



# International Journal of Research in Agronomy

E-ISSN: 2618-0618

P-ISSN: 2618-060X

© Agronomy

[www.agronomyjournals.com](http://www.agronomyjournals.com)

2024; SP-7(10): 43-46

Received: 20-08-2024

Accepted: 26-09-2024

**Charan K**

Department of Vegetable Science,  
College of Horticulture, Mudigere,  
Karnataka, India

**Prakash Kerure**

Department of Vegetable Science,  
College of Horticulture, Hiriya,  
Karnataka, India

**Srinivasa V**

Department of Vegetable Science,  
College of Horticulture, Mudigere,  
Karnataka, India

**Kantharaj Y**

Department of Post Harvest  
Management, College of  
Horticulture, Mudigere,  
Karnataka, India

**Ramesh AN**

Department of Crop Improvement  
and Biotechnology, College of  
Horticulture, Hiriya, Karnataka,  
India

**Corresponding Author:**

**Charan K**

Department of Vegetable Science,  
College of Horticulture, Mudigere,  
Karnataka, India

## Variability studies of okra (*Abelmoschus esculentus* L. Moench) F<sub>4</sub> population for yield and yield related traits

Charan K, Prakash Kerure, Srinivasa V, Kantharaj Y and Ramesh AN

DOI: <https://doi.org/10.33545/2618060X.2024.v7.i10Sa.1729>

### Abstract

The present investigation was carried out to understand the extent of genetic variability between yield and its traits in F<sub>4</sub> segregating populations of the three bi-parental crosses viz., IIHR-875 × IIHR-478, IIHR-478 × IIHR-567 and IIHR-604 × IIHR-347 at ZAHRS, Babbur Farm, Hiriya during 2023-24. The statistical design augmented design was followed to analyse the different traits. In F<sub>4</sub> segregating population of the bi-parental cross IIHR-875 × IIHR-478 recorded high GCV and PCV values for first fruit producing node. Whereas in F<sub>4</sub> populations of the bi-parental cross IIHR-478 × IIHR-567 exhibited moderate GCV and high PCV values for number of branches per plant. With regard to F<sub>4</sub> populations of the bi-parental cross IIHR-604 × IIHR-347 shown high PCV and GCV values for plant height and total yield per plant. The higher heritability coupled with high genetic advance as percent of mean was observed for inter nodal length, first fruit producing node, fruit length, fruit length and total yield per plant in the F<sub>4</sub> populations of the bi-parental cross IIHR-875 × IIHR-478. Whereas in F<sub>4</sub> populations of the bi-parental cross IIHR-478 × IIHR-567 exhibited high heritability with high genetic advance as percent of mean for first fruit producing node. With regard to F<sub>4</sub> populations of the bi-parental cross IIHR-604 × IIHR-347 manifested moderate heritability with high genetic advance as percent of mean for number of branches per plant.

**Keywords:** Okra, variability, heritability, genetic advance

### Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] commonly known as bhendi, lady's finger, gumbo or okra is a popular vegetable crop grown in both subtropical and tropical locations around the world. It belongs to the class dicotyledonae, order Malvales, family Malvaceae, and genus *Abelmoschus* (syn. *Hibiscus*) with chromosome number 2n=130 (Joshi and Hardas, 1953) <sup>[12]</sup>. Okra is native to Ethiopia, but recent studies suggest it is of African or Asian origin.

Bhendi or okra advantages because of its great nutritional content, medical worth, market value and export potential. Pests such as jassids and bollworms as well as diseases such as yellow vein mosaic and powdery mildew all cause difficulties for okra cultivation, reducing produce quality and increasing cultivation expenses. Some good varieties of okra have been developed in India, however many of them have one or more drawbacks. Crop improvement in okra should focus on plant height, higher yield, more branching, shorter and more internodes, fruit length, number of fruits and resistance to diseases and pests.

A systematic approach to initiating any breeding program involves evaluating the diversity of available materials. Maximizing genetic heterogeneity is essential for the effective selection of superior offspring. When beneficial diversity is limited, creating variation through processes such as hybridization, mutation, or hybridization followed by selection in a segregating population becomes necessary. A breeder's thorough understanding of genetic diversity facilitates the selection of appropriate lines for crossing. Promising inbred lines are generated only when these lines are crossed to produce heterotic hybrids, which have the potential to yield segregating populations.

Okra is an often cross pollinated crop, it thus provides an opportunity to breed homozygous true breeding and productive lines which may be used as variety and also to produce F<sub>1</sub> hybrids for commercial exploitation of heterosis. The breeders very often use segregating populations as source population to exercise selection for identifying homozygous lines with better

performance to develop varieties. At the same time, the breeding lines from the advanced generations are also used as parental lines for developing commercially exploitable heterotic hybrids. But, most often the source of early generations *i.e.*, F<sub>2</sub>, F<sub>3</sub>, F<sub>4</sub>, F<sub>5</sub> and F<sub>6</sub> segregating populations had offer wider opportunities for achieving high success, because of wider genetic base (Mallikarjun and Savitramma, 2017) [15].

Yield is considered to be a complex character and is also under the influence of numerous genes. Indeed, there are various reports that illustrate how direct selection for yield in plants is highly effective. In addition, the inheritance of quantitative characters is often also influenced by variation in other characters, either because of pleiotropy or genetic linkage. The genetic variability along with heritability, which expresses the relative amount of heritable portion of variation along with genetic advance, is more useful in predicting the resultant effect of selecting the best individuals (Burton and De Wane, 1953) [3].

### Materials and Methods

The experimental materials of the present study comprises of F<sub>4</sub> population of three okra crosses *viz.*, IIHR-875 × IIHR-478, IIHR-478 × IIHR-567, IIHR-604 × IIHR-347, along with four checks *viz.*, Arka Anamika, Arka Abhay, Shakti, Hiriyuru local. The seeds of F<sub>4</sub> populations were obtained by selfing F<sub>3</sub> hybrids of plants IIHR-875 × IIHR-478, IIHR-478 × IIHR-567, IIHR-604 × IIHR-347 and the selfed seeds of parents were used for the F<sub>4</sub> study.

During Late *kharif* (September) 2023 season, F<sub>4</sub> plants along with four check varieties were raised. The experiment plot was laid out in augmented block design with 10 blocks. The experiment comprised of 20 plants with four check varieties in each block and 200 plants each of the F<sub>4</sub> populations were sown at a spacing of 60 cm × 45 cm. The experiment was carried out at ZAHRS, Babbur farm, Hiriyur (Tq), Chitradurga (Dist.), Karnataka (State) during *kharif* season of 2023-2024.

All recommended agronomic practices and plant protection measures were followed during the crop growth period to ensure proper growth and good yield. The observations were recorded for all the plants.

Observations for individual plants were recorded for yield and yield related traits that includes *viz.*, plant height (cm), internodal length (cm), branches per plant (No.), first fruit producing node, fruit length (cm), fruit diameter (mm), average fruit weight (g), number of fruits per plant and total yield per plant (g) as per the NBPGR minimal descriptors.

Genotypic and phenotypic co-efficient of variation were calculated according to the method suggested by Burton and De-Vane (1953) [3]. Heritability in broad sense and the genetic advance as percent of mean to visualize the relative utility of

genetic gain were worked out as suggested by Johnson *et al.*, (1955) [11].

### Results and Discussion

The results on the variability, heritability and genetic advance for 9 characters in okra for the cross IIHR-875 × IIHR-478 have been presented in Table 1.

The estimated PCV was higher than GCV for all the studied parameters with close correspondence between them. This indicated the fact that the environmental influence is very low and hence selection for these characters could be made based on their phenotypic performance Katagi *et al.* (2013) [13], Duggi *et al.* (2013) [4] and Barche *et al.* (2014) [2].

The first fruit-producing node exhibited high levels of PCV and GCV, with a narrow difference between the two, suggesting less environmental influence and more variation within the populations. These findings align with previous studies by Kumar *et al.* (2012) [14], and Prakash *et al.* (2017) [19].

Moderate PCV and GCV observed for inter nodal length, number of fruits per plant, fruit diameter, fruit length, average fruit weight indicating the influence of environment on the expression of the traits. This indicates greater scope for selection to improve upon these characters in the cross studied. This findings conformity with the results of Singh *et al.* (2007) [22], Prakash *et al.* (2017) [19].

The high broad sense heritability values for the trait such as inter nodal length, first fruit producing node, fruit length, fruit diameter, average fruit weight, total yield per plant suggested that this character was less influenced by the environmental effects, which makes them effectively transmitted to the progeny. There is a strong influence of fixable additive gene effects for inheritance of this trait and therefore, selection for this trait may lead to the fast-genetic improvement.

The higher estimates of heritability coupled with high genetic advance as percent of mean is recorded in first fruit producing node, fruit length, fruit diameter, average fruit weight and total yield per plant which indicates due to additive gene effects, and suggests that effective progress in improvement through the selection could be achieved for improving first fruit producing node, fruit length, fruit diameter, average fruit weight and total yield per plant. Similar results are obtained by Hallur *et al.* (2015) [7] and Prakash *et al.* (2017) [19].

The moderate heritability with moderate to high genetic advance as percent of mean is recorded in number of fruits per plant and average fruit weight, this indicated the non-additive gene action and hybridization followed by selection would be useful for improving these traits. This findings in conformity with results of Hazar and Basu (2000) [8] for number of fruits per plant.

**Table 1:** Estimates of genetic parameters for growth, and yield attributes in F<sub>4</sub> population of the bi-parental cross IIHR-875 × IIHR-478

Sl. No.	Genetic Parameters	Mean	Range		GV	PV	GCV (%)	PCV (%)	h <sup>2</sup> bs (%)	GA	GAM (%)
			Min.	Max.							
1	Plant height (cm)	142.11	63.00	183.00	132.10	350.57	8.10	13.20	37.70	14.53	10.23
2	Number of branches per plant	2.47	2.00	6.00	0.01	0.36	5.20	24.40	4.60	0.05	2.29
3	Inter-nodal length (cm)	8.08	4.93	13.01	0.81	0.99	11.30	12.40	82.20	1.69	20.91
4	First fruit producing node	4.96	3.00	5.00	9.25	9.42	25.96	26.41	98.20	3.52	71.06
5	Number of fruits per plant	20.35	12.00	31.00	5.65	10.05	11.70	15.60	56.30	3.67	18.07
6	Total yield per plant (g)	266.26	146.40	883.30	2065.68	3287.38	17.10	21.60	62.90	74.21	27.84
7	Fruit length (cm)	13.76	10.20	19.80	2.87	4.13	12.40	14.80	69.60	2.91	21.17
8	Fruit diameter (mm)	14.39	10.60	19.90	3.33	3.99	12.70	13.90	83.60	3.44	23.91
9	Average fruit weight (g)	13.04	10.20	28.48	1.64	2.47	9.90	12.10	66.60	2.15	16.49

The results on the variability, heritability and genetic advance for 9 characters in okra for the cross IIHR-478 × IIHR-567 have been presented in Table 2. The estimated PCV was higher than GCV for all the studied parameters with close correspondence between them. This indicated the fact that the environmental influence is very low and hence selection for these characters could be made based on their phenotypic performance Katagi *et al.* (2013)<sup>[13]</sup>, Duggi *et al.* (2013)<sup>[4]</sup> and Barche *et al.* (2014)<sup>[2]</sup> Moderate PCV and GCV were observed for plant height, number of branches per plant, first fruit-producing node, fruit length and fruit diameter indicating the influence of environment on the expression of the traits. This indicates a greater scope for selection to improve upon these characters in the cross-studied. These findings conformity with the results of Hazar and Basu (2000)<sup>[8]</sup> for plant height and Singh *et al.* (2007)<sup>[22]</sup> for fruit length and fruit diameter.

The high broad sense heritability values for the trait such as plant height, first fruit producing node, fruit length, fruit diameter suggested that this character was less influenced by the

environmental effects, which makes them effectively transmitted to the progeny. There is a strong influence of fixable additive gene effects for the inheritance of this trait and therefore, selection for this trait may lead to fast genetic improvement.

The higher estimates of heritability coupled with high genetic advance as percent of mean is recorded in the first fruit producing node which indicates due to additive gene effects, and suggest that effective progress in improvement through the selection could be achieved for improving first fruit producing node. Similar findings were obtained by the results of Indurani and Veeragavathatham (2005)<sup>[9]</sup>.

The moderate heritability with moderate to high genetic advance as percent of mean is recorded in number of branches per plant and average fruit weight this indicated the non-additive gene action and hybridization followed by selection would be useful for improving these traits. This findings in conformity with results of Goswami *et al.* (2014)<sup>[6]</sup> for number of branches per plant.

**Table 2:** Estimates of genetic parameters for growth, and yield attributes in F<sub>4</sub> population of the bi-parental cross IIHR-478 × IIHR-567

Sl. No.	Genetic Parameters	Mean	Range		GV	PV	GCV (%)	PCV (%)	h <sup>2</sup> bs (%)	GA	GAM (%)
			Min.	Max.							
1	Plant height (cm)	152.70	121.00	187.00	20.36	24.96	13.33	16.35	81.57	8.40	5.50
2	Number of branches per plant	2.39	2.00	4.00	0.13	0.24	14.88	20.48	54.17	0.55	22.87
3	Inter-nodal length (cm)	7.89	4.32	11.23	0.07	0.84	3.24	11.64	8.33	0.16	1.99
4	First fruit producing node	5.11	3.00	6.00	0.49	0.65	13.64	15.80	75.38	1.25	24.50
5	Number of fruits per plant	20.90	14.00	27.00	1.25	5.97	5.35	11.70	20.94	1.05	5.04
6	Total yield per plant (g)	270.20	163.20	795.00	586.66	2079.41	8.95	16.86	28.21	26.50	9.81
7	Fruit length (cm)	13.96	10.20	19.40	2.43	3.80	11.16	13.96	63.95	2.57	18.39
8	Fruit diameter (mm)	14.63	12.40	19.80	2.56	4.07	10.94	13.80	62.90	2.61	17.87
9	Average fruit weight (g)	12.92	10.20	29.44	1.21	2.14	8.51	11.31	56.54	1.70	13.19

The results on the variability, heritability and genetic advance for 9 characters in okra for the cross IIHR-478 × IIHR-567 have been presented in Table 3. The estimated PCV was higher than GCV for all the studied parameters with close correspondence between them. This indicated the fact that the environmental influence is very low and hence selection for these characters could be made based on their phenotypic performance Katagi *et al.* (2013)<sup>[13]</sup>, Duggi *et al.* (2013)<sup>[4]</sup> and Barche *et al.* (2014)

Plant height and total yield per plant expressed high amount of PCV and GCV. The difference between PCV and GCV was found to be narrow indicating lesser influence of environment on these characters and the presence of more variation in the populations to select superior segregants in the advanced generation. The results obtained on yield and yield related characters in the present study are in agreement with the reports of Akotkar *et al.* (2010)<sup>[18]</sup>, Pradip *et al.* (2010)<sup>[17]</sup>, Prakash and Pitchaimuthu (2010)<sup>[18]</sup>, Shaikh *et al.* (2013)<sup>[20]</sup>, Sharma *et al.* (2016)<sup>[21]</sup>.

Moderate GCV and high PCV were observed for number of branches per plant, fruit diameter and average fruit weight indicating the influence of the environment on the expression of the traits. This indicates greater scope for selection to improve upon these characters in the cross studied. This findings

conformity with the results of Gangashetty *et al.* (2010)<sup>[5]</sup> for fruit diameter and average fruit weight.

The high broad sense heritability values for the trait such as plant height and total yield per plant suggested that this character was less influenced by the environmental effects, which makes them effectively transmitted to the progeny. There is a strong influence of fixable additive gene effects for inheritance of this trait and therefore, selection for this trait may lead to the fast genetic improvement.

The higher estimates of heritability coupled with low genetic advance as percent of mean is recorded in plant height and total yield per plant which indicates due to additive gene effects, and suggest that effective progress in improvement through the selection could be achieved for improving first fruit producing node. Similar findings were obtained by the results of Indurani and Veeragavathatham (2005)<sup>[9]</sup> and Jindal *et al.* (2010)<sup>[10]</sup> for plant height.

The moderate heritability with moderate genetic advance as percent of mean is recorded in fruit diameter and average fruit weight this indicated the non-additive gene action and hybridization followed by selection would be useful for improving these traits. This findings in conformity with results of Pal *et al.* (2010)<sup>[16]</sup> for fruit diameter.

**Table 3:** Estimates of genetic parameters for growth, and yield attributes in F<sub>4</sub> population of the bi-parental cross IIHR-604 × IIHR-347

Sl. No.	Genetic Parameters	Mean	Range		GV	PV	GCV (%)	PCV (%)	h <sup>2</sup> bs (%)	GA	GAM (%)
			Min.	Max.							
1	Plant height (cm)	147.70	97.00	185.97	35.60	49.10	24.10	33.24	72.51	10.47	7.09
2	Number of branches per plant	2.44	2.00	4.00	0.29	0.51	12.05	20.70	58.22	0.85	34.93
3	Inter-nodal length (cm)	8.58	4.69	11.42	0.09	0.85	1.04	9.88	10.50	0.20	2.32
4	First fruit producing node	4.84	3.00	6.00	0.07	0.29	1.53	6.03	25.34	0.28	5.83
5	Number of fruits per plant	20.72	13	33	1.84	8.58	8.87	41.39	21.43	1.29	6.24
6	Total yield per plant (g)	274.01	162.50	977.50	123.50	149.14	45.07	54.43	82.81	20.83	7.60
7	Fruit length (cm)	13.89	10.40	19.10	1.13	3.26	8.13	23.49	34.60	1.29	9.27
8	Fruit diameter (mm)	14.60	12.96	19.90	2.03	4.60	13.92	31.49	44.19	1.95	13.37
9	Average fruit weight (g)	13.21	9.52	27.20	1.91	2.88	14.42	21.79	66.17	2.31	17.51

### Conclusion

The study of variability, heritability, and genetic advance in okra for the crosses IIHR-875 × IIHR-478, IIHR-478 × IIHR-567, and IIHR-478 × IIHR-567 showed that traits such as the first fruit-producing node, fruit length, fruit diameter, average fruit weight, and total yield per plant exhibited high heritability along with genetic advance. This suggests strong additive gene effects, indicating rapid genetic improvement through selection. Traits like the number of fruits per plant showed moderate heritability and genetic advancement, suggesting hybridization followed by selection would be effective.

### References

- Akotkar PK, De DK, Pal AK. Genetic variability and diversity in okra (*Abelmoschus esculentus* L. Moench). *Electronic Journal of Plant Breeding*. 2010;1(4):393-398.
- Barche S, Nair R, Ramgiri M, Jain PK. Genetic variability in okra (*Abelmoschus esculentus* L. Moench). *An International Quarterly Journal of Environmental Sciences*. 2014;6:153-156.
- Burton GW, De Vane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*. 1953;45:418-481.
- Duggi D, Magadum MA, Srinivasraghavan DS, Kishor, Oommen SK. Genetic analysis of yield and yield-attributing characters in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Agricultural and Environmental Biotechnology*. 2013;6(1):45-50.
- Gangashetty PI, Shanthakumar G, Salimath PM, Patil BB, Mane RS, Haleshkumar B, Waghmore AN. Genetic variability studies in single and double cross advanced generation segregating progenies of bhendi (*Abelmoschus esculentus* (L.) Moench). *Electronic Journal of Plant Breeding*. 2010;1(5):1358-1362.
- Goswami A, Singh B, Singh A. Study of genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *Progress in Agriculture*. 2014;14(1):57-62.
- Hallur RH, Shantappa T, Shivanand B, Jagadeesha RC. Genetic variability, heritability and genetic advance in okra biparental progenies. *International Journal of Advanced Research*. 2015;3(4):1199-1203.
- Hazar P, Basu D. Genetic variability, correlation and path analysis in okra. *Annals of Agricultural Research*. 2000;21(3):452-453.
- Indurani C, Veeraragavathatham D. Genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *Indian Journal of Horticulture*. 2005;62(3):303-305.
- Jindal SK, Arora D, Ghai TR. Variability studies for yield and its contributing traits in okra. *Electronic Journal of Plant Breeding*. 2010;1(6):1495-1499.
- Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybean and their application in selection. *Agronomy Journal*. 1955;47:477-483.
- Joshi AB, Hardas MW. Chromosome number of *Abelmoschus esculentus* plant species related to cultivated bhindi. *Current Science*. 1953;22:384-385.
- Katagi A, Tirakannavar S, Jagadeesha RC, Jayappa J, Shankappa KS. Genetic analysis of association studies in segregating population of okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Forestry and Crop Improvement*. 2013;4(1):13-18.
- Kumar S, Annapurna, Yadav YC, Singh R. Genetic variability, heritability, genetic advance, correlation and path analysis in okra. *Horticultural Flora Research Spectrum*. 2012;1(2):139-144.
- Mallikarjun K, Savithramma DL. Genetic variability, heritability, correlation and regression in F<sub>3</sub> and F<sub>4</sub> segregating generation for traits related to WUE and yield in the cross NRCG 12274 × ICG 12370 of groundnut (*Arachis hypogaea* L.). *International Journal of Current Microbiology and Applied Sciences*. 2017;6(11):3912-3921.
- Pal MK, Singh B, Kumar R, Singh SK. Genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *Environment and Ecology*. 2010;28(1):469-4671.
- Pradip K, Akotkar DKD, Pal AK. Genetic variability and diversity in okra (*Abelmoschus esculentus* L. Moench). *Electronic Journal of Plant Breeding*. 2010;1(4):393-398.
- Prakash K, Pitchaimuthu M. Nature and magnitude of genetic variability and diversity studies in okra (*Abelmoschus esculentus* (L.) Moench). *Electronic Journal of Plant Breeding*. 2010;1(6):1426-1430.
- Prakash K, Pitchaimuthu M, Akshata H. Studies on variability, correlation and path analysis of traits contributing to fruit yield and its components in okra (*Abelmoschus esculentus* (L.) Moench). *Electronic Journal of Plant Breeding*. 2017;8(1):134-141.
- Shaikh M, Mazid SAMA, Mohrir MN, Jadhav RS. Genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *Electronic Journal of Plant Breeding*. 2013;4(3):1255-1257.
- Sharma KP, Mishra DP, Pandey A. Genetic variability studies for yield and its contributing traits in okra (*Abelmoschus esculentus* (L.) Moench). *Journal of Applied and Natural Science*. 2016;8(3):1634-1637.
- Singh AK, Ahmed N, Narayan R, Chatoo MA. Genetic variability, correlations and path coefficient analysis in okra under Kashmir conditions. *Indian Journal of Horticulture*. 2007;64(4):472-474.