

Genetic Component and Variance analysis of Okra (*Abelmoschus esculentus* L.)

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Abstract

Ten okra genotypes (includes two checks) were evaluated for yield and yield attributing traits. In the present study, wide variability was recorded for fruit yield per plant (g), fruit yield per plot (kg) and YVMV infestation (%) indicating the existence of more variability for these traits among the genotypes under study as they have high PCV and high GCV. High heritability coupled with high genetic advance as per cent of mean indicates the operation of additive gene action as in case of number of primary branches per plant, nodes on main stem, intermodal length, leaf area, number of fruits per plant, fruit girth, fruit yield per plant, fruit yield per plot and YVMV infestation (%). Hence, direct selection based on these traits in genetically diverse material could be effective for desired improvement. Moderate genetic advance as per cent of mean with high or moderate heritability indicates the action of both additive and non-additive genes as in case of petiole length, fruit length and fruit weight. Hence, direct selection has limited scope for further improvement of these traits.

Key words: Genetic variability, heritability, genetic advance, okra

Introduction

Okra (*Abelmoschus esculentus* (L.) Moesch) is a fast growing annual which has captured a prominent position among the vegetables and is commonly known as bhindi or lady's finger in India. Okra is specially valued for its tender, delicious green fruits which are cooked, canned and consumed in various forms in different part of the country. It gained popularity in many parts of the world for its unsurpassed medicinal value and commercial importance. Okra is generally amphidiploids in nature with $2n = 130$ chromosomes. Fruit yield in okra is depends upon many yield components, since it is polygenic character. The variability for various characters is a prerequisite for a plant breeder. Genetic variability is an important factor for any heritable improvement. Magnitude and nature of genetic variability determined the progress of breeding for the economic characters and plays an important role in a crop in selecting the best genotypes for making rapid improvement in yield and other desirable characters, reported by Vavilov (1951). In the present study, attempt has been made to assess the variability of important yield and yield contributing traits, along with indices of variability i.e., GCV and PCV, heritability (h^2) and genetic advance over mean (GAM) which would facilitate an understanding behind expression of character and also the role of environment.

Hybridization has been the most successful approach in increasing the productivity in vegetable crops. Selection of genetically superior and suitable genotypes is the most important stage from the standpoint of hybridization of vegetable crops in order to develop new genotypes having desirable characters. One of the main problems of vegetable breeders for developing high yielding varieties through either heterosis breeding or pedigree breeding is to select good parents and crosses. In a systematic breeding programme, it is essential to identify superior parents for hybridization and crosses to expand the genetic variability for selection of superior genotypes (Inamullah *et al.*, 2006). The value of any population depends on its potential per se and it's combining ability in crosses. Selection of parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior lines may not lead to expected degree of heterosis in F1 generation or throw superior transgresses segregates in segregating generations.

Materials and Methods

The material for present investigation comprised 10 genotypes of Okra namely Azad Ganga, BO-2, KS-315, KS-375, KS-408, KS-410, KS-415, KS-418, Parbhani Kranti and Pusa Sawani collected from the

germ plasm stock maintained in Department of vegetable science C. S. Azad University of Agriculture and Technology Kalyanpur- Kanpur. These comprised of commercial varieties and indigenous collection from different parts of India. All the homogenous parents parent procured from C.S. Azad University were grown at research farm of Kisan Post Graduate College Simbhaoli – Ghaziabad (U.P.). All the possible F1 crosses excluding reciprocal were made among these 10 parents during the season. All these F1 were selfed for procuring F2 seeds. The parents were also maintained through selfing. Parent and F1 were sown in double rows while F2 in three rows with 10 plants. Fertility of experimental plots was maintained uniformly. The experiment was laid out in randomized block design with three replications. Seeds were sown at a spacing of 60 cm between rows and 45 cm between the plants. The observations were recorded on five randomly selected plants per replication for each genotype for characters. The analysis of variance of was carried out as suggested by Panse and Sukhatme (1985). Genotypic and phenotypic coefficients of variation were estimated according to Burton and Devane (1953). Heritability in broad sense was estimated as per the formulae suggested by Allard (1960) and Genetic advance was estimated as per the formula proposed by Johnson *et al.* (1955).

Results and Discussion

The analysis of variance (Table 1) revealed significant differences among 10 okra genotypes for all characters suggesting the presence of good amount of variation. The characters viz., fruit yield per plant (g), and YVMV infestation (%) recorded wide range

of variation suggesting the presence of variability for these characters and also offers scope for selecting better variable genotype to exploit yield in okra. High magnitude of genetic variability for these traits has been reported earlier by Mulge *et al.* (2004) and kumar *et al.* (2006). The extent of variability present in the okra genotypes was measured for various traits in terms of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), genetic advance and genetic advance as per cent of mean were recorded.

While looking to estimates of GCV and PCV, it was observed that the characters like fruit yield per plant (g) (kg) and YVMV infestation (%) exhibited higher magnitudes of GCV and PCV (> 20%) indicating the existence of wide range of genetic variability in the germ plasm for these traits. There is a good scope for the further improvement of these characters through selection since they are controlled by additive gene action. Similar results were reported by Patro and Ravishankar (2004), Singh *et al.* (2007). Moderate to low variability was recorded for plant height, number of primary branches per plant, number of nodes on main stem, number of fruits per plant, fruit length, first flowering node, fruit weight, days to 50 % flowering, days to first picking, number of pickings and picking duration (Table 2). These outcomes are in accordance with the findings of Alam and Hossain (2006). To determine the amount of heritable variation estimate of GCV alone is not sufficient. Therefore, heritable variation can be found out with the greater degree of accuracy when heritability is studied in conjunction with genetic advance. High heritability coupled with high genetic advance as per cent of mean

Table 1: Analysis of variance for quantitative traits in okra genotypes

S. no.	Characters	Mean sum of squares		
		Replications (df = 2)	Treatments (df = 99)	Error (df = 199)
1	Plant height (cm)	42.02	558.72**	260.13
2	Number of primary branches/ plant	0.04	0.34**	0.05
3	Number of nodes on main stem	0.17	27.52**	2.28
4	No. of fruits/ plant	3.08	33.33**	4.39
5	Fruit length (cm)	4.25	11.77**	1.61
6	Fruit weight (g)	2.45	7.55**	0.87
7	Days to 50 % flowering	0.46	13.69**	1.43
8	Days to first picking	3.76	10.25**	3.56
9	Number of pickings	0.78	2.17**	0.88
11	Picking duration (days)	9.39	28.80**	4.82
12	Fruit Yield/Plant(g)	0.45	40378.11**	478.24

*, ** = significant at 5% and 1% level, respectively.

Table 2: Estimates of variability, heritability and genetic advance as per cent of mean for different characters in okra genotypes

S. no.	Characters	Mean	Variances		PCV (%)	GCV (%)	h ² (%)	Genetic advance	GA as % of mean
			Phenotypic	Genotypic					
1	Plant height (cm)	152.75	365.02	98.8	12.96	6.77	27.37	10.78	7.34
2	No. of primary branches/plant	1.92	0.15	0.10	20.42	16.83	67.39	0.55	28.24
3	No. of nodes on main stem	22.24	10.8	8.65	16.23	14.52	78.88	5.35	26.23
4	No. of fruits/plant	22.35	14.2	9.76	17.54	14.74	69.06	5.32	25.17
5	Fruit length (cm)	14.78	5.22	3.34	15.86	12.53	66.54	3.09	20.78
6	Fruit weight (g)	19.50	3.221	2.26	9.46	7.79	71.52	2.68	13.54
7	Days to 50% flowering	48.13	5.60	4.21	4.98	4.32	74.08	3.52	7.71
8	Node at which first flower appeared	4.79	0.38	0.18	13.43	7.89	35.38	0.46	9.73
9	Days to first picking	55.50	5.78	2.28	4.57	2.82	38.81	1.92	3.83
10	Number of pickings	13.28	1.26	0.45	9.24	5.43	34.72	0.88	6.64
11	Picking duration (days)	51.65	12.8	7.87	6.78	5.52	62.11	4.52	8.95
12	Fruit Yield/ plant (g)	417.23	13780.20	13285.96	28.54	27.95	96.59	233.50	56.32

indicates the operation of additive gene action as in case of number of primary branches per plant, nodes on main stem, number of fruits per plant, fruit yield per plant, fruit yield per plot and YVMV infestation (%). Hence, direct selection based on these traits in genetically diverse material could be effective for desired improvement. These results are in close conformity with the findings of Singh *et al.* (2006). Moderate genetic advance as per cent of mean with high or moderate heritability indicates the action of both additive and non-additive genes as in case of petiole length, fruit length and fruit weight. Hence, direct selection has limited scope for further improvement of these traits. Similar conclusion was obtained by Bendale *et al.* (2003) and Mohapatra *et al.* (2007).

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