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## Genetic variability, heritability and genetic advance in Okra (*Abelmoschus esculentus* (L.) Moench)

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#### Abstract

The present investigation was carried out during *kharif* 2020 at experimental farm, Department of Agricultural Botany, VNMKV, Parbhani. The experimental material consists of forty-two genotypes (including two checks) of which forty genotypes were the derivatives of segregating generations *i.e.* F<sub>2</sub> and Back crosses of Parbhani Kranti × VROR-159, Parbhani Kranti × Kashi Pragati, Kashi Satadhari × BO-2, Kashi Satadhari × VROR-159. These genotypes were evaluated for twelve traits in RBD design with two replications and data was recorded. The experiment has revealed that PBNLF 4, PBNLF 5, PBNLF 6, PBNLF 13, PBNLF 15 and PBNLF 33 genotypes were found superior for yield and yield attributing characters over rest of the genotypes and checks. The traits *viz.*, plant height (cm), internodal length (cm), number of nodes on main stem, number of branches per plant, 100 seed weight (g) and fruit yield per plant (g) have recorded the moderate values of GCV, PCV and high estimates of heritability along with high genetic advance, while the trait number of seeds per fruit have shown moderate estimate of GCV and PCV only. Hence characters showing high to moderate values of PCV, GCV and high estimate of heritability and genetic advance as per cent mean were considered as most important characters and selection of these traits will be more effective in improvement of fruit yield per plant.

**Keywords:** Okra, genotypes, genetic variability, GCV, PCV, heritability, genetic advance

#### Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) is an important vegetable and annual herbaceous crop. It is grown in subtropical and tropical parts of the world for its immature green fruits and fresh leaves. It is generally self-pollinated in nature but it is being an often-cross pollinated crop with an extent of 4-10 per cent out crossing in which insect assisted pollination occurs up to maximum of 42.2 per cent which provide a considerable amount of variability (Kumar, 2006). It is amphidiploid in nature with chromosome number 2n=130 and is belonging to the family Malvaceae. *Abelmoschus esculentus* is the only species which is known to be cultivated extensively as commercial vegetable among 34 species of *Abelmoschus*.

Okra contributes about 60 percent to the total fresh vegetable export, excluding potato, garlic and onion. In India, Okra is cultivated in an area of 0.51 million hectare with 6.18 million tonnes of produce with an average productivity of 12.04 tonnes per hectare (Anonymous, 2019) [4] and in Maharashtra it occupies an area of 13.98 thousand hectare with an annual production of 139.40 thousand tonnes and productivity of 9.97 tonnes per hectare (Anonymous, 2018) [3]. The states which are majorly involved in okra production are west Bengal, Gujarat, Orissa, Bihar and Andhra Pradesh.

Tender fruits of okra are used as vegetable in culinary preparation or it is eaten boiled or made it into slices and eaten after frying. It is having higher average nutritive values than tomato, eggplant and most of cucurbits. In thickening of soups and gravies it is used, as it is high in mucilage content. Its tender and scrumptious green fruits are used in preparing curries and soups or it can be canned and stored in dehydrated or frozen form for consumption during off season. Okra is highly remunerative as compared to leafy vegetables, while in India it is not adopted as leafy vegetable like East countries. In Turkey the seeds of okra are roasted and ground to use them as alternative for coffee and is also used in preparation of vegetable curds. In Thailand slimy soups and sauces are relished which are prepared by boiling okra in water. Okra seeds contain protein about 20 per cent and 20 per cent oil (Tindall 1983, Charrier 1984) and it is a rich source of essential unsaturated fatty acids like linoleic acid. The trial conducted in China have suggested that the alcohol extract of okra leaves can play a role in elimination of oxygen free radicals, alleviate renal tubular-interstitial diseases and reduce proteinuria, also it will improve the renal function (Kumar *et al.* 2009) [15].

Okra has found medical application as a plasma replacement or blood volume expander (Kumar *et al.* 2010) <sup>[17]</sup>. In paper industry stem and mature fruits are used, also they are used as clarifier of sugarcane juice which is further used in preparation of brown sugar and guar (Chauhan, 1972) <sup>[9]</sup>. In preparation of a medicant, the leaves of okra are used which plays a major role in reduction of inflammation. As it is a good source of iodine it controls goiter (Chadha, 2001) <sup>[7]</sup>. It is useful against Genito-urinary disorders, Spermatorrhoea and Chronic dysentery (Nadkarni, 1927) <sup>[19]</sup>.

Evaluation of potentialities of the existing cultivars is essential because it depicts the genetic diversity of the base materials on which depends the promise for further improvement. The success of a breeding programme for the improvement of quantitative attributes depends to a great extent on the magnitude of genetic variability existing in the germplasm. Heritability and genetic advance estimates help the breeder to apply appropriate breeding methodology in the crop improvement programme (Johnson *et al.* 1955) <sup>[12]</sup>. Thrust of any crop improvement programme is to enhance economic yield which is a complex dependent character, mostly inherited quantitatively and is determined by a number of yield components, greatly affected by environmental factors. In determining the potential of genetically different lines and cultivars, breeders have to observe various traits that influence yield. Accurate evaluation of these characters is made more difficult by the genotype by environment interaction. Thus, enabling the plant breeder for the variation and the estimates of the heritability and genetic advance are the important parameters on which the success of selection line depends.

### Materials and Methods

The present investigation was conducted at Experimental Farm, Department of Agricultural Botany, College of Agriculture, VNMKV, Parbhani, during *kharif* 2020. The experimental material consists 42 genotypes (including two checks) which are the derivatives of segregating generations *i.e.* F<sub>2</sub> and Back crosses of Parbhani Kranti × VROR-159, Parbhani Kranti × Kashi Pragati, Kashi Satadhari × BO-2, Kashi Satadhari × VROR-159. The study was carried out in Randomized Block Design with two replications and having a spacing of 60 cm × 30 cm in row to row: plant to plant respectively. The seeds were sown by dibbling 2-3 seeds on a plot of size 1.20 × 3 m<sup>2</sup>, the basal dose of 100:50:50 Kg/ha was given to crop. The agronomic and plant protection measures were given as per requirement. These genotypes were evaluated and observations were recorded on twelve characters *viz.*, Days to 50% flowering, Plant height (cm), Internodal length (cm), Number of nodes on main stem, Number of branches per plant, Fruit length (cm), Fruit diameter (cm), Number of ridges per fruit, Number of fruits per plant, 100 seed weight (g), Number of seeds per fruit and Fruit yield per plant (g). For statistical analysis mean values of five randomly selected plants were taken in each replication. The data were subjected to statistical analysis as per description of Panse and Sukhatme (1985) <sup>[21]</sup>. The genotypic and phenotypic variance was calculated by using mean square from variance table (Johnson *et al.* 1955) <sup>[12]</sup>. GCV and PCV will be calculated according to method suggested by Burton (1952) <sup>[6]</sup>. Heritability (broad sense) was calculated according to method suggested by Allard (1960) <sup>[2]</sup>. Genetic advance was calculated by formula suggested by Johnson *et al.* (1955) <sup>[12]</sup>.

### Results and Discussion

Analysis of variance for various yield and yield contributing traits have shown highly significant difference (Table 1) among all the twelve traits under study at 5% and 1% level of significance, except for the traits *viz.*, days to 50% flowering, number of seeds per fruit and number of ridges per fruit. The range and mean for all the characters presented in Table 2. The mean values for days to 50 per cent flowering was ranged from 44.00 days to 52.00 days; plant height has ranged from 104.20 cm to 165.80 cm; internodal length has ranged from 4.24 cm to 7.54 cm; number of nodes on main stem has ranged from 12.57 to 18.77; number of branches per plant have ranged from 2.04 to 4.06; fruit length has ranged from 11.86 cm to 15.21 cm; fruit diameter have exhibited a mean range of 1.80 cm to 2.01 cm; number of ridges per fruit have exhibited a range of 5.00 ridges to 6.50 ridges per fruit; number of fruits per plant have ranged from 13.54 of fruits per plant to 16.87 fruits per plant; 100 seed weight has ranged from 4.00 g to 7.00 g; number of seeds per fruit have shown a range of 30.15 seeds per fruit to 63.50 seeds per fruit; high range of variation was observed for fruit yield per plant ranging from 228.70 g to 315.00 g. Similar results were observed by Prakash and Pitchaimuthu (2010) <sup>[23]</sup> for plant height, internodal length, fruit length, fruit diameter, number of fruits, 100 seed weight and fruit yield per plant, Walling *et al.* (2020) <sup>[30]</sup> for plant height, number of branches per plant, number of fruits per plant, fruit length, fruit diameter and fruit yield per plant. Several workers including Singh *et al.* (2019) <sup>[28]</sup>, Kudari *et al.* (2020) <sup>[14]</sup> have reported wide range of variability for different yield attributing traits in okra.

According to Shivasubramanian and Menon (1973) <sup>[27]</sup> GCV and PCV were classified as Low (0-10%), Moderate (10-20%), High (20% and above). The phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the traits studied and there was a little difference between the values of PCV and GCV. Moderate PCV and GCV values were recorded for the traits *viz.*, plant height, internodal length, number of nodes on main stem, number of branches per plant, 100 seed weight, number of seeds per fruit and fruit yield per plant. Low PCV and GCV values were observed for days to 50% flowering, fruit length, fruit diameter and number of fruits per plant. Moderate PCV with low GCV was observed for number of ridges per plant. Similar results were obtained by Alam *et al.* (2020) <sup>[1]</sup> for internodal length, plant height, number of nodes on main stem, days to 50 per cent flowering, fruit yield per plant, Kerure *et al.* (2017) <sup>[13]</sup> for days to 50 per cent flowering, 100 seed weight, number of branches per plant and plant height, Kumari *et al.* (2019) <sup>[18]</sup> for plant height, fruit yield per plant, fruit diameter, fruit length, number of fruits per plant, number of branches per plant, Sharma *et al.* (2016) <sup>[26]</sup> for number of fruits per plant, plant height, number of ridges per fruit, fruit length, fruit diameter, number of nodes per plant, Das *et al.* (2012) <sup>[10]</sup> for number of seeds per plant.

According to Robinson *et al.* (1949) <sup>[25]</sup> heritability estimates were grouped as Low (0 - 30%), Moderate (31 - 60%) and High (61% and above). Genetic advance as percent of mean was grouped by Johnson *et al.* (1955) <sup>[12]</sup> as Low (<10%), Moderate (11 - 20%) and High (>20%). All the genotypes under study have shown high heritability coupled with high genetic advance as percent mean for characters *viz.*, plant height, internodal length, number of nodes on main stem, number of branches per plant, 100 seed weight and fruit yield per plant. High heritability indicates that the larger portion of

phenotypic variance has been attributed to genotypic variance and reliable selection should be made for these traits on the basis of phenotypic performance. High heritability along with moderate genetic advance was shown by fruit length and number of fruits per plant, whereas the traits like, days to 50 per cent flowering and fruit diameter have shown high heritability coupled with low genetic advance as per cent mean, indicating that the variations for such characters is due to interaction between both additive and non-additive genetic factors. Moderate heritability with moderate genetic advance as per cent mean was indicated by number of seeds per fruit. Similar results were obtained by Alam *et al.* (2020) [1] for plant height, internodal length, number of nodes on main stem, fruit yield per plant, Yadav *et al.* (2016) [32] for plant

height, number of branches per plant, fruit length, fruit yield per plant, Nikitha *et al.* (2016) [20] for days to 50 per cent flowering and fruit length, Bello *et al.* (2015) [5] fruit diameter, and Walling *et al.* (2020) [30] for fruit diameter and number of ridges per fruit, Kumari *et al.* (2019) [18] for fruit yield, fruit diameter, number of nodes on main stem. High heritability for number of fruits per plant is in accordance with the findings of Yadav *et al.* (2016) [32] and Phanikrishna *et al.* (2015) [22]. Moderate genetic advance as per cent mean for number of seeds per fruit is in accordance to Kumari *et al.* (2019) [18] and Rambabu *et al.* (2019) [24]. Gangashetty *et al.* (2010) [11] for 100 seed weight, fruit length, internodal length, number of branches per plant.

**Table 1:** Analysis of variance for yield and yield attributes in okra genotypes

Sr. No.	Characters	Mean sum of squares		
		Replication (1)	Treatment (41)	Error (41)
1	Days to 50% flowering	1.44	5.74	2.05
2	Plant height	437.80	354.27**	17.91
3	Internodal length	0.02	1.09**	0.07
4	Number of nodes on main stem	0.56	5.40**	0.14
5	Number of branches per plant	0.09	0.39**	0.02
6	Fruit length	0.00	1.12**	0.04
7	Fruit diameter	0.00	0.01**	0.00
8	Number of ridges per fruit	1.44	0.79	0.46
9	Number of fruits per plant	0.44	2.22**	0.16
10	100 seed weight	0.01	0.82**	0.01
11	Number of seeds per fruit	146.59	90.38	37.49
12	Fruit yield per plant (g)	1.78	2246.03**	7.45

**Table 2:** Genetic variability parameters for twelve characters in okra

Sr. no.	Characters	Range	Mean	Genotypic variance	Phenotypic variance	GCV %	PCV %	h <sup>2</sup> (bs) %	GA	GA as % of mean
1	Days to 50% flowering	44-52	45.03	1.84	2.87	3.01	3.76	64.30	2.24	4.98
2	Plant height (cm)	104.2-165.8	127.37	168.17	177.13	10.18	10.44	94.90	26.03	20.43
3	Internodal length (cm)	4.24-7.54	5.65	0.51	0.54	12.63	13.07	93.30	1.42	25.13
4	Number of nodes on main stem	12.57-18.77	14.91	2.63	2.70	10.87	11.02	97.30	3.29	22.10
5	Number of branches per plant	2.04-4.06	3.22	0.18	0.19	13.26	13.74	93.20	0.85	26.38
6	Fruit length (cm)	11.86-15.21	13.13	0.54	0.56	5.61	5.71	96.30	1.48	11.34
7	Fruit diameter (cm)	1.80-2.01	1.91	0.01	0.01	4.04	4.05	99.60	0.15	8.31
8	Number of ridges per fruit	5.00-6.50	5.53	0.16	0.39	7.28	11.35	41.20	0.53	9.62
9	Number of fruits per plant	13.54-16.88	15.40	1.03	1.11	6.59	6.84	92.80	2.01	13.08
10	100 seed weight (g)	4.00-7.00	5.67	0.40	0.41	11.22	11.31	98.60	1.30	22.96
11	Number of seeds per fruit	30.15-63.5	50.44	26.44	45.19	10.19	13.32	58.50	8.10	16.06
12	Fruit yield per plant (g)	228.7-350	273.04	1119.29	1123.01	12.25	12.27	99.70	68.80	25.19

\*\* Significant at 1% level of probability or level of significance, Values in parenthesis denote degrees of freedom

## Conclusion

Results from present investigation clearly indicated that greater variability exists among all the characters of selected genotypes. The trend of PCV was almost similar to GCV. The traits like plant height (cm), internodal length (cm), number of nodes on main stem (cm), number of branches per plant, 100 seed weight (g), number of seeds per fruit and fruit yield per plant (g) have exhibited moderate estimate of GCV and PCV, whereas low estimate of GCV and PCV were observed for days to 50 per cent flowering, fruit length (cm), fruit diameter (cm) and number of fruits per plant. The trait number of ridges per fruit has exhibited low estimate of GCV and high estimate of PCV. GCV values were lower than PCV and the values of GCV and PCV varied to a little extent, indicating the presence of variability in genotypes for all the studied traits is due to genetic and less influence of environment. High heritability coupled with high genetic advance were

recorded for the characters like plant height (cm), number of nodes on main stem, number of branches per plant, 100 seed weight (g) and fruit yield per plant (g) thus indicated the strong contribution of additive genetic variance in expression of the characters and hence simple selection scheme would be sufficient for these traits for the improvement in fruit yield per plant (g). Based on estimates of genetic parameters, it is evident that the characters showing high values of PCV, GCV, heritability and genetic advance as per cent mean were considered as most important characters and selection of these traits will be more effective in improvement of fruit yield per plant.

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