of nodes per plant, number of fruits per plant and fruit yield per plant suggested the preponderance of additive genes. The combined effect of high heritability and genetic advance is crucial in plant breeding. High heritability alone is insufficient as it does not guarantee substantial improvement and ensure significant genetic gain and efficient breeding efforts. Similar results were reported for fruit yield per plant and plant height at final harvest; number of fruits per plant (10, 25). Moderate heritability along with high genetic advance as percent of mean (GAM) as observed in cross-1 and cross-2 for days to first flowering. Similar findings were reported for days to first flowering, which indicated the role of both additive and non-additive gene actions that governs the inheritance of these traits and offers the best possibility of improvement through progeny selection or any modified selection procedures aiming to exploit the additive gene effects (11).

Correlation coefficient

Correlation study gives an idea about the extent of relationship between different variables. Direct selection for yield and yield component traits is not effective as it is a complex quantitative character and is highly influenced by environment. High genotype and environment interaction will restrict improvement, if selection is based on yield. In the present findings of F_2 populations of all the three crosses, fruit yield per plant exhibited positive and highly significant correlation with number of fruits per plant, fruit girth, number of nodes per plant and fruit weight. Similar results were obtained for fruit weight and number of fruits per plant (26-30). While, in cross-3 fruit length showed positive and highly significant correlation with fruit yield per plant. Similar results were obtained for fruit yield per plant (29). For the next generation selection, prioritize plants with a high number of fruits per plant, larger fruit girth, more nodes per plant and heavier fruit weight, as these traits are positively correlated with fruit yield. In F_2 populations of selected crosses, days to first flowering had highly significant and negative correlations with plant height at final harvest, fruit yield per plant and number of fruits per plant in cross-1. Similar results were obtained for plant height at final harvest (31). While it showed significant and negative correlation with fruit yield per plant, number of fruits per plant in cross-2 and fruit yield per plant in cross-3, which is in accordance with the earlier observations (31). In all the three crosses, fruit length in cross-1, internodal length in cross-2 exhibited non-significant correlation with fruit yield per plant, which is in accordance with the earlier observations (26).

In cross-1, plant height at final harvest exhibited negative and highly significant correlations with negative correlations with fruit yield per plant and number of fruits per plant (Table 2). Similar results were obtained for plant height at final harvest and fruit length (31, 32). In cross-2, plant height at final harvest exhibited negative and highly significant correlation with number of fruits per plant,

Table 2. Phenotypic correlation coefficients among nine traits in cross-1

Characters	Days to first flowering	Plant height (cm)	Internodal length (cm)	Fruit length (cm)	Fruit girth (cm)	No. of nodes / plant	No. of fruits / plant	Fruit weight (g)	Fruit yield / plant (g)
Days to first flowering	1.000								
Plant height (cm)	-0.403**	1.000							
Internodal length (cm)	0.328**	0.242*	1.000						
Fruit length (cm)	0.313**	0.032	0.135*	1.000					
Fruit grith (cm)	0.337**	0.128	0.294**	-0.008	1.000				
No. of nodes / plant	0.304**	-0.425*	-0.563**	0.154*	0.538**	1.000			
No. of fruits / plant	-0.241**	-0.635**	-0.156*	0.037	0.512**	0.548**	1.000		
Fruit weight (g)	0.068	0.145*	0.043	-0.207*	0.099	0.101	0.215*	1.000	
Fruit yield / plant (g)	-0.2185**	-0.549**	-0.1389*	0.088	0.5032**	0.5205**	0.9656**	0.4554**	1.000

Table 3. Phenotypic correlation coefficients among nine traits in cross-2

Characters	Days to first flowering	Plant height (cm)	Internodal length (cm)	Fruit length (cm)	Fruit girth (cm)	No. of nodes / plant	No. of fruits / plant	Fruit weight (g)	Fruit yield / plant (g)
Days to first flowering	1.000								
Plant height(cm)	-0.109	1.000							
Internodal length (cm)	0.046	0.164*	1.000						
Fruit length (cm)	0.082	0.050	-0.239**	1.000					
Fruit grith (cm)	0.131*	0.172*	0.213**	-0.233**	1.000				
No. of nodes / plant	0.078	-0.357**	-0.247**	-0.081	0.339**	1.000			
No. of fruits / plant	-0.151*	-0.321**	-0.149	0.130	0.456**	0.590**	1.000		
Fruit weight (g)	0.021	0.304**	0.144	-0.042	0.246**	0.150	0.309**	1.000	
Fruit yield / plant (g)	-0.1485*	-0.4688**	-0.097	0.157*	0.5928**	0.5658**	1.174**	0.749**	1.000

number of nodes per plant, fruit yield per plant and positive correlation with fruit weight (Table 3). While in cross-3, highly significant and negative correlation with number of fruits per plant, fruit weight and positive correlation with fruit girth, number of nodes per plant, number of fruits per plant were observed (Table 4). Similar results were obtained for fruit grith, number of nodes per plant, number of fruits per plant (25). For the next generation, in cross-1, select shorter plants to improve fruit yield and the number of fruits per plant. In cross-2, prioritize shorter plants with a higher number of nodes and fruits, balancing fruit weight while in cross-3, focus on selecting shorter plants with better fruit girth and higher node counts.

Across all crosses, emphasize traits like fruit yield and fruit girth, ensuring that plant height does not negatively impact key yield attributes. In cross-1, fruit length exhibited positive and significant correlation with number of nodes per plant. In cross-2, it showed significant and positive correlations with fruit yield per plant and in cross-3 it showed highly significant and positive correlations with fruit yield per plant, number of fruits per plant and number of nodes per plant (32-34). For the next generation, select plants with longer fruit lengths across all crosses, as this trait is positively correlated with key yield components.

In cross-1, prioritize plants with more nodes per plant. In cross-2 and cross-3, focus on plants with higher fruit yields, with cross-3 selections also considering the number of fruits and nodes per plant. This strategy will enhance both fruit length and overall yield. In all the three crosses, fruit weight exhibited positive and highly significant correlation with fruit yield per plant. For the next generation, focus on selecting plants with higher fruit weight, as it is positively and significantly correlated with fruit yield across all three crosses. Prioritize individuals with the heaviest fruits to enhance overall yield potential (32, 33). In all the three crosses, fruit grith exhibited positive and highly significant correlations with fruit yield per plant, number of fruits per plant, number of nodes per plant. Similar results were obtained for fruit yield per plant, number of fruits per plant and number of nodes per plant (27, 28). While, in cross-2 and cross-3, fruit grith had positive correlation with fruit weight highly significant and significant respectively. For the next generation, prioritize selecting plants with larger fruit girth, as it positively correlates with higher fruit yield, more fruits per plant and increased number of nodes, ensuring overall yield improvement.

In all the three crosses, number of nodes per plant exhibited positive and significant correlation with number of fruits per plant and fruit yield per plant. Similar results were obtained for number of fruits per plant (28). While, in cross-3 it had highly significant and negative correlation with fruit weight. In all the three crosses,

Table 4. Phenotypic correlation coefficients among nine traits in cross-3

Characters	Days to first flowering	Plant height (cm)	Internodal length (cm)	Fruit length (cm)	Fruit girth (cm)	No. of nodes / plant	No. of fruits / plant	Fruit weight (g)	Fruit yield / plant (g)
Days to first flowering	1.000								
Plant height (cm)	-0.027	1.000							
Internodal length (cm)	0.053	0.868**	1.000						
Fruit length (cm)	0.079	0.162	0.373**	1.000					
Fruit girth (cm)	0.212*	0.246**	0.356**	0.206*	1.000				
No. of nodes / plant	0.240**	0.646**	0.656**	0.306**	0.456**	1.000			
No. of fruits / plant	0.230**	0.600**	0.620**	0.265**	0.443**	0.946**	1.000		
Fruit weight (g)	0.201*	-0.256**	-0.148	-0.111	0.158*	-0.373**	-0.440**	1.000	
Fruit yield / plant (g)	-0.187*	-0.571**	-0.619**	0.257**	0.554**	1.186**	1.269**	0.853**	1.000

number of fruits per plant exhibited positive and highly significant correlation with fruit yield per plant. For the next generation, prioritize selecting plants with a higher number of fruits per plant, as this trait is strongly linked to increased fruit yield. This direct selection will effectively enhance overall yield in the subsequent generation (25, 35). Whereas, in cross-2 it had highly significant and positive correlation with fruit weight and negative correlation with fruit weight in cross-3.

Correlation coefficient analysis of the present investigation revealed that in F_2 populations of all the three crosses, fruit yield per plant exhibited positive and highly significant correlations with number of fruits per plant, fruit girth, number of nodes per plant and fruit weight, which indicating that these characters are the primary yield determinants in okra and selection criteria based on these characters would be beneficial for improvement of fruit yield per plant. These are the most important attributes, which contributed towards higher fruit yield.

Path coefficient

Path coefficient analysis is a powerful tool, which enable partitioning of the given relationship in its further components. In other words, it takes into account not only the relationship of component character with the dependent character but also simultaneously takes care of its relationship with others component also. Thus, it helps in understanding the casual system in a better way because it enables partitioning the total correlation coefficient into direct and indirect effects of various characters. In the present investigation, path coefficient analysis was carried out for character under study using simple correlation coefficient and taking fruit yield per plant as dependent variables in order to see the casual factor and identify the components, which are responsible for producing fruit yield per plant.

In the present study, F_2 populations of all the crosses, path coefficient analysis revealed that number of fruits per plant had highest positive direct effect on fruit yield per plant. This was in accordance with reports for highest positive direct effect on fruit yield per plant (36-39). The number of fruits per plant has the highest positive direct effect on fruit yield per plant, prioritize selecting plants with a higher number of fruits in the next generation. This will directly enhance fruit yield. Combine this selection with traits like early flowering to ensure overall productivity. Validate selections through field trials to confirm stability and performance. Aim for uniformity to achieve consistent yield improvements.

Positive and moderate direct effect on fruit yield per plant was recorded for fruit weight in F_2 populations of all three crosses. Positive and negligible direct effects on fruit yield per plant were recorded for fruit length, fruit girth, number of nodes per plant in F_2 populations of all the three crosses. Similar results were obtained for plant height at final harvest (40, 41). Direct selection practiced on these characters will result in improvement in yield. In F_2 populations of all the three crosses, days to first flowering, plant height, internodal length had negative and negligible direct effect on fruit yield per plant (28, 35). For the next generation, select plants based on traits that positively impact fruit yield, such as fruit weight and number of fruits. Avoid selecting based on days to first flowering, plant height or internodal length, as they have negligible direct effects on yield. Use a selection index focused on yield-related traits and validate selections through field testing. In F_2 populations of all the three crosses, fruit grith, number of nodes per plant, number of fruits per plant, fruit weight and fruit length except in cross-1 had highly significant and positive indirect effect on fruit yield per plant. Path coefficient analysis of the present investigation revealed that number of fruits per plant and fruit weight are important yield components having high direct and positive effects on the improvement of fruit yield in okra.

Transgressive segregation

Transgressive segregation produced hybrid progeny phenotypes that were superior to the parental phenotypes. Such plants were produced by accumulation of favorable genes (positive alleles) from both the parents as a consequence of recombination followed by segregation and additive gene action are also the main reasons for the occurrence of transgressive segregants. Unlike heterosis, extreme phenotypes caused by transgressive segregation were heritably stable. Transgressive segregation could be exploited for development of genotypes with positive characters from both the parents. In the present investigation, superior transgressive segregations for number of nodes per plant, number of fruits per plant, fruit weight and fruit yield per plant were identified in each of the F_2 segregating generations of selected three crosses (Table 5).

Table 4. Phenotypic correlation coefficients among nine traits in cross-3

S. No	cross-1					cross-2					cross-3				
	F_2 Plant number/ parents	Number of nodes per plant	Number of fruits per plant	Fruit yield per plant	Fruit weight	F_2 Plant number/ parents	Number of nodes per plant	Number of fruits per plant	Fruit yield per plant	Fruit weight	F_2 Plant number/ parents	Number of nodes per plant	Number of fruits per plant	Fruit yield per plant	Fruit weight
1	4	15	16	277	17.3	50	16	16	215	15.4	18	16	18	247	14.70
2	6	18	17	294.4	17.3	55	16	18	235	14.1	53	15	16	225	14.24
3	44	16	17	292	17.1	129	15	16	205	15.8	58	17	19	262	15.57
4	46	19	18	309.4	17.2	130	17	17	230	16.5	98	15	17	232	15.62
5	59	16	16	280	17.5	134	15	16	210	17.1	135	15	16	230	14.31
6	86	17	16	279.4	17.5	135	17	19	250	16.2	137	17	18	244	16.55
7	124	17	18	307	17	137	15	18	236	15.1	138	18	20	277	15.84
8	139	17	17	295	17.4	140	15	17	230	15.5	146	15	16	221	16.46
9	Parent 1	15.60	14.80	217.22	14.24	141	15	16	240	15	150	15	18	244	14.32
10	Parent 2	15.20	14.50	212.70	13.70	151	15	16	220	16.8	152	15	17	240	15.06
11.						Parent 1	14.90	14.60	185.33	14.01	155	15	16	218	16.53
12.						Parent 2	13.70	15.40	193.41	12.64	Parent 1	14.90	14.60	185.53	14.01
13.											Parent 2	13.20	15.90	195.43	12.43

Conclusion

The results of the present investigation indicated that hybridization involving six genotypes in F_2 populations of IC33087 × EC169336, IC33175 × IC29359 and IC33175 × EC169344 culminated in increased variability, heritability and genetic advance as percent over mean values. The F_2 populations of all the three crosses can be subjected to simple selection for improvement of fruit yield as they depicted high heritability along with high genetic advance as percent mean for traits like; plant height at final harvest, fruit length, fruit grith, fruit weight, number of nodes per plant, number of fruits per plant and fruit yield per plant. Simultaneous selection may be applied based on correlation and path analysis, yield associated attributes like; number of nodes per plant, number of fruits per plant and fruit weight for genetic improvement in okra. Overall, Cross-2 (IC33175 × IC29359) combines high genetic variability, strong heritability and high direct effects on yield-related traits, making it the most promising for selection and improvement in okra breeding.

Authors' contributions

ER carried out the experiment and recorded the observation. MS pooled and analysed the data and tabulated. MV involved in drafting and aligned the article. DD analysed the D2 analysis and interpreted the results. VA drafting the article. SS did the crossing of F2 generation and conceived of the study and participated in its design and coordination. All authors read and approved the final manuscript.

Compliance with ethical standards

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

Ethical issues: None

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Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

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