



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(7): 3560-3563
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www.thepharmajournal.com
Received: 02-04-2022
Accepted: 08-05-2022

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Study of variation among the genotypes of okra [*Abelmoschus esculentus* (L.) Moench]

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Abstract

The experiment was conducted to estimate the genetic variability in 75 okra genotypes. The variability parameters like range, coefficient of range, mean, genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance as percentage of mean were estimated for 12 different characters. The values of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the 12 characters indicating the influence of environmental factors. The magnitude of heritability was observed to be high for all the characters except days to first picking under study indicated that the larger portion for total variation would be under genetic control therefore selection based on phenotypic levels would be useful for the improvement of these characters. High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for plant height, number of branches per plant, number of nodes on main stem per plant, internodal length (cm), number of fruits per plant, fruit length (cm), fruit girth (cm), fruit weight (g), total number of pickings and fruit yield per plant (g). Which may be attributed to the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitably be applied on this character for their improvement. The analysis of variance for experimental design indicated highly significant differences among all the genotypes for all the twelve traits studied suggesting the presence of considerable amount of variability in the experimental material, which can be exploited for improvement of fruit yield and yield attributes in okra. In a true agreement with the GCV and PCV values in the present investigation for most of the characters was noticed, indicating additive genetic variance governing the high heritability (>60%) with high genetic advance as per cent of mean was high (>20%) for plant height, number of branches per plant, number of nodes on main stem per plant internodal length (cm), number of fruits per plant, fruit length (cm), fruit girth (cm), fruit weight (g), total number of pickings and fruit yield per plant (g). Hence there could be exercised for improvement through selection.

Keywords: Genetic variability, heritability, GCV, PCV, genetic advance, okra

Introduction

Okra (*Abelmoschus esculentus* L.) is one of the most widely known and utilized species of the *malvaceae* family. It is an economically important vegetable crop grown in tropical and sub-tropical parts of the world. Okra originated in Ethiopia. Okra is known by many local names in different parts of the world. It is called lady's finger in England, gumbo in United States of America, guino-gombo in Spanish, guibeiro in Portuguese and bhindi in India. Okra plants are grown commercially in many countries such as an India, Japan, Turkey, Iran, Western Africa, Yugoslavia, Bangladesh, Afghanistan, Pakistan, Myanmar, Malaysia and Thailand. Okra is a multipurpose crop due to its various uses of the fresh leaves, buds, flowers, pods, stems and seeds. Okra immature fruits, which are consumed as vegetables, can be used in salads, soups and stews, fresh or dried, fried or boiled. It offers mucilaginous consistency after cooking. Okra mucilage has medicinal applications when used as a plasma replacement or blood volume expander. The mucilage of okra binds cholesterol and bile acid carrying toxins dumped into it by the liver. The immature pods are also used in making pickle. The entire plant is edible and is used to have several foods. Okra seeds are a potential source of oil, with concentrations varying from 20% to 40%, depending on the extraction method. The oil mainly consists of linoleic acid (up to 47.4%). Okra seed oil is a rich source of linoleic acid, a polyunsaturated fatty acid essential for human nutrition. Proteins play a particularly important role in human nutrition. The amino acid contents, proportions, and their digestibility by humans characterize a protein's biological value.

Fresh okra pods are the most important vegetable source of viscous fiber, an important dietary component to lower cholesterol. Seven-days-old fresh okra pods have the highest concentration of nutrients. Okra contains high fiber, which “helps to stabilize blood sugar by regulating the rate at which sugar is absorbed from the intestinal tract”. The frequent usage of okra might help avoid kidney disease.

Materials and Methods

The present investigation was conducted to assess the genetic variability in okra [*Abelmoschus esculentus* (L.) Moench]. The study was carried out during *kharif* 2020 at the Vegetable Research Station, Junagadh Agricultural University, Junagadh. Geographically Junagadh is situated at 21.5°N latitude and 70.5°E longitude with an elevation of 82.92 meters above the mean sea level. The soil of the experimental site is medium black with pH 7.8. The climate of the area represents semi-arid and tropical. The weather during the growing season was favourable for normal growth and development of crop. The experimental material consisted of 75 diverse genotypes of okra representing different geographic origin. The experimental materials of these genotypes were obtained from the Vegetable Research Station, Junagadh Agricultural University, Junagadh. Seventy five genotypes of okra were sown in a Randomized Block Design with two replications during *kharif* 2020 at Vegetable Research Station, Junagadh Agricultural University, Junagadh. Plot size was 1.20 m x 2.40 m length with spacing of 60 cm x 30 cm. The genotypes were randomly allotted to the plots in each replication. The observations were recorded on five randomly selected plants from sixteen plants in each genotype from each replication. The observations were recorded for 12 different characters, viz., days to 50% flowering, days to first picking, plant height, number of branches per plant, number of nodes on main stem per plant, internodal length, number of fruit per plant, fruit length, fruit girth, fruit weight, total number of pickings and fruit yield per plant.

Analysis of variance for randomized block design (RBD) was done as per Panse and Sukhatme (1985) [14]. Phenotypic coefficient of variation (PCV) and genotypic co-efficient of variation (GCV) were calculated as per the formula suggested by Burton and De Vane (1953) [6]. Heritability and genetic advance were estimated using the formula suggested by Allard (1960) [4].

Results and Discussion

The analysis of variance for experimental design indicated highly significant differences among all the genotypes for all the twelve traits. The high magnitude of GCV and PCV were observed for number of branches per plant, fruit yield per plant, number of fruits per plant and number of nodes on main stem per plant. This is in relation with the earlier reports of Duggi *et al.* (2013) [9] for number of branches per plant, number of fruits per plant and fruit yield per plant; Yonas *et al.* (2014) [19] for number of branches per plant; Khajuria *et al.* (2016) [12] for number of fruits per plant; Chandramouli *et al.* (2016) [7] for fruit yield per plant and Das *et al.* (2012) [8] for number of nodes on main stem per plant.

The moderate magnitude of GCV and PCV were observed internodal length, plant height, fruit length, fruit weight, fruit girth and total number of pickings. This is in relation with earlier reports of Reddy *et al.* (2012) [17] for internodal length,

plant height and fruit length; Chandramouli *et al.* (2016) [7] for internodal length, fruit length and fruit girth; Koundinya *et al.* (2013) [13] for plant height; Das *et al.* (2012) [8] and Goswami *et al.* (2012) [10] for fruit length; Goswami *et al.* (2012) [10] for internodal length; Ahamed *et al.* (2015) [3] for fruit weight.

Heritability (h^2_{bs})

In the present investigation, high heritability estimates were observed for days to 50% flowering, plant height, number of branches per plant, number of nodes on main stem per plant, internodal length, number of fruits per plant, fruit length, fruit girth, fruit weight, total number of pickings and fruit yield per plant. High heritability estimates indicated that the characters were least influenced by the environmental effects. This also recommended that the phenotypes were the true representative of their genotypes for these traits and selection based on phenotypic value could be more reliable.

Similar results of high heritability were reported by Ahamed *et al.* (2015) [3] and Kerure *et al.* (2017) [11] for fruit weight; Chandramouli *et al.* (2016) [7] and Kerure *et al.* (2017) [11] for number of fruits per plant; Chandramouli *et al.* (2016) [7] for number of branches per plant; Chandramouli *et al.* (2016) [7] and Rambabu *et al.* (2019) [16] for internodal length; Chandramouli *et al.* (2016) [7] and Amba Kumari *et al.* (2019) [5] for fruit girth and number of nodes per plant; Kerure *et al.* (2017) [11] for fruit length; Kerure *et al.* (2017) [11], Amba Kumari *et al.* (2019) [5] and Rambabu *et al.* (2019) [16] for fruit yield per plant; Sharma *et al.* (2016) [18], Kerure *et al.* (2017) [11] and Rambabu *et al.* (2019) [16] for plant height; Phani Krishna *et al.* (2015) [15] for total number of pickings; Duggi *et al.* (2013) [9] for days to 50% flowering.

Genetic advance (G_s)

The expected genetic advance value was high for characters; plant height and fruit yield per plant. Similar results were also observed by Ahamed *et al.* (2015) [3], Kerure *et al.* (2017) [11] and Rambabu *et al.* (2019) [16] for plant height and Kerure *et al.* (2017) [11], Amba Kumari *et al.* (2019) [5] and Rambabu *et al.* (2019) [16] for fruit yield per plant.

The expected genetic advance value was moderate for fruit weight. Similar results were also observed by Rambabu *et al.* (2019) [16] for fruit weight.

In the present investigation, low genetic advance was observed for number of nodes on main stem per plant, number of fruits per plant, days to 50% flowering, total number of pickings, fruit length, days to first picking, internodal length, fruit girth and number of branches per plant. The results are in agreement with the findings of Chandramouli *et al.* (2016) [7] and Amba Kumari *et al.* (2019) [5] for number of nodes on main stem per plant; Amba Kumari *et al.* (2019) [5] and Rambabu *et al.* (2019) [16] for number of fruits per plant; Chandramouli *et al.* (2016) [7], Kerure *et al.* (2017) [11] and Amba Kumari *et al.* (2019) [5] for days to 50% flowering; Chandramouli *et al.* (2016) [7] and Rambabu *et al.* (2019) [16] for total number of pickings; Kerure *et al.* (2017) [11], Amba Kumari *et al.* (2019) [5] and Rambabu *et al.* (2019) [16] for fruit length; Chandramouli *et al.* (2016) [7] for days to first picking; Amba Kumari *et al.* (2019) [5] and Rambabu *et al.* (2019) [16] for internodal length; Chandramouli *et al.* (2016) [7] and Rambabu *et al.* (2019) [16] for fruit girth and Kerure *et al.* (2017) [11], Amba Kumari *et al.* (2019) [5] and Rambabu *et al.* (2019) [16] for number of branches per plant.

Table 1: Analysis of variance showing mean squares of 12 characters in 75 genotypes of okra

Source	d. f.	Days to 50% flowering	Days to First picking	Plant Height (cm)	No. of branches per plant	No. of nodes per plant	Internodal length (cm)
Replications	1	14.11	19.44	227.33	0.14	4.64	0.40
Genotypes	74	14.78**	12.56**	592.12**	0.70**	19.84**	2.69**
Error	74	5.59	6.76	67.02	0.04	1.59	0.18

Table 1: Contd....

Source	d. f.	No. of fruits per plant	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Total number of pickings	Fruit yield per plant (g)
Replications	1	1.12	0.61	0.26	7.39	1.31	282.71
Genotypes	74	11.28**	4.17**	1.14**	154.95**	2.82**	2326.73**
Error	74	0.51	0.36	0.08	10.39	0.43	138.79

*, ** Significant @ 5% and 1% levels, respectively

Table 2: Range, coefficient of range, mean, genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability, genetic advance (Gs) and genetic advance expressed as percentage of mean (GAM) for various characters in okra

Sr. No.	Characters	Range	Coefficient of range (%)	Mean	GCV (%)	PCV (%)	Heritability (broad sense) h^2_{bs} (%)	Genetic advance (Gs)	Genetic advance as % of mean (GAM %)
1	Days to 50% flowering	41.50 - 54.50	13.54	49.20	4.36	5.53	62.17	3.48	7.08
2	Days to first picking	51.00 - 61.50	9.33	55.47	3.07	4.52	46.14	2.38	4.29
3	Plant height (cm)	64.17 - 145.00	38.62	105.01	15.43	16.39	88.68	31.43	29.93
4	No. of branches per plant	0.90 - 3.30	57.14	1.79	32.21	33.08	94.84	1.16	64.63
5	No. of nodes on main stem per plant	8.33 - 20.50	42.36	14.72	20.52	21.39	91.98	5.97	40.53
6	Internodal length (cm)	3.58 - 8.92	41.26	6.23	17.97	18.59	93.47	2.23	35.80
7	No. of fruits per plant	5.00 - 14.83	49.49	9.20	25.21	25.80	95.47	4.67	50.75
8	Fruit length (cm)	7.15 - 13.55	30.76	9.92	13.90	14.55	91.24	2.71	27.35
9	Fruit girth (cm)	4.45 - 7.95	28.00	5.89	12.39	12.82	93.40	1.45	24.66
10	Fruit weight (g)	48.50 - 82.20	25.78	62.47	13.61	14.09	93.30	16.92	27.08
11	Total number of pickings	7.50 - 12.50	25.00	9.82	11.12	12.08	84.80	2.07	21.10
12	Fruit yield per plant (g)	67.90 - 234.55	55.10	116.76	28.33	29.21	94.03	66.07	56.58

Conclusion

The analysis of variance revealed that mean squares due to genotypes were found highly significant for all the characters indicating the existence of ample genetic variability in the experimental material.

Number of branches per plant recorded the maximum coefficient of range followed by fruit yield per plant, number of fruits per plant, number of nodes on main stem per plant and internodal length.

The values of phenotypic coefficient of variation were slightly higher than that of genotypic coefficient of variation for all the characters studied, representing less effect of environment on the expression of characters studied. This suggests that phenotypic variation can be used to judge genetic variation.

The high to moderate genotypic coefficient of variation and phenotypic coefficient of variation was observed for number of branches per plant followed by fruit yield per plant, number of fruits per plant, number of nodes on main stem per plant, internodal length, plant height, fruit length, fruit weight, fruit girth and total number of pickings. The results indicated the presence of wide variation for the traits under study to allow further improvement by selection of the individual traits. This indicated that existence of genetic variation for these characters and selection of better segregated populations on the basis of phenotypic performance.

The high heritability (broad sense) values were observed for all the twelve characters except days to first picking. The high heritability values point out that heritability may be due to higher contribution of genotypic components in these characters.

The genetic advance expressed as percentage of mean was

found high for number of branches per plant followed by fruit yield per plant, number of fruit per plant, number of nodes on main stem per plant, internodal length, plant height, fruit length, fruit weight, fruit girth and total number of pickings. It was found low for days to 50% flowering and days to first picking.

High heritability along with high genetic advance was reported for plant height, number of branches per plant, number of nodes on main stem per plant, internodal length, number of fruits per plant, fruit length, fruit girth, fruit weight, total number of pickings and fruit yield per plant, it indicate presence of additive gene action for these traits. So, direct selection is effective.

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