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Genetic Analysis Studies in Okra [*Abelmoschus esculentus* (L.) Moench]

Neeraj Singh*, Dhirendra Kumar Singh, Umesh Chandra Sati, Monisha Rawat and Pooja Pandey

Department of Vegetable Science, College of Agriculture, GBPAU&T, Pantnagar, Uttarakhand – 263145

*Corresponding Author E-mail: neerajsingh9838@gmail.com

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ABSTRACT

An experiment was undertaken on One hundred eighty accessions of okra [Abelmoschus esculentus (L.) Moench] to assessed to determine their genetic variability, heritability and genetic advance in all genotypes. The wide range of variability was observed among fifteen characters of all genotypes. The phenotypic coefficient of variance (PCV) was generally higher than their respective genotypic coefficient of variance, thus revealing the role of environmental factors. The genotypic and phenotypic coefficient of variability were high for fruit width, intermodal length, plant height, number of primary branches, first flower production node and first fruit production node (23.01 and 23.43, 21.65 and 21.88, 20.68 and 20.78, 19.47 and 20.93, 19.35 and 19.40, 18.29 and 20.57 respectively) indicating maximum amount of variability present in the genotypes for these characters which would be amenable for further selection. High heritability coupled with high genetic advance per cent of mean was observed for plant height, first flower producing node, number of ridges per fruit, intermodal length, fruit width, stem diameter, number of fruits per plant and first fruit producing node (99.00 and 38.22, 99.00 and 39.77, 99.00 and 33.99, 98.00 and 44.13%, 96.00% and 46.54%, 96.00% and 23.95%, 92.00% and 27.56% and 79.00% and 33.50% respectively) indicates predominance additive gene action. Thus, there is ample scope for improving these characters through direct selection.

Key words: *Genetic advance, Heritability, Okra, Genetic variability.*

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench] also known as lady's finger and Bhendi is an important spring - summer and rainy season vegetable crop cultivated in tropical and sub-tropical parts of the world. Looking to the potentials of okra its improvement is inevitable. So, before taking up any breeding programme, a thorough knowledge is required regarding the nature and magnitude of genetic variability, heritability and genetic advance over mean. The key for any success of any breeding program lies in the availability of genetic variability for desired traits[6].

The phenotypic expression of the plant is mainly controlled by genetic makeup of plant and its interaction with environment. It is necessary to partition the observed phenotypic variability into its heritable and non heritable components with suitable parameters[18].

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Yield is a complex character and is a function of large number of characters, their interaction and is also influenced to a great extent by environment. Therefore, selection for yield alone is not effective and it is imperative to depend on traits which are highly heritable and contribute greatly for yield[9].

This study was conducted by keeping objective to improve the productivity, by generating information about the nature and magnitude of genetic variability, which is quite necessary to select and plane effective breeding programme.

MATERIAL AND METHODS

The current study on genetic variability studies in okra were undertaken during the year 2014 in *kharif* season at Vegetable Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar. The experimental site falls under agro-climatic zone-IV. One eighty genotypes were evaluated through a field experiment conducted in augmented block design with four blocks and five checks, ridges and furrows were opened at a distance of 60 cm apart. Two to three seeds per hill were dibbled at a distance of 30 cm in a row. For recording observations, five plants in each experimental plot were chosen at randomly as per NBPGR minimal descriptors from five competitive plants from each replication on fifteen parameters.

The mean values of the data collected were used for analysis of variance (ANOVA) was estimated[14] (Table 1). With a view to understand the extent to which the observed mean, range, genotypic variance (GV), phenotypic variance (PV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2bs), genetic advance and genetic advance as per cent over mean (GAM) were worked out for 26 plant traits[3,9,22] (Table 2).

RESULTS AND DISCUSSION

The analysis of variance showed that the genotypes under study differed significantly among themselves for all the 15 characters (Table 1). The mean, range, genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance as per cent of mean for all the characters are presented in Table 2. The magnitude of PCV was higher than that of GCV for all the traits revealing little influence of the environment in the expression of these traits[7]. The high ratio of GCV and PCV indicate that some of the characters were influenced by the environment. The genotypic and phenotypic coefficient of variability were high for fruit width (23.01% and 23.43% respectively), intermodal length (21.65% and 21.88% respectively), plant height (20.68% and 20.78% respectively), number of primary branches (19.47% and 20.93% respectively), first flower production node (19.35% and 19.40% respectively) and first fruit production node (18.29% and 20.57% respectively) which indicating maximum amount of variability present in the genotypes, for these characters which would be amenable for further selection and characters like number of ridges per fruit (16.55% and 16.60% respectively), number of fruits per plant (13.92% and 14.49% respectively), yield per plant (12.87% and 15.48% respectively), number of seeds per fruit (12.59% and 13.13% respectively), stem diameter (11.88% and 12.14% respectively), fruit length (9.23% and 10.16% respectively), 100 seed weight (8.52% and 8.84% respectively), 50 per cent flowering (7.22% and 7.31% respectively) and fruit weight (3.08% and 3.78% respectively) indicating the existence of limited variability in the genotypes evaluated for the traits showing low genetic variability in the genotypes stock studied. This necessitates need for generation of new variability for these characters. Similar observations have been reported by Dhankar and Dhankar[5]; Mehta *et al*[10].,; Prakash and Pitchaimuthu[16]; Pradip *et al*[15]., and Nwangburuka *et al*[11].

Heritability alone provides no clear indication about the amount of genetic improvement that expected to come out from selection of individual genotype, estimation of heritability without genetic advance will not be of practical value, hence knowledge of genetic advance as per cent of mean coupled with heritability becomes more useful to assist in framing out an effective selection criterion. Genetic advance as per-cent of mean is the improvement in the mean of the selected family over the base population. Since heritability includes additive and non- additive gene effects, a breeder should take care of this fact while going for selection based on heritability. High heritability (>80 %) coupled with high genetic advance (>20 %) as per cent of mean was observed for plant height (99.00% and 42.39% respectively), first flower producing node (99.00% and 39.77% respectively), number of ridges per fruit (99.00% and 33.99 respectively), intermodal length (98.00% and 44.13% respectively), fruit width (96.00% and 46.54% respectively), number of seeds per fruit (92.00% and 24.87% respectively), number of primary branches (87.00% and 37.33% respectively), stem diameter (96.00% and 23.95% respectively) and number of fruits per plant (92.00% and 27.56% respectively) indicating predominance of additive genetic component in governing of these traits and improvement of these traits through simple selection would be rewarding. Similar results were noticed in earlier studies by Vishalkumar *et al*[21].,; Sharma *et al*[19].,; Jindal *et al*[8].,; Adeoluwa and Kehinde[1]; Adiger *et al*[2].,; Das *et al*[4].,; Reddy *et al*[17]., and Om Prakash Meena and Vijay Bahadur[12].

Moderate heritability coupled with high genetic advance as per cent of mean was observed for first fruit producing node (79.00% and 33.51% respectively). This indicates the importance of additive effects for this trait and selection may be rewarding. These same results were also observed by Mehta *et al*[10].,; Sharma *et al*[19]., and Osekita and Akinyele[13].

High heritability coupled with moderate genetic advance as per cent of mean was observed for fruit length (82.00% and 17.28% respectively), 100 seed weight (93.00% and 16.89% respectively) and 50 per cent flowering (97.00% and 14.67% respectively) indicating non-additive gene action. The high heritability was being exhibited due to favorable influence environment rather than genotype and selection for such traits may not be rewarding. These results were confirmative with results obtained by Singh *et al*[20].

High genetic advance as per cent of mean coupled with moderate heritability was observed for marketable yield per plant (69.00% and 22.05% respectively) indicates the importance of additive effects for this trait and selection may be rewarding. These same results were also observed by Mehta *et al*[10]., and Sharma *et al*[19].

Moderate heritability coupled with low genetic advance as per cent of mean was observed for fruit weight (67.00% and 5.17% respectively) indicating non-additive gene action and selection for such traits may not be rewarding. These same results were also observed by Mehta *et al*[10].

Table 1: Analysis of variance (mean sum of square) for different parameters in okra genotypes

	df	first flower producing node	Ist fruit producing node	internodal length	Fruit length (cm)	fruit width (cm)	No. of ridges per fruit	no. of seeds/ fruit	100 seed weight (g)	50 % flowering	plant height(cm)	no. of primary branches	stem diameter (mm)	no. fruits/ plant	fruit weight (g)	marketable yield / plant (g)
Block	5	4.124	4.741	2.456	7.498	0.797	1.546	227.766	1.120	19.344	1905.984	2.445	8.182	19.517	1.063	4511.337
Entries (ignoring Blocks)	184	1.583	2.279	3.222	1.937	0.294	0.903	77.710	0.316	12.873	463.263	0.912	9.595	6.241	0.367	1270.833
Checks	4	2.999	3.807	1.378	9.174	0.020	0.007	20.675	0.160	87.934	5717.458	0.831	3.118	50.104	2.085	4687.586
Varieties	179	1.426	1.828	2.589	1.849	0.275	0.929	53.520	0.337	11.084	399.614	0.680	6.730	2.032	0.348	507.233
ERROR	20	0.006	0.344	0.048	0.290	0.009	0.005	3.801	0.022	0.251	3.462	0.082	0.252	0.138	0.107	142.726

Table 2: Estimates of mean, range, components of variance, heritability and genetic advances for 15 characters in okra genotypes

Characters / **Genetic Parameter**		**first flower producing node**	**Ist fruit producing node**	**internodal length**	**Fruit length (cm)**	**fruit width (cm)**	**No. of ridges per fruit**	**no. of seeds/ fruit**	**100 seed weight (g)**	**50 % flowering**	**plant height (cm)**	**no. of primary branches**	**stem diameter (mm)**	**no. fruits/ plant**	**fruit weight (g)**	**market able yield / plant (g)**
Average mean		5.78	6.24	6.90	12.68	2.10	5.44	52.46	6.18	42.72	90.15	3.72	20.07	9.26	5.78	6.24
Range	**Max**	9.00	9.80	19.24	25.02	5.28	11.00	75.60	7.50	49.00	160.00	7.20	29.40	14.80	9.00	9.80
	Min	3.60	3.80	4.18	9.76	1.54	5.00	6.00	5.20	32.00	55.20	2.20	13.20	6.20	3.60	3.80
GCV		19.35	18.29	21.65	9.23	23.01	16.55	12.59	8.52	7.22	20.68	19.47	11.88	13.92	3.08	12.87
PCV		19.40	20.57	21.88	10.16	23.43	16.60	13.13	8.84	7.31	20.78	20.93	12.14	14.49	3.78	15.48
ECV		1.32	9.40	3.16	4.25	4.42	1.31	3.72	2.39	1.17	2.06	7.67	2.50	4.01	2.19	8.60
Hb		100	79	98	82	96	99	92	93	97	99	87	96	92	67	69
GA		2.29	2.09	3.04	2.19	0.98	1.85	13.05	1.04	6.27	38.22	1.39	4.81	2.55	0.77	30.63
GA % of mean		39.77	33.51	44.13	17.26	46.54	33.99	24.87	16.89	14.67	42.39	37.33	23.95	27.56	5.17	22.05

PCV- Phenotypic co-efficient of variation GCV- Genotypic co-efficient of variation

ECV- Environmental co-efficient of variation hb- Heritability (Broad sense)

GA- Genetic advance

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