



Assessment of Genetic Variability in Okra (*Abelmoschus esculentus* L. Moench) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was carried out at New Orchard, Main Agricultural Research Station, UAS, Raichur, during late *Kharif* 2021-22 using thirty-one genotypes and laid out in Randomized Block Design (RBD) with three replications. High magnitude GCV and PCV were reported for the traits *viz.*, fruit yield per hectare, fruit yield per plant, number of fruits per plant, plant height, leaf area per plant, number of ridges on fruit surface, fruit girth and fibre content indicates that maximum variability exists in these traits. The traits *viz.*, number of nodes per plant, fruit length, ten fruits weight, shelf-life, stem girth, harvesting period and first flowering node recorded the medium GCV

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and PCV values. While, low GCV and PCV values were observed for the characters viz., number of leaves per plant, chlorophyll content, days to 50 per cent flowering and days to first flowering showing little variability for these characters. High heritability accompanied by high genetic advance over per cent mean was observed for number of ridges on fruit surface, number of fruits per plant, fruit yield per plant, fruit yield per hectare, fruit girth, leaf area per plant, plant height, number of nodes per plant, fruit length, fibre content, stem girth and ten fruits weight which indicates additive gene effects and selection based on these characters may be effective. Hence, characters showing high to moderate values of PCV, GCV and high estimate of heritability and genetic advance as per cent mean were considered as most important characters and selection of these traits will be more effective in improvement of fruit yield per plant.

Keywords: Okra genotypes; variability; heritability.

1. INTRODUCTION

“Okra, scientifically known as *Abelmoschus esculentus* L. Moench and also referred to as lady’s finger and bhendi, is a significant vegetable crop grown during the spring-summer and rainy seasons in tropical and sub-tropical regions worldwide. In areas with mild winters, it can be cultivated year-round. India is the largest producer of okra in the world with an annual production of 6.87 million tonnes from an area of 550 thousand hectares in 2019 – 2020” [1]. “Major okra-producing states in India include Uttar Pradesh, Bihar, Orissa, West Bengal, Andhra Pradesh, Karnataka, and Assam. The Agricultural and Processed Food Products Export Development Authority (APEDA) has established Agriculture-Export Zones in Punjab, Uttar Pradesh, Gujarat, Andhra Pradesh, Bihar, and West Bengal to boost vegetable exports, including okra. Okra holds substantial potential as a fresh vegetable crop contributing to India’s foreign exchange earnings. Currently, it is exported to the United Arab Emirates, United Kingdom, Nepal, Bahrain, Saudi Arabia, Singapore, Kuwait, Qatar, and Sri Lanka” [2].

“It is an annual herbaceous plant and belongs to the family Malvaceae under the order Malvales, having a chromosome number of $2n=130$ and is considered to be an amphidiploid. Okra being an often cross-pollinated crop, outcrossing to an extent of 20 per cent by insects, which renders a considerable amount of variability. Emasculation and pollination processes are easier in okra due to large flower and monadelphous stamens” [3].

The present investigation was conducted to study the variability, heritability, and genetic advance for different quantitative traits in okra, aiming to evaluate the potentialities of existing genotypes. This evaluation is crucial as it illustrates the genetic diversity of the base

materials, which underpins the promise for further improvement. “The success of a breeding programme targeting quantitative attributes heavily relies on the extent of genetic variability within the germplasm. Breeders can utilize heritability and genetic advance estimates to employ appropriate breeding methodologies in crop improvement, with economic yield being a complex, inheritably quantitative character influenced by multiple yield components and environmental factors” [4]. “Evaluating genetically different genotypes and cultivars requires observing various traits influencing yield, complicated by genotype by environment interactions. Hence, providing breeders with information on genetic coefficient of variation (GCV), broad-sense heritability (h^2), genetic advance (GA), and genetic advance as a percentage of the mean (GAM) offers insights into the nature of gene action governing specific traits, facilitating effective genotype-based selection” [5].

2. MATERIALS AND METHODS

The study was conducted at New Orchard, Department of Horticulture, MARS, UAS, Raichur during late Kharif (2021 - 2022). The experimental location is situated in North Eastern Dry Zone (Zone-II) of Karnataka $16^{\circ}15' N'$ latitude, $77^{\circ}21' E'$ longitude at an altitude of 389 m above mean sea level having red sandy loamy soil. Average rainfall of the site is 660 mm. The mean maximum temperature is more than $31.2^{\circ}C$ throughout the year. The relative humidity is high in monsoon months which ranged from 55 to 70 per cent. The major rainfall is confined to late kharif to early rabi (August to December). “The experimental material included 31 okra genotypes obtained from ICAR- National Bureau of Plant Genetic Resources (NBPGR), New Delhi, and ICAR- Indian Institute of Horticultural Research (IIHR), Bengaluru (Table 1). These

genotypes were evaluated in a Randomized Block Design (RBD) with three replications” [3]. Each plot measured 3.6 m in length and 2.4 m in width, plants were spaced at 60 cm x 45 cm. Recommended agronomic practices and plant protection measures were followed as per the package of practices, UHS, Bagalkot.

The observations were recorded on twenty different growth, reproductive, yield, and quality characters, with five randomly selected plants per plot in each replication. These characters included plant height, number of leaves per plant, leaf area per plant, internodal length, number of nodes per plant, stem girth, chlorophyll content (SPAD readings), days to first flowering, days to 50 per cent flowering, first flowering node, fruit length, fruit girth, ten fruits weight, number of fruits per plant, harvesting period, fruit yield per plant, fruit yield per hectare, number of ridges on fruit surface, shelf-life, and fibre content. Genotypic and phenotypic variances were calculated using mean square from variance tables [4]. Genotypic coefficient of variation and phenotypic coefficient of variation were categorized as low (0-10%), moderate (11-20%), and high (21% and above) following the method suggested by Burton and Devane [5]. Broad-sense heritability was calculated using the method suggested by Weber and Moorthy [6] and categorized as low (0-30%), moderate (30-60%), and high (60 % and above) as given by Robinson et al. [7]. Genetic advance as a percentage over mean was calculated and categorized as low (0-10%), moderate (11-20%), and high (21 % and above) according to Johnson et al. [4].

3. RESULTS AND DISCUSSION

The analysis of variance revealed that all the twenty characters exhibited highly significant differences among the genotypes thus, suggesting existence of sufficient variability in the germplasm studied [Table 2 (a-b)]. Range values for various characters studied (Table 3) indicated presence of sufficient genetic variability for all the characters, which is prerequisite for making improvement through selection. The results obtained are in agreement with Rambabu et al. [8] Keerthana et al. [9] Madhumitha and Senthilkumar [10]. “The range in the values reflect the amount of phenotypic variability, which is not very reliable since it includes genotypic, environmental and genotype x environmental interaction components and does not reveal as to which character is showing higher degree of variability. Further, the phenotype of crop is influenced by additive gene effect (heritable), dominance (non-heritable) and epistasis (no allelic interaction). Hence, it becomes necessary to split the observed variability into phenotypic coefficient of variation and genotypic coefficient of variation, which ultimately indicates the extent of variability existing for various traits” [9]. The estimates of phenotypic and genotypic coefficients of variation of all the characters studied are presented in Table 3. In general, the phenotypic and genotypic coefficients of variation were almost similar with slightly higher phenotypic coefficients of variation, which indicates the role of environment in the expression of traits under observation. This was in agreement with the study of Ranga et al. [11] Vani et al. [12] and Mohita et al. [13] in okra.

Table 1. List of genotypes used under study with their source of collection

Genotype	Source of collection	Genotype	Source of collection
OPL-2101	NBPGR-New Delhi	OPL-2117	NBPGR-New Delhi
OPL-2102	NBPGR-New Delhi	OPL-2118	NBPGR-New Delhi
OPL-2103	NBPGR-New Delhi	OPL-2119	NBPGR-New Delhi
OPL-2104	NBPGR-New Delhi	OPL-2120	NBPGR-New Delhi
OPL-2105	NBPGR-New Delhi	OPL-2121	NBPGR-New Delhi
OPL-2106	NBPGR-New Delhi	OPL-2122	NBPGR-New Delhi
OPL-2107	NBPGR-New Delhi	OPL-2123	NBPGR-New Delhi
OPL-2108	NBPGR-New Delhi	OPL-2124	NBPGR-New Delhi
OPL-2109	NBPGR-New Delhi	OPL-2125	NBPGR-New Delhi
OPL-2110	NBPGR-New Delhi	OPL-2126	NBPGR-New Delhi
OPL-2111	NBPGR-New Delhi	OPL-2127	NBPGR-New Delhi
OPL-2112	NBPGR-New Delhi	OPL-2128	NBPGR-New Delhi
OPL-2113	NBPGR-New Delhi	OPL-2129	NBPGR-New Delhi
OPL-2114	NBPGR-New Delhi	OPL-2130	NBPGR-New Delhi
OPL-2115	NBPGR-New Delhi	Arka Anamika	IIHR, Bengaluru, Karnataka
OPL-2116	NBPGR-New Delhi	(Check variety)	

Table 2(a). Analysis of variance with respect to MSS for various growth and flowering parameters in okra

Source of variation	d.f	Plant height	Number of leaves per plant	Leaf area per plant	Internodal length	Number of nodes per plant	Stem girth	Chlorophyll content	Days to first flowering	Days to 50 per cent flowering	First flowering node
Treatment	1	819.06**	8.24**	0.54**	1.59*	8.47**	7.51**	35.26*	4.48**	9.39**	0.52**
Replication	30	8.70	2.64	0.01	0.16	0.02	0.35	11.24	0.79	17.56	0.03
Error	30	28.58	1.41	0.02	0.71	0.45	0.84	17.05	0.66	2.73	0.06

, **= Significant at 5% and 1%, respectively

Table 2(b). Analysis of variance with respect to MSS for various yield and quality parameters in okra

Source of variation	d.f	Fruit length	Fruit girth	10 fruits weight	Harvesting period	Number of fruits per plant	Fruit yield per plant	Fruit yield per hectare	Number of ridges on fruit surface	Shelf life	Fibre content
Treatment	1	8.23**	39.46**	1382.30**	58.85**	31.59**	9440.49**	29.81**	4.26	0.96**	11.16**
Replication	30	0.60	0.35	7.32	45.31	3.07	255.96	0.07	0.00	0.02	0.69
Error	30	0.51	1.10	311.38	11.74	1.30	206.98	0.69	0.00	0.35	1.17

, **= Significant at 5% and 1%, respectively

Table 3. Estimates of genotypic and phenotypic coefficient of variation, heritability and genetic advances as per cent of mean for different parameters in okra genotypes

Sl. No.	Characters	Range		GrandMean	GV	PV	GCV (%)	PCV (%)	h ² BS(%)	GA (%)	GAM (%)
		Lowest	Highest								
1	Plant height (cm)	49.61	131.06	72.92	395.24	423.82	27.26	28.23	93.26	39.54	54.23
2	Number of leaves per plant	16.92	29.29	22.41	3.42	4.83	8.24	9.80	70.76	3.20	14.28
3	Leaf area index	0.66	3.62	2.13	0.26	0.28	24.01	24.83	93.47	1833.45	47.82
4	Internodal length (cm)	4.94	12.64	7.62	0.44	1.15	9.94	17.45	32.46	0.88	11.66
5	Number of nodes per plant	7.10	16.51	10.60	4.01	4.46	18.87	19.92	89.82	3.90	36.85
6	Stem girth (mm)	10.74	20.83	15.19	3.34	4.18	12.02	13.45	79.88	3.36	22.13
7	Chlorophyll content (SPAD readings)	41.32	64.26	55.51	9.11	26.16	5.12	8.68	34.81	6.77	6.23
8	Days to first flowering	34.00	41.00	37.01	1.91	2.57	3.73	4.33	74.43	2.45	6.64
9	Days to 50 per cent flowering	28.00	45.00	40.30	3.33	6.06	4.52	6.10	54.93	2.78	6.91
10	First flowering node	4.00	5.80	4.55	0.23	0.29	10.44	11.85	77.70	0.86	18.96
11	Fruit length (cm)	7.66	19.06	14.22	3.86	4.37	13.80	14.69	88.24	3.80	26.71
12	Fruit girth (mm)	14.44	44.72	19.08	19.18	20.28	22.94	23.59	94.59	8.77	45.97
13	10 fruits weight (g)	121.30	264.20	168.63	535.46	846.84	13.72	17.25	63.23	37.90	22.47
14	Harvesting period (days)	40.00	64.00	47.59	23.55	35.29	10.19	12.48	66.74	8.16	17.15
15	Number of fruits per plant	13.81	77.70	35.72	15.79	15.80	55.62	55.62	99.98	40.92	114.56
16	Fruit yield per plant (g)	207.36	1522.10	608.49	4616.76	4823.73	55.83	57.06	95.71	684.67	112.51
17	Fruit yield per hectare (t)	2.28	16.73	6.82	14.56	15.25	55.93	57.23	95.51	7.68	112.60
18	Number of ridges on fruit surface	8	5	6.16	2.13	2.13	24.06	24.06	100.00	3.01	49.56
19	Shelf life (days)	3.00	5.50	4.24	0.31	0.66	13.05	19.09	46.72	0.78	18.38
20	Fibre content (%)	6.75	16.09	11.45	4.99	6.17	20.52	21.69	80.97	4.14	36.19

3.1 Genotypic Co-efficient of Variation

High genotypic co-efficient of variation was reported for the traits viz., fruit yield per hectare (55.93 %), fruit yield per plant (55.83 %), number of fruits per plant (55.62 %), plant height (27.26 %), leaf area per plant (24.01 %), number of ridges on fruit surface (24.06 %), fruit girth (22.94 %) and fibre content (20.52 %). Number of nodes per plant (18.87 %), followed by fruit length (13.80 %), ten fruits weight (13.72 %), shelf-life (13.05 %), stem girth (12.02 %), harvesting period (10.19 %) and first flowering node (10.44 %) recorded the medium GCV values. While, low GCV values were observed for the characters viz., internodal length (9.94 %), number of leaves per plant (8.24 %), chlorophyll content (5.12 %), days to 50 per cent flowering (4.52 %) and days to first flowering (3.73 %).

The high GCV values indicated that maximum variability exists in these traits and there is enough scope for further improvement. The results of high GCV were in consonance to the earlier findings of Singh et al. [14] for plant height, fruit girth and number of ridges on fruit surface, Priyanka et al. [15] Samim et al. [16] and Ranga et al. [11] for number of fruits per plant and fruit yield per plant, Karadi et al. [17] for fruit yield per hectare and Rambabu et al. [8] for fiber content in okra.

3.2 Phenotypic Co-efficient of Variation

High phenotypic co-efficient of variation was reported for the traits viz., fruit yield per hectare (57.23 %), fruit yield per plant (57.06 %), number of fruits per plant (55.62 %), plant height (28.23 %), leaf area per plant (24.83 %), number of ridges on fruit surface (24.06 %), fruit girth (23.59 %) and fibre content (21.69 %). Number of nodes per plant (19.92 %), shelf-life (19.09 %), internodal length (17.45 %), ten fruits weight (17.25 %), fruit length (14.69 %), stem girth (13.45 %), harvesting period (12.48 %) and first flowering node (11.85 %) recorded the medium PCV values. While, low PCV values were observed for the characters viz., number of leaves per plant (9.80 %), chlorophyll content (8.68 %), days to 50 per cent flowering (6.10 %) and days to first flowering (4.33 %).

The results of high PCV were in consonance to the earlier findings of Singh et al. [14] for plant height, fruit girth and number of ridges on fruit surface, Priyanka et al. [15] Samim et al. [16] and Ranga et al. [11] for number of fruits per plant

and fruit yield per plant, Karadi et al. [17] for fruit yield per hectare and Rambabu et al. [8] for fiber content in okra.

The scope for improvement through selection is higher for characters with moderate to high coefficients of variation. High estimates of the phenotypic and genotypic coefficients of variation, together with a wide range of variability, further suggest that these traits would be responsive to selection. Despite a small difference in the values, phenotypic coefficients of variation were larger than the comparable genotypic coefficients of variation. This demonstrated that the variation was mostly attributable to genetic variations and that the environment had little impact on the expression of the observed features, selection based upon phenotypic expression for these characters would be effective for improvement of this crop Ranga et al. [11] Vani et al. [12] and Mohita et al. [13].

3.3 Heritability and Genetic Advance as Per Cent Over Mean

“The phenotypic and genotypic coefficients of variation do not give a true picture about the extent of inheritance of the character. Therefore, the heritability of a character can be relied upon, as it enables the breeder to decide the extent of selection pressure to be applied under a particular environment, which separates out the environmental influence from the total variability. The estimation of heritability has a greater role to play in determining the effectiveness of selection of a character provided it is considered in conjunction with the predicated genetic advance” [4]. Furthermore, “the progress in selection is also directly proportional to the amount of genetic gain. Therefore, the effect of selection is realized more quickly in those characters which have high heritability as well as high genetic gain. When high heritability is accompanied with high GAM (Genetic advance as per cent of mean), it indicates additive gene effects and selection may be effective. High heritability with low GAM indicates importance of non-additive gene action where high heritability is exhibited due to favorable influence of environment rather than genotype and the selection for such traits may not be rewarding” [13].

Low heritability with high GAM is governed by additive gene effects in which low heritability is exhibited due to high environmental effects and the selection may not be effective in such cases.

Low heritability coupled with low GAM indicates that character is highly influenced by environmental effects and selection would not be ineffective [16,13].

Heritability plays an important role in estimating the heritable variations, because GCV does not offer full scope to estimate the heritable variations. In present investigation heritability was ranged between 32.46 to 100 per cent and genetic advances as per cent of mean was ranged between 6.23 to 114.56 per cent.

High heritability (h^2 BS) accompanied by high genetic advance over mean (GAM) was observed for the traits number of ridges on fruit surface (h^2 BS= 100 % and GAM= 49.56 %), number of fruits per plant (h^2 BS= 99.98 % and GAM= 114.56 %), fruit yield per plant (h^2 BS= 95.71 % and GAM= 112.51 %), fruit yield per hectare (h^2 BS= 95.51 % and GAM= 112.60 %), fruit girth (h^2 BS= 94.59 % and GAM= 45.97 %), leaf area per plant (h^2 BS= 93.47 % and GAM= 47.82 %), plant height (h^2 BS= 93.26 % and GAM= 54.23 %), number of nodes per plant (h^2 BS= 89.82 % and GAM= 36.85 %), fruit length (h^2 BS= 88.24 % and GAM= 26.71 %), fibre content (h^2 BS= 80.97 % and GAM= 36.19 %), stem girth (h^2 BS= 79.88 % and GAM= 22.13 %) and ten fruits weight (h^2 BS= 63.23 % and GAM= 22.47 %) which indicates involvement of additive gene effect and characters are heritable to next generation. Selection based on these characters would be more effective. The results of high heritability coupled with high genetic advance over per cent mean in the present investigation are in agreement with the earlier findings of Kumari et al. [18] for fruit yield per hectare, Singh et al. [14] for plant height, stem girth, number of fruits per plant, fruit yield per plant and number of ridges on fruit surface, Morey et al. [19] and Rambabu et al. [8] for fibre content, Samim et al. [16] for number of nodes per plant and ten fruits weight and Ranga et al. [11] for fruit length and fruit girth in okra [20].

High heritability with moderate genetic advance over mean was observed for first flowering node (h^2 BS= 77.70 % and GAM= 18.96 %), number of leaves per plant (h^2 BS= 70.76 % and GAM= 14.28 %) and harvesting period (h^2 BS= 66.74 % and GAM= 17.15 %) while high heritability with low genetic advance over mean was observed for days to first flowering (h^2 BS= 74.43 % and GAM= 6.64 %). Days to 50 per cent flowering (h^2 BS= 54.93 % and GAM= 6.91 %) and chlorophyll content (h^2 BS= 34.81 % and GAM= 6.23 %)

showed moderate heritability with low genetic advance over mean. Shelf-life (h^2 BS= 46.72 % and GAM= 18.38 %) and internodal length (h^2 BS= 32.46 % and GAM= 11.66 %) showed moderate heritability with moderate genetic advance over mean indicates involvement of non-additive gene effects which can be exploited by hybridization or heterosis breeding.

4. CONCLUSION

In present investigation high genetic variability (GCV and PCV) indicating that characters offer great scope for selection due to high variation in genotypes. High heritability coupled with high GAM was observed for number of ridges on fruit surface, number of fruits per plant, fruit yield per plant, fruit yield per hectare, fruit girth, leaf area per plant, leaf area index, plant height, number of nodes per plant, fruit length, fibre content, stem girth and ten fruits weight indicate involvement of additive gene effect and characters are heritable to next generation. Selection based on these characters would be more effective.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. NHB. Area and Protection of Horticultural Crops (second advance estimate report): All India NHB database, Gurgaon, India; 2019.
2. Anonymous; 2020. Available:www.apeda.gov.in
3. Veeresh and Pampanna Y. Correlation Analysis of Quantitative Characters in Okra (*Abelmoschus esculentus* L. Moench). Biological Forum – An International Journal. 2023;15(10):1113-1115
4. Johnson HW, Robinson HF, Comstock RS. Estimation of genetic and environmental variability in soyabean. Agron. J. 1955;41:314-318.
5. Burton GW, Devane RW. Estimating heritability in tall fescue (*Festuca*

- arubdinaces) from replicated clonal material. Agron. J. 1953;45:478-481.
6. Weber CR, Moorthy HR. Heritable and non- heritable relationship and variability of oil content and agronomic characters in the F₂ generation of soyabean crosses. Agron. J. 1952;44:202-209.
 7. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and degree of dominance in corn. Agron. J. 1949;41:353-359.
 8. Rambabu B, Waskar DP, Khandare VS. Genetic variability, heritability and genetic advance in okra. Int. J. Pure App. Biosci. 2019;7(1):374-382.
 9. Keerthana SS, Joshi JL, Anbuselvam Y, Ruban J, Sam. Exploration of Genetic Variations In Okra [*Abelmoschus Esculentus* (L.) Moench] Accessions Based On Quantitative Morphometric Traits. J. of Adv. Zoology. 2024;45(1): 811
 10. Madhumitha Y, Senthilkumar P. Estimation of simple correlation and genetic variability studies in F₂ population of three different crosses in bhendi (*Abelmoschus esculentus* L. Moench). Environment and Ecology. 2024;42(1A):207—212.
 11. Ranga AD, Kumar S, Darvhankar MS. Variability among different yield and yield contributing traits of okra (*Abelmoschus esculentus* L. Moench) genotypes. Electron. J. Plant Breed. 2021;12(1):74–81.
 12. Vani VM, Singh BK, Raju SVS, Singh AK. Studies on genetic variability, heritability and genetic advance for various quantitative traits in okra (*Abelmoschus esculentus* (L.) Monech) genotypes under north gangetic plains of Uttar Pradesh. J. Pharmacogn Phytochem. 2021;10:272-274.
 13. Mohita S, Vikanksha T, Jatinder S. Comparative studies of different okra genotypes under Punjab's Doaba region. Int. J. Adv. Biochem. Res. 2024;8(3):672-676.
 14. Singh N, Singh DK, Pandey, Panchbhaiya A, Monisha R. Correlation and path coefficient studies in okra (*Abelmoschus esculentus* (L.) Moench). Int. J. Curr. Microbio. App. Sci. 2017;6(7): 1093-1101.
 15. Priyanka DV, Thirupathi MR, Begum H, Sunil N, Jayaprada M. Studies on genetic variability, heritability and genetic advance in genotypes of okra (*Abelmoschus esculentus* (L.) Moench). Int. J. Curr. Microbiol. App. Sci. 2018; 7(5):401-411.
 16. Samim S, Sonia S, Singh A. Genetic assessment for fruit yield and horticultural traits in okra (*Abelmoschus esculentus* (L.) Moench). Int. J. Curr. Microbiol. App. Sci. 2018;7(10):947-957.
 17. Karadi SM, Hanchinamani CN. Basavaraja N, Kulkarni MS, Tatagara MH, Satish D. Nature and magnitude of genetic variability studies in okra (*Abelmoschus esculentus* (L.) Moench). Int. J. Chem. Stud. 2018;6(6):638-641.
 18. Kumari M, Solankey SS, Akhtar S, Neha P. Assessment of genetic variability and character association in okra genotypes for yield and contributing characters. J. App. Nat. Sci. 2017;9(3): 1825-1830.
 19. Morey AL, Nagre PK, Dod VN, Kale VS. Genetic variability in okra. Asian J. Hort. 2012;7(1):1-4.
 20. Integrated Horticultural crops management (Kannada). Univ. Hort. Sci., Bagalkot. 58-62.

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