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ASSESSMENT OF VARIABILITY IN F$_2$ GENERATION OF OKRA (*ABELMOSCHUS ESCULENTUS* L. MOENCH)

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ABSTRACT

A field experiment entitled "Evaluation of F$_2$ generation population in Okra (*Abelmoschus esculentus* L. Moench)" was undertaken during *Kharif* 2024 in randomized block design with two replications at Experimental Farm, Horticulture Research Scheme (Vegetable), VNMKV, Parbhani. Twenty-five genotypes (9 parents and 14 crosses) including two checks Radhika and Parbhani Kranti to estimate the variability to select the superior genotypes. Analysis of variance were studied for mean sum of squares revealed significant differences for all the eighteen characters examined. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). High estimates of genotypic and phenotypic coefficient of variation were observed for YVMV infestation on plants (%), fruit length (cm), number of seeds per fruit, weight of 10 seeds (g) and total number of fruits per plant. The characters *viz*., plant height (cm), fruit length (cm), total number of fruits per plant, number of seeds per fruit, weight of 10 seeds (g) and weight of 100 seeds (g). Further selection of these characters will improve the breeding efficiency of the okra genotypes.

Key words : Okra, Variability, Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), YVMV.

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] is an important vegetable crop cultivated annually in tropical and subtropical regions worldwide for its immature green fruits and tender leaves. Although, primarily self-pollinated, okra is often cross-pollinated with an outcrossing rate ranging from 4% to 10%, which can reach up to 42.2% through insect-assisted pollination contributing significantly to its genetic variability (Kumar *et al*., 2006). A member of the family Malvaceae okra is amphidiploid in nature possessing a chromosome number of 2n = 130. The geographical origin of okra remains debated among researchers. One hypothesis suggests its origin in northern India, where *Abelmoschus tuberculatus* a potential progenitor species is native. Alternatively, another theory proposes that okra was domesticated in Ethiopia or northern Egypt, citing evidence of ancient cultivation in East Africa and the presence of *Abelmoschus ficulneus*, another possible ancestor. However, conclusive evidence supporting either origin theory is still lacking. The genus *Abelmoschus* includes several species such as *A. moschatus*, *A. manihot*, *A. esculentus*, *A. tuberculatus*, *A. ficulneus*, *A. crinitus* and *A. angulosus* (Charrier, 1984).

Okra plays a vital role in the fruit and vegetable industry due to its numerous benefits including high nutritional and medicinal value, adaptability to various climates, ease of cultivation, year-round production, high yield potential and suitability for export (Reddy, 2010). It is an excellent source of essential vitamins and minerals particularly vitamin A and B, calcium, phosphorus and iron (Lamont, 1999). Its rich iodine content makes it a potential remedy for goiter (Purewal and Randhawa, 1947). The mucilaginous properties of okra aid digestion and contribute to its high carbohydrate, protein and mineral content (Adeniji and Kehinde, 2012). Beyond its culinary uses, mature okra fruits and stems serve as raw materials in the paper industry, while mucilaginous extracts from green stems are used in sugar cane juice clarification in India. Additionally, dried okra seeds contain approximately 40% oil and 20-30% crude protein (Berry *et al*., 1988) and can be roasted as a coffee substitute (Martin, 1982). It is a very nutritious vegetable, rich in vitamins, calcium, potassium and other mineral matters (Aykroyd, 1963).

Despite its commercial importance and adaptability, the average productivity of okra in India remaining low, primarily due to limited genetic variability among cultivated varieties and the absence of targeted selection strategies for yield improvement (Ranga and Darvhankar, 2022). Knowledge on extent of genotypic and phenotypic variations present in any crop species perform an important role in success of breeding programme for releasing superior varieties. Genetic variability plays a crucial role in achieving heritable improvements making it essential to assess the nature and extent of diversity when selecting desirable genotypes from a germplasm. The broad genetic variability present in available germplasm provides valuable opportunities for further genetic enhancement and crop improvement. Okra has good amount of variability so there is a great scope for improvement of okra crop. Vegetable breeders making efforts to increase the productivity by improving high yielding varieties which can suitable for all environmental conditions.

Materials and Methods

The experimental material constituted twenty-five okra genotypes (9 parents, 14 crosses and 2 checks) collected from F_1 generation and the experiment was conducted at the Experimental Farm, Horticulture Research Scheme (Vegetable), VNMKV, Parbhani, during *Kharif* 2024. The study was carried out in Randomized Block Design with two replications and having a spacing of 60 cm × 45 cm in row to row and plant to plant, respectively. The seeds were sown by dibbling 2-3 seeds with a plot size of 3 m × 2.7 m, the basal dose of 100:50:50 Kg/ha was given to crop. These genotypes were evaluated and observations were recorded on eighteen characters *viz*., plant height (cm), number of primary branches per plant, internodal length (cm), days to 50 % flowering , first flowering node, first fruiting node, fruit length (cm), fruit width (cm), fruit weight (g), total number of fruits per plant, number of ridges per fruit, number of seeds per fruit, weight of 10 seeds (g), weight of 100 seeds (g), total yield per plant (g), number of marketable fruits per plant, marketable yield per plant (g) and YVMV infestation (%). For statistical analysis mean values of five randomly selected plants were taken in each replication. The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated according to Burton (1952).

Table 1 : Parents and checks used in experiment.

S. no.	Parents	Code
1.	Parbhani Kranti	P_1
2.	Arka Anamika	P_2
3.	Arka Abhay	P_3
4.	Phule Utkarsha	P_4
5.	Varsha Uphar	P_5
6.	Pusa Sawani	P_6
7.	Kashi Satdhari	P_7
8.	*Abelmoschus manihot*	P_8
9.	*Abelmoschus tetraphyllus*	P_9
10.	Radhika	Check1
11.	Parbhani Kranti	Check2

Table 2 : Parentage of crosses used in experiment.

S. no.	Crosses	Parentage
1.	C_1	Parbhani Kranti x *Abelmoschus manihot*
2.	C_2	Parbhani Kranti x *Abelmoschus tetraphyllus*
3.	C_3	Arka Anamika x *Abelmoschus manihot*
4.	C_4	Arka Anamika x *Abelmoschus tetraphyllus*
5.	C_5	Arka Abhay x *Abelmoschus manihot*
6.	C_6	Arka Abhay x *Abelmoschus tetraphyllus*
7.	C_7	Phule Utkarsha x *Abelmoschus manihot*
8.	C_8	Phule Utkarsha x *Abelmoschus tetraphyllus*
9.	C_9	Varsha Uphar x *Abelmoschus manihot*
10.	C_{10}	Varsha Uphar x *Abelmoschus tetraphyllus*
11.	C_{11}	Pusa Sawani x *Abelmoschus manihot*
12.	C_{12}	Pusa Sawani x *Abelmoschus tetraphyllus*
13.	C_{13}	Kashi Satdhari x *Abelmoschus manihot*
14.	C_{14}	Kashi Satdhari x *Abelmoschus tetraphyllus*

Results and Discussion

Analysis of variance

Analysis of variance revealed that all the twenty-five genotypes differed significantly for all the eighteen characters studied, which revealed the existence of sufficient variations in all the characters for effective selection in the material under study (Table 3).

Estimation of genetic parameters

The Phenotypic coefficient of variation (PCV) was observed greater than genotypic coefficient of variation (GCV) for all the traits shown in Table 4 differences were minimal in the majority of characters. The highest

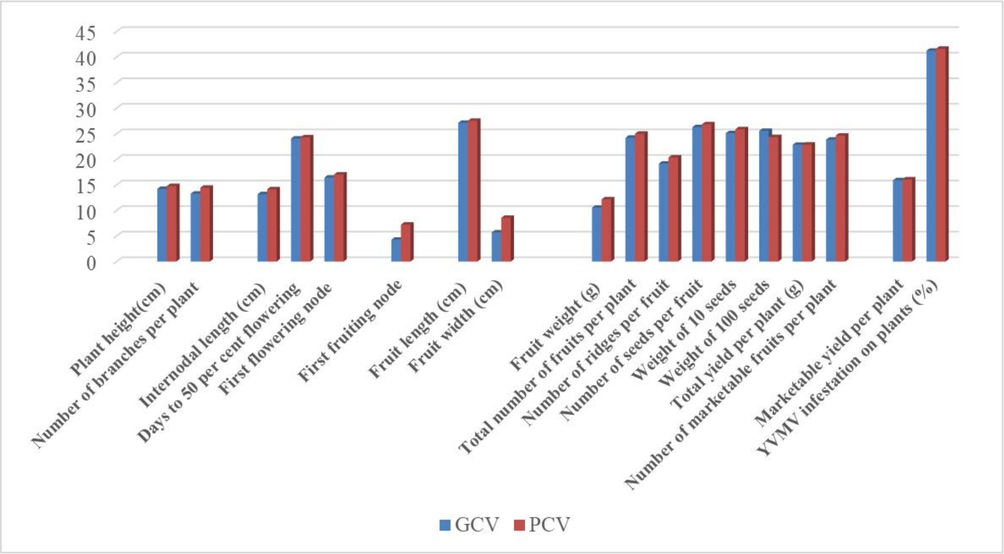

Fig. 1 : Graphical representation of genotypic and phenotypic coefficient of variation for quantitative and qualitative traits in Okra.

Table 3 : Analysis of variance (ANOVA) for different characters in Okra.

S. no.	**Characters**	**Source of variance**			
		Replication		**Treatment**	**Error**
		D.F	1	24	24
1.	Plant height (cm)	0.320		572.23**	21.94
2.	Number of branches per plant	0.001		0.570**	0.047
3.	Internodal length (cm)	0.074		1.573**	0.110
4.	Days to 50 % flowering	1.445		190.21**	1.781
5.	First flowering node	0.039		0.365**	0.013
6.	First fruiting node	0.034		0.083**	0.040
7.	Fruit length (cm)	0.028		24.78**	0.341
8.	Fruit width (cm)	1.72		2.914**	1.118
9.	Fruit weight (g)	0.275		6.538**	0.932
10.	Total number of fruits per plant	0.007		13.329**	0.424
11.	Number of ridges per fruit	0.192		2.332**	0.140
12.	Number of seeds per fruit	0.080		71.09**	1.497
13.	Weight of 10 seeds (g)	0.001		0.049**	0.002
14.	Weight of 100 seeds (g)	0.066		4.046**	0.304
15.	Total yield per plant (g)	0.110		2356.75**	3.622
16.	Number of marketable fruits per plant	0.020		3.591**	0.115
17.	Marketable yield per plant (g)	0.020		633.086**	6.507
18.	YVMV infestation on plants (%)	0.510		34.284**	0.315

*and ** indicates significance at 5% and 1%, respectively.

phenotypic and genotypic coefficient of variation were observed for YVMV infestation on plants (41.61% and 41.22%), fruit length (27.52 cm, 27.14 cm)), number of seeds per fruit (26.84 and 26.28), weight of 10 seeds (25.87 g and 25.10)) and total number of fruits per plant (25.0 and 24.21). The moderate phenotypic and genotypic coefficient of variation were observed in number of marketable fruits per plant (24.62 and 23.85), days to 50% flowering (24.29 and 24.06), weight of 100 seeds (24.33 g and 22.56 g), total yield per plant (22.87 g and 22.84 g) and number of ridges per fruit (20.35 and 19.16). Lowest phenotypic and genotypic coefficient of variation observed for first fruiting node (7.21 and 4.27), fruit width (8.54 cm and 5.7 cm) and fruit weight (12.17 g and 10.54

Table 4 : Parameters of variability for quantitative traits of okra.

Characters	Range	Mean	GCV	PCV	Heritability %	Genetic advance %	GA in % of mean
Plant height(cm)	100.5-165.2	116.72	14.21	14.76	92.61%	32.88	28.17
Number of branches per plant	3.30-5.70	3.84	13.29	14.43	84.89%	0.97	25.23
Internodal length (cm)	4.90-8.90	6.49	13.17	14.13	86.94%	1.64	25.30
Days to 50 per cent flowering	33.6- 73.0	40.33	24.06	24.29	98.14%	19.80	49.11
First flowering node	2.10-3.85	2.55	16.43	17.03	93.13%	0.83	32.67
First fruiting node	3.10-3.90	3.42	4.27	7.21	35.08%	0.17	5.21
Fruit length (cm)	6.85-18.50	12.87	27.14	27.52	97.28%	7.10	55.16
Fruit width (cm)	1.45-1.90	1.66	5.70	8.54	44.54%	1.30	7.83
Fruit weight (g)	11.95-19.15	15.87	10.54	12.17	75.06%	2.98	18.82
Total number of fruits per plant	13.20-24.0	10.48	24.21	25.00	93.84%	5.06	48.32
Number of ridges per fruit	4.5-7.90	5.46	19.16	20.35	88.66%	2.03	37.17
Number of seeds per fruit	4.5-31.5	22.44	26.28	26.84	95.88%	11.89	53.02
Weight of 10 seeds (g)	0.16-0.89	0.61	25.10	25.87	94.12%	0.30	50.16
Weight of 100 seeds (g)	1.35-8.09	6.06	22.56	24.33	86.01%	2.61	43.10
Total yield per plant (g)	185.8-428.2	150.1	22.84	22.87	99.69%	70.55	46.98
Number of marketable fruits per plant	1.95-7.50	5.52	23.85	24.62	93.82%	2.63	47.58
Marketable yield per plant (g)	137.4-288.3	111.2	15.90	16.07	97.97%	36.08	32.43
YVMV infestation on plants (%)	5.30-20.85	9.99	41.22	41.61	98.18%	8.41	84.15

g). Similar results were also reported in okra by Adeoluwa and Kehinde (2011) for fruit length. Singh *et al*. (2007) and Kolakar *et al*. (2018) reported moderate PCV and GCV values for number of marketable fruits per plant and total yield per plant. While Khalid *et al*. (2018) for total number of fruits per plant and yield per plant.

The high heritability estimates were observed in traits total yield per plant (99.69 g) followed by YVMV infestation on plants (98.18%) and days to 50 percent flowering (98.14). While moderate heritability was observed for traits number of branches per plant (84.89), internodal length (86.9 cm) and weight of 100 seeds (86.0 g). Lowest heritability was observed in first fruiting node (35.0) and fruit width (44.5 cm). Similarly, highest genetic advance (%) was observed in character total yield per plant (70.5 g) followed by marketable yield per plant (36.0 g) and plant height (32.8 cm). While moderate genetic advance was observed for weight of 100 seeds (2.61 g), fruit weight (2.98 g) and total number of fruits per plant (5.06). Lowest genetic advance observed for first fruiting node (0.178) followed by weight of 10 seeds (0.309 g) and first flowering node (0.834). Kolakar e*t al*. (2018) reported high heritability for total number of fruits per plant and YVMV infestation on plants. Ankinyele and Osekita (2006) also found the similar findings.

Conclusion

In the 25 genotypes studied all the traits exhibited a wide and substantial range of variability. For every trait assessed the phenotypic coefficient of variation (PCV) was found to be higher than the genotypic coefficient of variation (GCV). The small gap between these values indicates that environmental influence on these traits is minimal and making phenotypic selection effective. All traits showed high heritability coupled with high genetic advance as a percentage of the mean suggesting that additive gene effects primarily govern their expression. Hence direct selection would be highly effective method for improving these traits.

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