



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(11): 151-155
© 2021 TPI
www.thepharmajournal.com

Received: 02-08-2021
Accepted: 13-09-2021

Ullangula Sravanthi
Scientist, KVK, BPA, ICAR,
PJ TSAU, Hyderabad,
Telangana, India

B Neeraja Prabhakar
Hon'ble Vice Chancellor SKLTS
HU, Telangana, India

P Saidaiah
Associate Professor, COH,
Mojerla, SKLTS HU, Telangana,
India

A Manohar Rao
Professor (Rtd.), PJ TSAU,
Hyderabad, Telangana, India

D Lakshmi Narayana
Associate Professor, COH,
Rajendranagar, SKLTS HU,
Telangana, India

G Sathish
Assistant Professor, COH,
Mojerla, SKLTS HU, Telangana,
India

Corresponding Author:
Ullangula Sravanthi
Scientist, KVK, BPA, ICAR,
PJ TSAU, Hyderabad,
Telangana, India

Studies on genetic variability in okra (*Abelmoschus esculentus* (L.) Moench)

Ullangula Sravanthi, B Neeraja Prabhakar, P Saidaiah, A Manohar Rao, D Lakshmi Narayana and G Sathish

Abstract

In the present investigation was carried out at College of Horticulture, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad during the period during s *Kharif*, 2016-17 to study the variability, heritability and genetic advance for different morphological and agronomic traits. Analysis of variance revealed significant variability among the genotypes of okra for all character's studied. Genetic variability revealed that a lot of variation among the genotypes. In general, the lowest difference in phenotypic and genotypic coefficients of variation indicates lowest environmental influence in controlling the expression of the traits. Based on genetic variability studies, high PCV and GCV and high heritability coupled with high genetic advance as per cent of mean were recorded for plant height (cm), number of fruits per plant, number of fruits per plot and number of fruits per plant, number of fruits per plot and overall YVMV PDI (%) indicating the existence of wider genetic variability for these traits in the germplasm under study.

Keywords: Genetic variability, heritability, genetic advance, okra, *Abelmoschus esculentus*

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench.] is a member of the family Malvaceae and an important vegetable crop grown in tropical and subtropical regions of the world. The green tender fruits of okra are good source of carbohydrate, protein, vitamins (A, B and C) and rich in calcium, potassium and other mineral matters. It contains 1.9 g protein, 1.2 g fiber, 1.5 mg Fe and 88 IU Vit-A per 100 g of edible portion. India is a major okra producing country in the world comprising of 72 per cent of total area under okra. In India it was cultivated on an area of 526 thousand-hectare with annual production of 6460 thousand tones and productivity of 12.28 t ha⁻¹ and in Telangana area 12.16 thousand-hectare, production 167.25 MT and productivity 13.68 t ha⁻¹ (2019-2020 2nd advance NHB). Genetic improvement of any crop mainly depends on the amount of genetic variability present in the population and the germplasm serves as a valuable source of base population and provide scope for wide variability (R.T. Gavade and B.A. Ghadage, 2015) [2]. Further, the crop exhibits rich genetic diversity and scope for improvement for various horticultural traits. Heritability is the heritable portion of phenotypic variance. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations. Heritability indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance but it fails to indicate the expected genetic progress in one cycle of selection. Heritable variation can be effectively used with greater degree of accuracy when heritability is studied in conjunction with genetic advance (Johnson *et al.* 1955) [4]. Genetic advance denotes the improvement in the mean genotypic values of selected families over base population and thus helps the breeder to select the progenies in the earlier generation itself. An improvement in yield and quality of okra is normally achieved by selecting the genotypes with desirable character combination existing in nature or by hybridization. With this objective, the present investigation was carried out with okra germplasm.

Material and Methods

The present research was conducted at College of Horticulture, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad during the period during *Kharif*, 2016-17. The details of 32 genotypes included in the present study along with their source of the collection are presented in table 1. The genotypes which were chosen for the present study were grown in a randomized block design with three replications.

Standard cultural and agronomic practices were followed to maintain healthy crop growth. Thirteen observations were recorded on five randomly selected plants in each replication for the morphological traits *viz.*, plant height (cm), days to initiation for first flowering, days to 50% flowering, number of branches plant⁻¹, fruit length (cm), diameter of fruit (cm), weight of fruit (g), number of fruits plant⁻¹, number of fruits plot⁻¹, fruit yield plant⁻¹ (g), fruit yield (t ha⁻¹), fiber content (%) and overall YVMV PDI (%). The data were statistically analyzed the analysis of variance as per the standard statistical procedure (Panse and Sukhatme, 1985). Phenotypic and genotypic components of variance were estimated as per the formulae suggested by (Lush, 1940) [8]. The broad sense heritability was estimated by following the procedure suggested by Weber and Moorthy. Estimates of phenotypic

and genotypic coefficients of variation were calculated as per the standard formulae (Burton and Devane, 1953) [1]. Genetic advance for each character was predicted by the formula given by (Johnson *et al.*, 1955) [4]. He reported that heritability along with genetic gain is more useful than the heritability alone, in predicting the resultant effect for selecting the best individuals. He categorized the heritability values, as the values greater than 60 per cent indicate the high heritability, the values ranged between 30 to 60 per cent indicate the moderate heritability, while the values less than 30 per cent indicate the low heritability. Similarly, the values greater than 20 per cent indicate high genetic advance, the values ranged between 10 to 20 per cent indicate moderate genetic advance, while the values less than 10 per cent indicate low genetic advance.

Table 1: List of germplasm lines of Okra selected for genetic diversity studies

S. No.	Genotype	Source
1.	RHBG-1	VRS, SKLTSHU, HYDERABAD
2.	RHBG-2	VRS, SKLTSHU, HYDERABAD
3.	RHBG-3	VRS, SKLTSHU, HYDERABAD
4.	RHBG-4	VRS, SKLTSHU, HYDERABAD
5.	RHBG-5	VRS, SKLTSHU, HYDERABAD
6.	RHBG-6	VRS, SKLTSHU, HYDERABAD
7.	RHBG-7	VRS, SKLTSHU, HYDERABAD
8.	VRO-6	VRS, SKLTSHU, HYDERABAD
9.	IC-42490	NBPGR- New Delhi
10.	IC-43743	NBPGR- New Delhi
11.	IC-45730	NBPGR- New Delhi
12.	IC-90219	NBPGR- New Delhi
13.	IC-10533	NBPGR- New Delhi
14.	IC-10265	NBPGR- New Delhi
15.	RHBG-8	VRS, SKLTSHU, HYDERABAD
16.	IC-18960	VRS, SKLTSHU, HYDERABAD
17.	IC-04328	VRS, SKLTSHU, HYDERABAD
18.	RHBG-9	VRS, SKLTSHU, HYDERABAD
19.	RHBG-13	VRS, SKLTSHU, HYDERABAD
20.	IC-90004	NBPGR- New Delhi
21.	IC-111515	NBPGR- New Delhi
22.	RHBG-10	VRS, SKLTSHU, HYDERABAD
23.	RHBG-11	VRS, SKLTSHU, HYDERABAD
24.	RHBG-12	VRS, SKLTSHU, HYDERABAD
25.	Arka Anamika	IIHR-Banglore
26.	Pusa Sawani	IARI-New Delhi
27.	Arka Abhay	IIHR-Banglore
28.	Pusa A-4	IARI-New Delhi
29.	EC-755648	NBPGR- New Delhi
30.	IC-29119	NBPGR- New Delhi
31.	IC-22237	NBPGR- New Delhi
32.	EC-755647	NBPGR- New Delhi

Results and Discussion

The analysis of variance showed that the genotypes under study differed significantly among themselves for all the 13 characters (Table 2).

Estimating variability in a population is an effective tool for the breeder to design the selection procedures more accurately for identifying superior genotypes. Variability helps to choose the potential genotype, since it indicates the extent of recombination for implementing effective selection. The

magnitudes of phenotypic and genotypic coefficients of variation have been assessed to know the real worth of material.

The results with regard to mean, the source overall range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2b) and expected genetic advance as per cent of mean (GA) for all the 13 characters are furnished in Table 3. The details of these variability parameters are presented below.

Table 2: Analysis of variance for 13 characters in okra 32 genotypes

Source of Variation	d.f	Mean sum of squares						Weight of the fruit (g)
		Plant height (cm)	Days to initiation for first flowering	Days to 50% flowering	Number of branches per plant	Fruit length (cm)	Diameter of fruit (cm)	
Replications	1	0.155	0.006	4.111	0.090	0.000	0.000	0.052
Genotypes	31	1349.966 ***	23.521 ***	10.074 ***	2.007 ***	4.192 ***	0.044 ***	9.418 ***
Error	31	9.726	2.104	2.389	0.040	0.146	0.006	0.366
S.Em ±	63	669.05	12.61	6.198	1.009	2.135	0.024	4.815
CV (%)		5.006	3.454	3.267	6.539	5.647	5.035	8.769
CD (P=0.05)		6.36	2.96	3.15	0.41	0.77	0.15	1.23

Continue...

Source of Variation	d.f	Mean sum of squares					Overall YVMV (%)
		Number of fruits per plant	Number of fruits per plot	Fruit yield per plant (g)	Fruit yield per hectare (t)	Fiber content (%)	
Replications	1	1.35	542.89	19.52	0.063	0.480	87.89
Genotypes	31	17.29 ***	6918.58***	4126.85 ***	12.742 ***	12.77 ***	944.85***
Error	31	0.485	194.062	94.901	0.294	0.738	41.12
S.Em ±	63	8.77	3508.49	2077.68	6.42	6.65	4.53
CV (%)		5.3366	5.3366	10.3866	10.4101	7.3041	17.50
CD (P=0.05)		1.4206	28.4116	19.8683	1.1055	1.7523	13.08

*Significant at 5 per cent level; ** Significant at 1 per cent level; *** Significant at less than 1 per cent level;

Table 3: Estimation of variability, heritability and genetic advance as per cent of mean for 13 characters in 32 genotypes of okra

S. No.	Characters	Range		Mean	Variance		PCV (%)	GCV (%)	h ² b (%)	Genetic Advance	GA as per cent of mean
		Minimum	Maximum		Phenotypic	Genotypic					
1	Plant height (cm)	26.65	106.15	62.3	679.85	670.12	41.85	41.55	98.57	52.94	84.98
2	Days to initiation for first flowering	35.25	50.5	41.99	12.81	10.71	8.52	7.79	83.58	6.16	14.68
3	Days to 50% flowering	43.74	54.65	47.3	6.23	3.84	5.28	4.14	61.67	3.17	6.7
4	Number of branches per plant	2.00	6.3	3.05	1.02	0.99	33.12	32.47	96.1	2.00	65.57
5	Fruit length (cm)	3.14	9.54	6.76	2.17	2.02	21.8	21.06	93.29	2.83	41.9
6	Diameter of fruit (cm)	1.15	1.78	1.49	0.03	0.02	10.56	9.29	77.27	0.25	16.82
7	Weight of fruit (g)	3.33	10.73	6.9	4.89	4.53	32.05	30.83	92.51	4.22	61.08
8	Number of fruits per plant	8.07	19.95	13.05	8.9	8.41	22.85	22.21	94.54	5.81	44.49
9	Number of fruits per plot	161.3	399	261.04	3556.32	3362.26	22.85	22.21	94.54	116.14	44.49
10	Fruit yield per plant (g)	41.08	182.21	93.79	2110.88	2015.98	48.99	47.87	95.5	90.39	96.37
11	Fruit yield per hectare (t)	2.28	10.12	5.21	6.52	6.22	49.03	47.91	95.49	5.02	96.45
12	Fiber content (%)	7.55	14.65	11.76	6.76	6.02	22.1	20.86	89.07	4.77	40.55
13	Overall YVMV PDI (%)	0	67.5	35.94	524.9	485.38	63.75	61.3	92.47	43.64	121.44

PCV and GCV: Phenotypic and genotypic coefficient of variation, h²: Heritability in broad sense, GA: Genetic Advance

Genetic Variability

Plant height (cm) showed very high phenotypic and genotypic variances (679.846 and 670.12) were recorded which were coupled with high PCV and GCV of 41.853 and 41.552 percent respectively. High heritability (98.57%) with high genetic advance (52.94) and high GA as per cent mean (84.98). Days to initiation for first flowering showed moderate phenotypic and genotypic variances (12.813 and 10.708 respectively) with low PCV (8.524) and GCV (7.793). High heritability (83.58%), low genetic advance (6.16) and moderate GA as per cent mean (14.68) estimates were recorded for this trait. Days to 50% flowering showed low phenotypic and genotypic variances (6.232 and 3.849 respectively) with low PCV (5.277) and low GCV (4.144), high heritability (61.67%), low genetic advance (3.17) and low GA as per cent mean (6.70) estimates were recorded for this trait. Number of branches plant⁻¹ recorded low phenotypic and genotypic variances of 1.024 and 0.984 respectively with high PCV (33.123) and high GCV (32.471) values. The high heritability (96.10%), low genetic advance (2.00) and high GA as per cent mean (65.57) were also reported for this trait. With respect to fruit length, very low phenotypic and genotypic variances (2.169 and 2.023), high PCV (21.801) and GCV (21.057), high heritability (93.29%), low genetic

advance (2.83) and high GA as per cent mean (41.90) estimates were recorded. Very low phenotypic (0.25) and genotypic variances (0.19) were recorded for fruit diameter, with moderate PCV (10.563) and low GCV (9.286), high heritability (77.27%), low genetic advance (0.25) and moderate GA as per cent mean (16.82). Low phenotypic (4.892) and genotypic (4.526) variances, moderate PCV (10.563) and GCV (9.286) were recorded for weight of fruit. High heritability (77.27%), very low genetic advance (0.25) and moderate GA as per cent mean (16.82) estimates were observed for this trait. Low phenotypic and genotypic variances (8.891 and 8.406) were recorded in okra genotypes with high PCV (22.845) and GCV (22.213) values for number of fruits plant⁻¹. This character showed high heritability (94.54%) but low genetic advance (5.81) and high GA as per cent mean (44.49). Number of fruits per plant showed very high phenotypic and genotypic variances (3556.323 and 3362.262) were recorded in okra genotypes with high PCV (22.845) and GCV (22.213) values. High heritability (94.54%) but high genetic advance (116.14) and high GA as per cent mean (44.49). Very high phenotypic (2110.877) and genotypic variances (2015.976) were recorded in okra genotypes with high PCV (48.986) and GCV (47.872) values for Fruit yield per plot (g). It showed high heritability

(95.50%) but high genetic advance (90.39) and GA as per cent mean (96.37). Low phenotypic (6.518) and genotypic variances (6.224) were recorded in okra genotypes with high PCV (49.03) and GCV (47.912) values for Fruit yield per hectare (t). It showed high heritability (95.49%) but low genetic advance (5.02) and high GA as per cent mean (96.45). Low phenotypic (6.756) and genotypic (6.018) variances, high PCV (22.097) and GCV (20.855) were recorded for fiber content (%). High heritability (89.07%), low genetic advance (4.77) and high GA as per cent mean (40.55) estimates were observed for this trait. High phenotypic (524.9) and genotypic (485.38) variances, high PCV (63.75) and GCV (61.30) were recorded in overall YVMV PDI (%). High heritability (92.47%), high genetic advance (43.64) and high GA as per cent mean (121.44) estimates were observed for this trait.

High PCV and GCV for the traits *viz.*, observed for plant height (cm), number of branches per plant, fruit length (cm), weight of fruit (g), number of fruits per plant, number of fruits per plot, fruit yield per plant (g), fruit yield per hectare (t), fiber content (%), overall YVMV PDI (%). Hence these characters can be improved through direct selection from existing genotypes. Low PCV and GCV for the traits *viz.*, days to initiation for first flowering, days to 50% flowering.

In the present study, by comparing phenotypic and genotypic coefficient of variation, most of the characters were low indicating the greater role of genetic factors. This clearly shows that phenotypic values can be used for selection. High phenotypic and genotypic coefficients of variation were recorded for plant height (cm), number of branches per plant, fruit length (cm), weight of fruit (g), number of fruits per plant, number of fruits per plot, fruit yield per plant (g), fruit yield per hectare (t), fiber content (%) and overall YVMV PDI (%) suggesting that variability in these characters is due to genetic constitution. These characters offer much scope for improvement by selection.

The phenotypic and genotypic coefficients of variation were low for the characters *viz.*, days to initiation for first flowering, days to 50% flowering. The low estimates of coefficient of variation indicated that the genotypes included in the present study possessed less genetic variability for these characters, while characters having high estimates of coefficient of variation indicated greater genetic variability among the genotypes for these attributes for making effective selection.

Heritability and Genetic Advance

Heritability estimates give a measure of transmission of characters from one generation to another, thus giving an idea of heritable portion of variability and enabling the plant breeder in isolating the elite genotype in the crop. The heritability expresses the portion of total variances that was attributed to the average effect of genes and that determines the degree of resemblance between parents and off springs. It also expresses the reliability of phenotypic values as a guide to the breeding value.

Heritability in broad sense is the portion of genotypic variance to phenotypic variance, which indicates the relative success of selection. It is useful in selection of elite genotype from diverse genetic population.

High heritability estimates are helpful in selecting superior genotypes on the basis of performance of quantitative characters. In the present study, the heritability in broad sense was found to be high for all the characters. High heritability estimates indicated the presence of large number of fixable

additive gene, hence, these traits can be improved by selection. Heritability coupled with genetic advance is an important selection parameter. In the present study, high heritability coupled with high genetic advance as per cent of mean was observed for the characters *viz.*, plant height, number of fruits per plant, fruit yield per plant and overall YVMV PDI (%). Further, high heritability accompanied with high genetic advance indicated the involvement of additive gene action, therefore selection may be effective.

Whereas, high heritability and low genetic advance was observed for the characters *viz.*, days to initiation for first flowering, days to 50% flowering, number of branches per plant, fruit length (cm), diameter of fruit (cm), weight of the fruit (g), number of fruits per plant, fruit yield per hectare (t) and fiber content (%) which implied equal importance of additive and non-additive gene action. The high heritability might be due to unfavorable influence of environment rather than genetic constitution and offers a little scope for selection.

Conclusion

On the basis of the present study, it could be concluded that simultaneous selection based on multiple characters *viz.*, plant height, number of fruits plant⁻¹, fruit yield plant⁻¹ and overall YVMV PDI (%) having high estimates of heritability and genetic advance could be exercised for improvement through simple direct selection.

Declaration: The authors declare no conflict of interest.

Acknowledgement

Authors wishes to thank the College of Horticulture, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad for undertaking the research and their financial support.

References

- Burton GW, De-Vane EH. Estimating heritability in tall fescue from replicated clonal material. *Agron. J* 1953;45:478-481.
- Gavade RT, Ghadage BA. Genetic variability, heritability and genetic advance in generation of Brinjal (*Solanum elongata* L.). *Bioinfolet* 2015;12(1C):325-328.
- Jagan K, Ravinder RK, Sujatha M, Sravanthi V, Madhusudhan SR. Studies on genetic variability, heritability and genetic advance in Okra (*Abelmoschus esculentus* (L.) Moench). *J Agri. Vet. Sci.* 2013a;5(1):59-61.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability of Soybeans. *Agron J* 1955;47:314-318.
- Karthika N, Uma MT. Genetic variability, heritability and genetic advance in Okra (*Abelmoschus esculentus* L. Moench). *Annals of Plant and Soil Research.* 2019;21(1):98-99.
- Katagi A, Thirakannavar S, Jagadeesha RC. Genetic variability and association studies in single and double cross F2 population of Okra. *Hort. Flora Res. Spectrum* 2014;3(3):232-238.
- Lalunaik B, Lal GM, Singh, Devi. Genetic Variability and Character Association for Yield and its Components of Okra (*Abelmoschus esculentus* (L.) Moench) Hybrids. *Indian Horti. J* 2017;7(2):132-135.
- Lush JL. Inter-size correlation regression of offspring on dairy as a method of estimating heritability of

- characters. Proceedings American Society of Animal Production 1940;33:293-301.
9. Mukesh KAK, Yadav RK, Yadav HC, Singh, Shwethga Y, Yadav PK. Genetic analysis of yield and its components in Okra (*Abelmoschus esculentus* (L.) Moench). Vegetable Sci 2013;40(2):198-200.
 10. National Horticulture Board. 2019-20. Indian Horticulture Database, department of Agriculture and cooperation, Government of India. Retrieved from www.nhb.gov.in.
 11. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers, 2nd Edition, Indian Council of Agricultural Research, New Delhi 1967.
 12. Ranga AD, Kumar S, Darvhankar SM. Variability among different yield and yield contributing traits of Okra (*Abelmoschus esculentus* (L.) Moench) genotypes. Electronic J of Plant Breeding 2021;12(1):74-81.
 13. Singh AP, Kumar PP, Kumar A, Bahadur V. Studies on genetic variability, heritability and character association in Okra. Inter. J Bio-resource Stress Management. 2017;8(3):457-462.