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Assessment of morphological variation among F₂ segregating population of Okra (*Abelmoschus esculentus* (L.) Moench)

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Abstract

Eight hundred F₂ population generated by crossing eight diverse parents in structured mating design were evaluated in an augmented design during rabi 2021-22. These 800 F₂ population were assessed for genetic variability for fruit yield and yield related traits viz., days to 50 per cent flowering, plant height (cm), number of branches, number of internodes, inter nodal length (cm), fruit length (cm), fruit diameter (cm), average fruit weight (g), number of fruits per plant, number of seeds per fruit, test weight (g) and fruit yield per plant (g). The analysis of variance revealed highly significant difference among genotypes for all the characters studied. The genetic variability studies revealed high PCV and GCV values for traits viz., number of primary branches, and fruit yield per plant. Moderate PCV and GCV were recorded for traits viz., number of internodes, fruit length, average fruit weight, number of fruits per plant, number of seeds per fruit and test weight. The high heritability coupled with high genetic advance as per cent mean was observed for the traits viz., fruit yield per plant, number of seeds per fruit, number of fruits, average fruit weight, fruit length and number of primary branches per plant, which suggested that most of the traits were highly heritable and the expression of the traits were more of controlled by genetic factor with less influence of environmental factors which allows breeders to improve the crop yield and other desirable traits through selection. Thus, further indicating the predominance of additive gene action for these traits.

Keywords: Okra, variability, heritability, PCA

Introduction

Okra (*Abelmoschus esculentus* L. Moench) is a vegetable crop belongs to the family Malvaceae, with chromosome number of $2n = 8x = 72$ or 144, originated in Southeast Asia^[1]. The crop is widely adaptable because of its ease of cultivation, high export potential, high monetary returns and suited to regions with moderate rainfall^[2]. India ranks first in production and 12th in productivity in the world. The annual production of okra in India is 6.46 million tonnes from an area of 5.30 lakh hectares with a productivity of 12.19 tons per hectare. In Karnataka, okra is grown in an area of 5.35 thousand hectares with production and productivity of 64.01 thousand tonnes and 11.97 tonnes per hectare, respectively^[3].

Okra is commonly used as vegetable and is widely employed in culinary preparations. It has good nutritional value, particularly vitamin C (30 mg/100 g), vitamin A (20mg/100g), zinc (6 mg/100 g), β carotene (300 μ g/100 g) and is a rich source of folic acid (300 μ g/100g)^[4]. A high level of dietary fibre, low caloric value and rich source of minerals like Ca, P, K and Mg have made okra an important component of the human diet. It is a rich source of iodine that helps to cure goitre and leaves are used as a remedy for dysentery. Seeds are also a good source of vitamins, minerals and has medicinally important compounds^[5].

Hybrid breeding in okra is one of the most successful programme in India. To improve productivity, information about the nature and magnitude of genetic divergence would help in selecting diverse parents, which might lead to effective gene recombination upon hybridization. Hybridization breeding is desirable to break the yield barrier in existing genotypes and also breed for different market types. Among the various approaches for developing inbred lines, selection in potential segregating populations is essential. Selecting segregating populations developed from multiple parent cross combinations involving parents with desired diversity may prove better than segregating populations derived from single cross combinations. The multi parent cross combinations generated by employing single cross combinations which are diverse, may produce desired transgressive segregants, such segregating populations help in identifying pureline varieties.

The assessment of variability present in any crop species is an essential prerequisite for formulating an effective breeding programme, as the existing variability can be used to enhance the yield level of cultivars following appropriate breeding strategies. However, the success of any progress in a breeding programme depends not only on the magnitude of genetic variability present in that population but also on the extent to which its desirable characters are heritable.

Materials and Methods

The experimental material comprised 800 F₂ progenies of multi parent crosses. The 800 F₂ progenies were grown during rabi 2021-22 at the experimental plots of the ZAHRS, KSNUAHS, Shivamogga. The 800 F₂ progenies along with five checks (Arka Anamika, Varsha Uphar, SVOK 515, Raadhika and NS 864) were grown in an augmented design with a spacing of 60 × 45 cm. The recommended crop production and protection practices were followed to raise a healthy crop. The observations were recorded on each F₂ plant on the twelve characters. Days to 50% flowering, Plant height (cm), Number of primary branches, Number of internodes on the main stem, Internodal length (cm), Fruit length (cm), Fruit diameter (cm), Average fruit weight (g), Number of fruits per plant, Number of seeds per fruit, Test weight (g) and Fruit yield per plant (g).

Analysis of variance was performed to split the total variability into different sources. The analysis was performed by using the 'augmented RCBD' package of R software (v 4.1.3). Principal component analysis for yield traits was done by 'Facto Mine R' and 'ggplot2' package of R software (v 4.2). Eigen values of principal components was used for selecting the optimum number of principal components.

Results and Discussion

Analysis of variance

The analysis of variance indicated the presence of significant variability among the multi parent cross F₂ population for all the yield contributing characters studied viz., days to fifty per cent flowering, plant height, number of primary branches, number of internodes, inter nodal length, fruit length, fruit diameter, average fruit weight, number of fruits per plant, test weight, number of seeds per fruit and fruit yield per plant (Table 1). Walling *et al.*,^[6] and Ranga *et al.*,^[7] were also observed similar significant variability in okra. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h²), genetic advance (GA) and genetic advance as per cent mean (GAM) for different morphological, yield and yield related traits were presented in Table 2.

Table 1: Analysis of variance for fruit yield and its component traits in F₂ Population of okra

Source of Variation	Degrees of freedom	Mean Sum of Squares											
		DFF	PH	NPB	NIN	IL	FL	FD	AFW	NOF	TW	TW	FYPP
Block (Ignoring genotypes)	3	1.08	36.48	0.01	0.09	0.01	0.40	0.004	0.10	0.32	0.22	1.25	101.4
Genotypes+ Checks (Ignoring blocks)	804	15.37	169.26*	0.58**	6.34**	0.59	6.43**	0s.04	8.01**	11.23**	0.77**	47.84**	7453.60**
Genotypes	799	15.31	163.70*	0.57**	6.24*	0.51	6.36**	0.04	7.91**	10.84**	0.72*	47.20**	7069.89**
Checks	4	27.24	1283.39**	0.48**	21.57**	15.75**	21.02**	0.16**	25.31**	10.33*	3.41**	163.87**	28796.22**
Checks vs Genotypes	1	13.56	157.40	10.36**	27.62**	0.52	2.55	0.14*	20.78**	325.41**	35.41**	95.59*	228664.18**
Error	12	8.89	57.75	0.02	2.60	0.33	1.68	0.02	2.10	2.19	0.29	10.61	483.16

*-Significant at 5% **- Significant at 1%

Where,

DFF = Days to fifty per cent flowering

NOF = Number of fruits per plant

FL = Fruit length (cm)

NPB = Number of primary branches

NOS = Number of seeds per fruit

AFW = Average fruit weight (g)

IL = Internodal length (cm)

PH = Plant height (cm)

TW = Test weight (g)

FD = Fruit diameter (cm)

NIN = Number of internodes

FYPP = Fruit yield per plant (g)

Days to 50 per cent flowering

The variability observed for days to 50 per cent flowering ranged from 36 to 57 days with an average value of 45.94 days. The recorded GCV and PCV values for days to fifty per cent flowering were 5.52 and 8.52 per cent, respectively with

41.96 per cent heritability. The observed genetic advance was 3.39 while, genetic advance as per cent mean was 7.37. These results are in conformity with the findings of Adewusi and Adeweso^[8] reported moderate heritability coupled with low genetic advance as per cent mean.

Table 2: Estimates of variability parameters for yield and its contributing traits in F₂ population of Okra

Sl. No.	Traits	Mean	Range		GCV (%)	PCV (%)	h ² (bs) (%)	GA	GAM
			Minimum	Maximum					
1	Days to 50 per cent flowering	45.94	36.00	57.00	5.52	8.52	41.96	3.39	7.37
2	Plant height (cm)	124.70	84.00	153.00	8.25	10.26	64.72	17.08	13.70
3	Number of primary branches	1.25	0.00	4.00	59.09	60.13	96.56	1.5	119.78
4	Number of internodes	16.41	11.00	24.00	11.63	15.23	58.34	3.01	18.33
5	Internodal length (cm)	7.77	4.83	10.56	5.44	9.22	34.82	0.51	6.62
6	Fruit length (cm)	17.02	8.96	24.36	12.71	14.82	73.55	3.83	22.48
7	Fruit diameter (cm)	1.69	1.20	2.64	8.02	11.77	46.47	0.19	11.28

8	Average fruit weight (g)	20.27	11.23	28.32	11.88	13.87	73.40	4.26	20.99
9	Number of fruits per plant	18.29	11.75	28.95	16.08	18.00	79.79	5.42	29.63
10	Number of seeds per fruit	51.14	32.25	84.23	11.83	13.44	77.53	10.99	21.49
11	Test weight (g)	5.90	4.02	8.63	11.11	14.35	59.88	1.05	17.73
12	Fruit yield per plant (g)	369.41	154.32	621.25	21.97	22.76	93.17	161.61	43.75

*-Significant at 5% **- Significant at 1%

Plant height (cm)

The plant height ranged from 84 to 153 cm with an average of 124.70 cm. The genotypic and phenotypic coefficient of variability were 8.25 and 10.26, respectively. The heritability estimate was high with 64.72 per cent coupled with a moderate genetic advance of 17.08 per cent and the genetic advance over mean was 13.70. Heritability estimates was high and genetic advance as per cent mean was moderate for plant height hence, selection can be made for this trait. Walling *et al.*,^[6] and Temam *et al.*,^[9] reported high heritability for plant height in okra.

Number of primary branches

Number of primary branches ranged from 0 to 4 with an average of 1.25 branches per plant. The recorded GCV and PCV was 59.09 and 60.13 per cent, respectively. For number of primary branches 96.56 per cent heritability was recorded. The observed genetic advance was 1.5 while, genetic advance as per cent mean was 119.78. The results of Alam *et al.*,^[10] and Ashraf *et al.*,^[11] reported high heritability.

Number of internodes

Number of internodes varied from 11 to 24 across the population with a grand mean of 16.41. Observed GCV and PCV for number of internodes is 11.63 and 15.23 per cent respectively and heritability of 58.34 per cent was observed. Genetic advance and genetic advance as per cent mean for number of internodes was 3.01 and 18.33 respectively. Shwetha *et al.*,^[12] reported moderate heritability and moderate genetic advance as per cent mean in their investigation.

Internodal length (cm)

The internodal length ranged from 4.83 to 10.56 with an average of 7.77. The recorded GCV and PCV are 5.44 and 9.22 per cent, respectively internodal length. A moderate heritability of 34.82 per cent with a genetic advance of 0.51 and 6.62 genetic advance as per cent mean was recorded. Thulisarm *et al.*,^[13] and Raval *et al.*,^[14] reported high heritability.

Fruit length (cm)

The mean value for fruit length was 17.02 cm with a range of 8.96 to 24.36 cm. Moderate genotypic and phenotypic coefficients of variation of 12.71 and 14.82 respectively were recorded for this trait. High heritability estimate (73.55%) accompanied with low GA (3.83) and high GAM of 22.48 as per cent of mean was observed among the genotypes. These findings are in agreement with the earlier works of Alake *et al.*,^[15] and Temam *et al.*,^[9].

Fruit diameter (cm)

A range of 1.20 to 2.64 cm was observed for fruit diameter with a mean value of 1.69 cm. The recorded GCV and PCV for fruit diameter was 8.02 and 11.77 per cent, respectively. For fruit diameter 46.47 per cent heritability was recorded. The observed genetic advance was 0.19 while, genetic

advance as per cent mean was 11.28. The results of Badiger *et al.*,^[16] and Ashraf *et al.*,^[11] showed moderate heritability with lower genetic advance as per cent mean.

Average fruit weight (g)

Average fruit weight ranged from 11.23 to 28.32g with an average of 20.27 g. It recorded 11.88 per cent GCV and 13.87 per cent PCV. Heritability of average fruit weight was 73.40 per cent and observed genetic advance was 4.26. While, genetic advance as per cent mean was 20.99. Average fruit weight showed high heritability and genetic advance as per cent mean. Temam *et al.*,^[9] and Shwetha *et al.*,^[12] in their studies reported high heritability for average fruit weight and it was comparable with present investigation.

Number of fruits per plant

Number of fruits per plant found varied from 11.75 to 28.95 across the population with a grand mean of 18.29. Moderate phenotypic and genotypic coefficients of variation of 18.29 and 16.08 respectively were noticed for number of fruits per plant. Whereas, number of fruits per plant had a high heritability of 79.79 per cent was recorded. The observed genetic advance was 5.42 with genetic advance as per cent mean of 29.63. Due to high heritability supported with moderately high coefficient of variation and narrow difference between GCV and PCV, plant height exhibited high genetic advance. Hence, substantial improvement of this trait could be achieved through selection. Similar observations were also recorded by Alam *et al.*,^[10] and Ashraf *et al.*,^[11].

Number of seeds per fruit

The variability observed for number of seeds per fruit ranged from 32.25 to 84.23 with an average value of 51.14. Moderate PCV (13.44 %) and GCV (11.83 %) were observed for this trait with high heritability (77.53 %) with moderate GA (10.99) and high GAM (21.49 %). Temam *et al.*,^[9] and Walling *et al.*,^[6] reported high heritability and genetic advance as per cent mean for number of seeds per fruit.

Test weight

Hundred seed weight significantly varied among the population ranging from 4.02 to 8.63 g with a grand mean of 5.90 g. The phenotypic and genotypic coefficient of variability were moderate at 14.35 and 11.11 per cent, respectively. The heritability estimate was moderate (59.88 %) with genetic advance and genetic advance as per cent mean of 1.05 and 17.73 respectively for test weight. Mohammed *et al.*,^[17] reported moderate heritability and moderate genetic advance as per cent mean for test weight.

Fruit yield per plant (g)

The fruit yield per plant ranged from 154.23 to 621.25 g with an average value of 369.41 g. High phenotypic and genotypic coefficients of variation of 22.76 and 21.97 respectively were noticed for fruit yield per plant. High heritability of 93.17 per cent coupled with higher genetic advance of 43.75 per cent over mean was recorded. Due to high heritability supported

with moderately high coefficient of variation and narrow difference between GCV (21.97) and PCV (22.76), plant height exhibited the high genetic advance. Hence, substantial improvement of this trait could be achieved through selection. Similar observations were also recorded by Alam *et al.*,^[10] and Melaku *et al.*,^[18].

Principal component analysis

The main goal of Principal component analysis (PCA) is to reduce the dimensionality in a set of correlated attributes into a smaller set of uncorrelated attributes that explain the majority of the variation in the original attributes. PCA was done to transform the original variables into a limited number of uncorrelated new variables and to allow the visualization of differences among characters. Choosing the number of principal components that represents the original data set is one of the key features in PCA.

The number of principal components that has a practical significance is determined by the eigenvalues. One of the

simple but arbitrary thumb rule is to consider the principal components, which have eigenvalues of one or greater as having practical significance. Usually, components with eigen values less than 1 are excluded^[19]. The PCA transformed the 12 raw set of data into 12 factors loadings or principal components. Results of PCA biplot based on phenotypic traits revealed that the first five PC (which account for about 77.63 per cent of the total variability) had eigen values greater than 1 displaying significant variability compared to the rest of the PCs which had eigen values less than 1. These latter PCs had not been considered, as they were not significantly influencing the variability among the cultivars. A biplot analysis was carried out based on the two most important PCs to visualize the percentage contribution of each trait to the total variability were determined. The percentage of variation explained by the first five PCs, their Eigen value and the factor scores for the 12 morphological traits are presented in Table 3.

Table 3: Principal component analysis of 12 traits in okra cultivars studied showing Eigen vectors, Eigen values, total and cumulative percentage of variance explained by the first five PC axes

Trait	PC1	PC2	PC3	PC4	PC5
DFE	0.11	-0.00	-0.16	0.09	0.43
PH	0.82	-0.14	-0.11	-0.10	-0.05
NPB	0.24	-0.01	-0.05	0.05	0.82
NIN	0.91	-0.17	-0.19	-0.09	-0.19
IL	-0.54	0.11	0.21	0.03	0.40
FL	0.09	0.22	0.65	-0.62	0.04
FD	0.13	0.19	0.15	0.89	-0.09
AFW	0.33	0.38	0.77	0.19	-0.07
NOF	0.90	-0.09	-0.18	-0.03	0.15
NOS	-0.06	-0.86	0.33	0.08	0.06
TW	0.07	0.84	-0.38	-0.11	0.01
FYPP	0.88	0.16	0.31	0.08	0.11
Eigen value	3.61	1.77	1.55	1.27	1.10
Total variance (%)	30.12	14.76	12.97	10.59	9.17
Cumulative variance (%)	30.12	44.89	57.86	68.45	77.63

Where

DFE = Days to fifty per cent flowering

PH = Plant height (cm)

NPB = Number of primary branches

NIN = Number of internodes

IL = Internodal length (cm)

FL = Fruit length (cm)

FD = Fruit diameter (cm)

AFW = Average fruit weight (g)

NOF = Number of fruits

NOS = Number of seeds per fruit

TW = Test weight (g)

FYPP = Fruit yield per plant (g)

From the loading of the variables in PCA I was found that plant height, number of internodes, number of fruits and fruit yield per plant were the dominant features which contributed to 30.12 per cent of the total variation. In PCA II, test weight and average fruit weight exerted a maximum influence which accounts for 14.76 per cent of the total variation. Fruit length and average fruit weight were dominant characters in PCA III which accounted for 12.97 per cent of the total variation. However, fruit diameter and number of primary branches per plant showed dominant features in PCA IV and V accounting for 10.59 and 9.17 per cent of the total variation, respectively. Thus, it is suggested that the use of these traits will help in saving a considerable amount of time for the identification of superior okra genotypes.

The first component is more important, since it accounted for 30.12 per cent of the variation, while the second accounted for 14.76 per cent. The traits *viz.*, plant height, number of internodes, number of fruits and fruit yield per plant exhibited

significant association with PC1, indicating that breeding in this component will lead to increase in these characters. The high contribution of fruit length, test weight, number of seeds per fruit and fruit yield per plant towards total variation had been reported earlier by Amoatey *et al.*,^[20] and Ranga *et al.*,^[7] in okra. Biplot analysis was carried out based on the first two PCs and the traits were shown on the biplots (Fig. 1) to clearly visualize their associations and differences.

High PCV and GCV values were observed for fruit yield per plant and number of primary branches and moderate GCV and PCV values were recorded for number of internodes, average fruit weight, number of fruits per plant, fruit length, number of seeds per fruit and test weight. Hence, these characters can be improved through direct selection from existing genotypes.

The traits which have shown high heritability and coupled with high genetic advance as per cent mean *viz.*, fruit yield per plant, number of seeds per fruit, number of fruits per

plant, average fruit weight, fruit length and number of primary branches could be further improved through simple

selection.

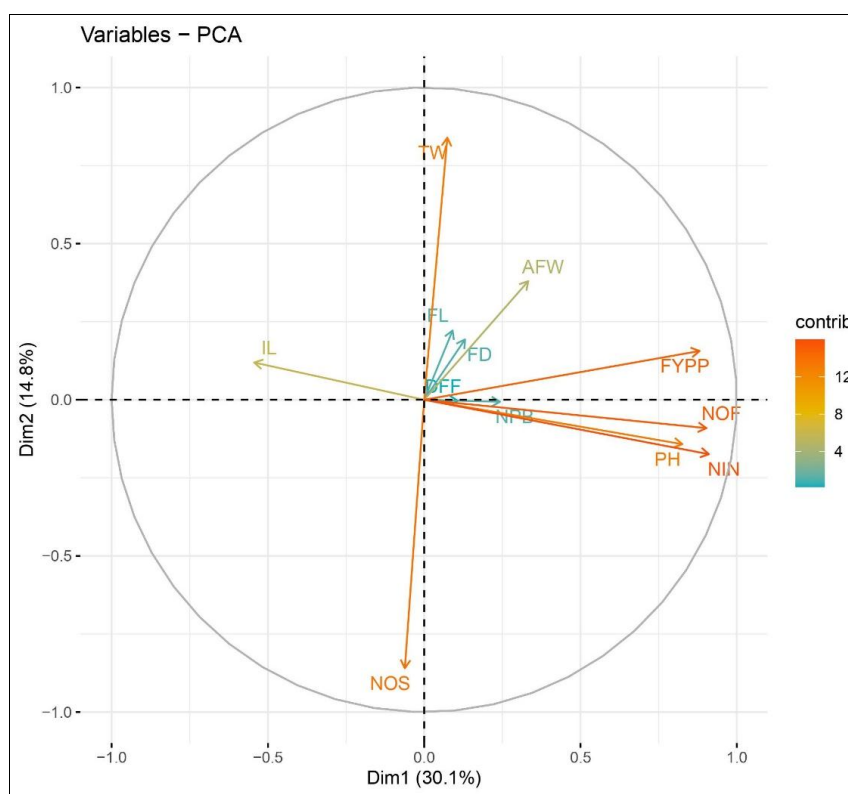


Fig 6: Biplot between PC1 and PC2 showing contribution of various traits responsible for variability in F₂ population of okra

Where

DFF = Days to fifty per cent flowering

PH = Plant height (cm)

NPB = Number of primary branches

NIN = Number of internodes

IL = Internodal length (cm)

FL = Fruit length (cm)

FD = Fruit diameter (cm)

AFW = Average fruit weight (g)

NOF = Number of fruits

NOS = Number of seeds per fruit

TW = Test weight (g)

FYPP = Fruit yield per plant (g)

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