

STUDIES ON GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN OKRA [*ABELMOSCHUS ESCULENTUS* (L.) MONECH] GENOTYPES

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Abstract

Thirty 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 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 Moench) is an important vegetable crop grown all over India and tropical and sub tropical parts of the world. It gained popularity in many parts of the world for its unsurprised 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 (h2) and genetic advance over mean (GAM) which would facilitate an understanding behind expression of character and also the role of environment.

Materials and Methods

The experiment was conducted at Horticultural College and Research Institute, Dr. Y. S. R. Horticultural University, Venkataramannagudem, West Godavari district (A.P.), India; with 30 diverse okra genotypes during *kharif*, 2014. 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 eighteen 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 Lush (1940) and Johnson *et al.* (1955).

Results and Discussion

The analysis of variance (table 1) revealed significant differences among 30 okra genotypes for all characters suggesting the presence of good amount of variation. The characters viz., fruit yield per plant (g), fruit yield per plot (kg) 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 Dhall et al. (2003), Mulge et al. (2004), Vishalkumar et al. (2006) and Reddy et al. (2012). 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 are given in table 2.

While looking to estimates of GCV and PCV, it was observed that the characters like fruit yield per plant (g),

fruit yield per plot (kg) and YVMV infestation (%) exhibited higher magnitudes of GCV and PCV (> 20%) indicating the existence of wide range of genetic variability in the germplasm 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), Jindal et al. (2010), Prakash and Pitchaimuthu (2010), Adiger et al. (2011) and Reddy et al. (2012). Moderate to low variability was recorded for plant height, number of primary branches per plant, number of nodes on main stem, intermodal length, leaf area, petiole length, number of fruits per plant, fruit length, fruit girth, first flowering node, fruit weight, days to 50 % flowering, days to first picking, number of pickings and picking duration. These outcomes are in accordance with the findings of Alam and Hossain (2006), Jindal et al. (2010), Kumar et al. (2012). Goswami (2012) and Shaikh et al. (2013).

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 indicates the operation of additive gene action as in case of number

S no	Characters	Mean sum of squares						
5.10.		Replications (df=2)	Treatments (df=29)	Error (df=58)				
1.	Plant height (cm)	40.02	558.79**	262.13				
2.	Number of primary branches/ plant	0.03	0.32**	0.04				
3.	Number of nodes on main stem	0.15	27.51**	2.26				
4.	Internodal length (cm)	1.46	4.48**	0.60				
5.	Leafarea (cm²)	0.04	8034.37**	44.78				
6.	Petiole length (cm)	9.54	14.99**	2.58				
7.	No. of fruits/ plant	3.01	33.38**	4.35				
8.	Fruit length (cm)	4.06	11.71**	1.68				
9.	Fruit girth (cm)	0.28	0.97**	0.15				
10.	Fruit weight (g)	2.33	7.57**	0.88				
11.	Days to 50 per cent flowering	0.31	13.65**	1.43				
12.	Node at which first flower appeared	0.46	0.67**	0.25				
13.	Days to first picking	3.63	10.26**	3.53				
14.	Number of pickings	0.70	2.12**	0.81				
15.	Picking duration (days)	9.34	28.81**	4.86				
16.	Fruit Yield/Plant(g)	0.43	40376.11**	479.24				
17.	Fruit yield/ plot (kg)	0.00	37.11**	0.48				
18.	YVMV infestation (%)	10.08	1529.45**	8.09				

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

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

S. no.	Characters	Mean	Variances		PCV	GCV	h ²	Genetic	GA as %
			Phenotypic	Genotypic	(%)	(%)	(%)	advance	of mean
1.	Plant height (cm)	147.05	361.02	98.88	12.92	6.76	27.39	10.72	7.29
2.	No. of primary branches/plant	1.82	0.14	0.09	20.39	16.73	67.34	0.51	28.29
3.	No. of nodes on main stem	20.26	10.68	8.42	16.13	14.32	78.83	5.31	26.19
4.	Inter nodal length (cm)	7.38	1.90	1.29	18.65	15.40	68.14	1.93	26.19
5.	Leafarea (cm ²)	313.02	2707.96	2663.20	16.62	16.49	98.35	105.43	33.68
6.	Petiole length (cm)	21.32	6.72	4.13	12.16	9.54	61.54	3.27	15.41
7.	No. of fruits/plant	21.24	14.02	9.68	17.63	14.64	69.00	5.32	25.06
8.	Fruit length (cm)	14.71	5.022	3.34	15.24	12.43	66.55	3.07	20.89
9.	Fruit girth (cm)	3.72	0.43	0.27	17.69	13.89	61.64	0.84	22.46
10.	Fruit weight (g)	19.27	3.11	2.23	9.15	7.74	71.59	2.60	13.50
11.	Days to 50% flowering	47.09	5.50	4.08	4.98	4.29	74.08	3.58	7.60
12.	Node at which first flowerappeared	4.73	0.39	0.14	13.23	7.86	35.35	0.46	9.63
13.	Days to first picking	53.60	5.77	2.24	4.48	2.79	38.87	1.92	3.59
14.	Number of pickings	12.23	1.25	0.43	9.14	5.39	34.77	0.80	6.54
15.	Picking duration (days)	51.56	12.85	7.98	6.95	5.48	62.15	4.59	8.90
16.	Fruit Yield/ plant (g)	414.13	13778.20	13298.96	28.34	27.85	96.52	233.40	56.36
17.	Fruit Yield/ plot (kg)	11.14	12.69	12.21	31.98	31.38	96.25	7.06	63.41
18.	YVMV infestation (%)	42.09	515.21	507.12	53.93	53.51	98.43	46.02	109.36

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

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. These results are in close conformity with the findings of Dhall et al. (2000), Hazra and Basu (2000), Patro and Ravishankar (2004), Singh et al. (2006), Nasit et al. (2009), Goswami (2012) and Yonas et al. (2014). 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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