



VARIABILITY AND CORRELATION STUDIES IN OKRA (*Abelmoschus esculentus* L. Moench)

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ABSTRACT

A study was conducted to evaluate fourteen genotypes of okra for yield and various yield attributing traits at Vegetable Breeding Station, Agricultural Research Institute, Rajendranagar, Hyderabad during *kharif* 2006 and 2007. The data were utilized to estimate the genetic variability in terms of mean, genotypic and phenotypic coefficients of variation, heritability, expected genetic advance and expected genetic advance as per cent mean. The present investigation showed that phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits suggesting the influence of environment in their expression. The estimates of GCV, heritability and heritability coupled with genetic advance as per cent of mean were higher for number of fruits plant⁻¹, internode length and plant height. The correlation study indicated that the yield plant⁻¹ had high positive association with number of fruits plant⁻¹, plant height, internode length and fruit girth at both genotypic and phenotypic levels. Among the traits studied, number of fruits plant⁻¹ had maximum direct contribution on yield and indirect contribution via plant height, internode length and fruit girth.

KEYWORDS: Correlation, genetic variability, heritability, okra, path analysis

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is an important vegetable crop grown for its tender fruits throughout India. It is an important protective food because of its high nutritional value which plays a pivotal role in human nutrition. Now a days, the productivity of okra shows a declining trend. In India, it occupied an area of 530.27 ha with an annual production of 6350.27 kg (National Horticulture Base data base 2012-13). Hence, developing high yielding varieties bestowed with fruits of high quantity as well as quality is of utmost importance in this crop. To improve the yield and other characters, information on genetic variability and interrelationship among different traits is necessary. The improvement in any crop is proportional to the magnitude of its genetic variability present in the population. Keeping in this in view, an attempt has been made to generate information on genetic variability, association of different characters and path analysis to select promising genotypes for utilization in okra breeding.

MATERIALS AND METHODS

A field experiment was conducted at Vegetable Breeding Station, Agricultural Research Institute, Rajendranagar, Hyderabad during *kharif* 2006 and 2007

in a randomized block design with three replications. The experimental plot size was 4 x 4 m. The experimental material consisted of fourteen okra genotypes was obtained from All India Coordinated Research Centers of Indian Council of Agricultural Research. Seeds were sown with a spacing of 45 × 30 cm. All the agronomic recommended package of practices including plant protection measures was taken up to get healthy crop. Data were recorded on randomly selected five plants from each genotype on plant height (cm), number of branches, node number at first fruit appeared, number of nodes plant⁻¹, number of fruits plant⁻¹, average fruit weight (g), fruit length (cm), fruit girth (cm) and yield plant⁻¹ (g). The generated data were subjected to analysis of variance as per Panse and Sukhatme, (1987) and genotypic and phenotypic coefficients of variation according to Burton and De Vane, (1953). Heritability and genetic advance were calculated according to Johanson *et al.* (1955) and Robinson *et al.* (1949) respectively. Correlation coefficients were computed at phenotypic and genotypic levels between pairs of characters adopting the formula given by Al-Jibori *et al.* (1958) and Path coefficient of various characters was done as suggested by Wright (1956).

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RESULTS AND DISCUSSION

The extent of variability measured in terms of range, genotypic variance (V_g), phenotypic variance (V_p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, expected genetic advance (GA) and expected genetic advance as per cent of mean were presented in Table 1. Maximum range of mean values was observed for yield plant⁻¹ (101 to 296 g) while minimum range was found for fruit girth (5.77 to 6.87 cm). Among the characters, yield plant⁻¹ and plant height showed wide range of variation, indicating the presence of variability for these characters and offers ample scope for selecting better genotypes. Bendale *et al.* (2003) and Hazra and Basu (2000) also reported wide range of variation for yield and plant height for other genotypes in okra. Phenotypic coefficient of variation was found to be more than genotypic coefficient of variation for all characters indicating the influence of environment on expression of the characters. These results were in agreement with that of Pathk and Singh (1999). The fruit yield plant⁻¹ exhibited high phenotypic coefficient of variation estimate (31.19) followed by number of fruits plant⁻¹ (26.34), internode length (25.60) and plant height (22.43) indicated that these characters were highly influenced by environmental factors. Fruit length and fruit girth recorded minimum value of phenotypic coefficient of variation compared to other characters. The genotypic coefficient of variation (GCV) would be more useful for assessing the variability since high estimates of phenotypic coefficient of variation (PCV) alone will not be enough to determine exact nature of variability. The relative magnitude of difference between PCV and GCV was low for plant height, fruit girth and yield plant⁻¹ indicating the low influence of environmental factors on these characters.

The genotypic coefficient of variation along with heritability estimate would give the best scope for selection (Burton and De Vane, 1953). In the present study, the estimates of heritability varied from 0.35 to 0.89. Highest heritability values were found for plant height (0.89) followed by yield plant⁻¹ (0.88) internode length (0.88) and number of fruits plant⁻¹ (0.84). High heritability for these characters might be useful for plant breeder for making effective selection. Low heritability value was observed for fruit length (0.35) followed by number of nodes plant⁻¹ (0.47) suggested that environmental factors constituted a major portion of total phenotypic variation

and hence direct selection for these characters would not be appropriate.

Though heritability gives a useful indication of relative value of selection based on phenotypic expression, it cannot be reliable unless genetic advance under selection is not taken into consideration along with heritability (Johanson *et al.* 1955). Genetic advance as per cent mean was found to be highest for internode length (46.11) followed by number of fruits plant⁻¹ (45.89) and plant height (40.97). These results suggesting the important role of genetic factors in the expression of these characters as genetic advance was estimated on the basis of heritability in broad sense (since, heritability in narrow sense give the information on additive type of gene action where the character expression was not influenced by environment). Hence, these characters would be selected on the basis of phenotypic values. According to Johanson *et al.* (1955) heritability estimate along with genetic advance is more useful than the heritability alone in predicting the resultant effect for selection. In the present investigation, high estimates of heritability accompanied with high genetic advance as per cent mean were recorded for internode length, number of fruits plant⁻¹ and plant height indicating the suitability of characters for phenotypic selection. Low heritability associated with low expected genetic advance as per cent mean was observed for fruit length, and girth.

The correlation study (Table-2) revealed that the genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic correlation coefficients. The results from Table 3 revealed that all the characters were positively and significantly correlated with yield plant⁻¹ except node number at first fruit appeared which showed negative association with yield. Among the characters, number of fruits plant⁻¹ exhibited highest positive correlation (1.035, 0.902) with yield followed by plant height (0.789, 0.748) both at genotypic and phenotypic levels and fruit girth (0.797) at genotypic level only. These results indicated that these characters can be considered for selection. These results are in confirmation with that of Bendale *et al.* (2003).

Plant height had high positive and significant correlation coefficients with internode length (0.894, 0.841), fruit girth (0.849, 0.621), number of fruits plant⁻¹ (0.811, 0.711) and number of nodes plant⁻¹ (0.750, 0.578) at genotypic and phenotypic levels respectively. Number of fruits plant⁻¹ expressed positive correlation with plant

Table 1. Estimates of mean, range, variance components and genetic parameters for different characters

Characters	Mean \pm SE	Range	CV	GCV	PCV	Heritability (broad sense)	Genetic Advance	Genetic Advance as % of mean
Plant height (cm)	87.86 \pm 3.82	56.13 - 117.6	7.53	21.13	22.43	0.89	36.00	40.97
Internode length (cm)	5.66 \pm 0.29	3.87 - 9.27	9.02	23.96	25.60	0.88	2.61	46.11
Node No. at 1 st fruit appeared	4.63 \pm 0.28	3.67 - 5.73	10.33	12.96	16.59	0.61	0.96	20.73
Number of nodes plant ⁻¹	18.51 \pm 0.83	15.20 - 21.53	7.74	7.27	10.61	0.47	1.88	9.72
Number of fruits plant ⁻¹	17.74 \pm 1.06	9.00 - 25.3	10.38	24.21	26.34	0.84	8.14	45.89
Average fruit weight (g)	20.04 \pm 0.86	17.50 - 23.33	7.47	7.94	10.91	0.53	2.38	11.88
Fruit length (cm)	15.42 \pm 0.59	14.03 - 18.20	6.67	4.90	8.28	0.35	0.92	5.97
Fruit girth (cm)	6.33 \pm 0.15	5.77 - 6.87	4.13	5.00	6.32	0.58	0.52	8.21
Yield plant ⁻¹ (g)	197.83 \pm 12.32	101.00 - 296.67	10.79	29.26	31.19	0.88	11.91	6.02

CV: Coefficient of variation; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation

Table 2. Estimates of genotypic and phenotypic correlation coefficients for different characters in Okra

Character	Level	Plant height	Internode length	Node number at 1 st fruit	Number of nodes plant ⁻¹	Number of fruits plant ⁻¹	Avg. fruit weight	Fruit length	Fruit girth	Yield plant ⁻¹
Plant height	G	1.000	0.894**	0.311*	0.750**	0.811**	0.290*	0.136	0.849**	0.798**
	P	1.000	0.841**	0.255*	0.578**	0.711**	0.148	0.111	0.621**	0.748**
Internode length	G		1.000	0.227	0.547*	0.807**	0.429*	0.189	0.850**	0.789**
	P		1.000	0.209	0.469*	0.693**	0.303*	0.096	0.661**	0.747**
Node number at 1 st fruit	G			1.000	0.555*	0.007	-0.184	-0.413*	-0.023	-0.015
	P			1.000	0.392*	0.017	-0.098	-0.038	-0.020	-0.014
Number of nodes plant ⁻¹	G				1.000	0.392*	0.139	-0.304*	0.420*	0.407*
	P				1.000	0.275*	0.079	-0.024	0.213	0.297*
Number of fruits plant ⁻¹	G					1.000	0.212	0.260*	0.763**	1.035**
	P					1.000	0.164	0.237	0.578**	0.902**
Average fruit weight	G						1.000	0.595**	0.453*	0.306*
	P						1.000	0.457*	0.416*	0.284*
Fruit length	G							1.000	0.609**	0.390*
	P							1.000	0.329*	0.193
Fruit girth	G								1.000	0.797**
	P								1.000	0.662**
Yield plant ⁻¹	G									1.000
	P									1.000

*, ** Significant at 0.05% and 0.01% probability respectively; G, P: Genotypic and Phenotypic Coefficient of correlation

Table 3. Estimates of direct and indirect effects of yield and yield related characters in Okra

Character	Level	Plant height	Internode length	Node number at 1 st fruit	Number of nodes plant ⁻¹	Number of fruits plant ⁻¹	Avg. fruit weight	Fruit length	Fruit girth	Correlation with yield
Plant height	G	-0.245	-0.403	-0.003	0.073	1.148	-0.004	0.022	-0.028	0.876
	P	0.172	-0.013	-0.004	-0.015	0.405	0.014	-0.005	0.024	0.766
Internode length	G	-0.216	-0.458	-0.003	0.085	1.009	-0.018	0.047	-0.029	0.789
	P	0.127	-0.018	-0.006	-0.020	0.401	0.042	-0.006	0.026	0.747
Node number at 1 st fruit	G	-0.056	-0.104	-0.013	0.087	0.008	0.008	-0.104	-0.000	-0.015
	P	0.026	-0.004	-0.028	-0.017	0.010	-0.014	0.003	-0.001	0.014
Number of nodes plant ⁻¹	G	-0.115	-0.251	-0.007	0.156	0.490	-0.006	-0.076	-0.014	0.407
	P	0.060	-0.008	-0.011	-0.043	0.159	0.011	-0.002	0.008	0.297
Number of fruits plant ⁻¹	G	-0.225	-0.370	-0.000	0.061	1.251	-0.001	0.065	-0.026	0.662
	P	0.120	-0.12	-0.001	-0.012	0.578	0.023	-0.016	0.023	1.035
Average fruit weight	G	-0.022	-0.197	0.002	0.022	0.266	-0.043	0.149	-0.015	0.306
	P	0.017	-0.005	0.003	-0.003	0.095	0.140	-0.030	0.017	0.284
Fruit length	G	-0.021	-0.087	0.005	-0.048	0.325	-0.025	0.251	-0.021	0.390
	P	0.014	-0.002	0.001	-0.001	0.137	0.064	-0.066	0.013	0.193
Fruit girth	G	-0.200	-0.390	-0.000	0.066	0.954	-0.019	0.153	-0.034	0.193
	P	0.106	-0.012	0.001	-0.009	0.334	0.058	-0.022	0.040	0.797

height (0.811, 0.711) and fruit girth (0.763, 0.578) at both genotypic and phenotypic levels. Fruit length had positive association with fruit girth at genotypic level (0.609) and phenotypic (0.329) level. These findings suggested that these traits should be considered during direct selection for genetic improvement for yield in okra. Dhall *et al.* (2000) also reported similar association among for these characters.

Path coefficient analysis studies revealed that number of fruits plant⁻¹ showed the highest positive effect (1.251) on yield plant⁻¹ (Table 3). Among the characters studied, all the traits showed positive direct effect on yield except internode length which showed negative direct effect on yield plant⁻¹. The highest indirect effect of number of fruits plant⁻¹ was observed with plant height (1.148), internode length (1.009) followed by fruit girth (0.954). These characters also showed significant positive correlation with yield. These findings indicating that direct selection for these traits might be effective and there is possibility of improving yield plant⁻¹. Similar results have been reported by Nasit *et al.* (2010) and Mehta *et al.* (2006).

The above findings suggested that for getting higher yield, selection should be practiced for yield related traits giving equal importance to number of fruits, number of nodes, plant height and the selected genotypes may be tested under potential areas for identification of best cultivar either for general cultivation or for using in future breeding programme.

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