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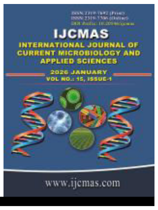

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Studies on Variability, Heritability and Genetic Advance in Okra [*Abelmoschus esculentus* (L.) Moench.]

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ABSTRACT

Thirty four accessions of okra were assessed for variability for nineteen characters with with checks Arka Anamika and Parbhani Kranthi. High phenotypic and genotypic coefficient of variation was observed for number of leaves per plant, fruit yield per plot, incidence of yellow vein mosaic virus, enation leaf curl virus and fruit and shoot borer indicating the existence of wider genetic variability. High heritability accompanied with high genetic advance was observed for plant height, internodal length, number of leaves per plant, fruit length, fruit weight, fruit diameter, number of seeds per fruit, number of fruits per plant, fruit yield per plant, fruit yield per plot, yellow vein mosaic virus, enation leaf curl virus and fruit and shoot borer suggesting that they can be improved through direct selection due to predominant additive variation.

Introduction

Okra (*Abelmoschus esculentus* L.) is an annual herbaceous vegetable crop belonging to the family Malvaceae, possessing a somatic chromosome number of 2n = 130 and is regarded as an amphidiploid (Siemonsmo, 1982). In India, it is popularly known as *bhendi* or lady's finger. Okra is predominantly an often cross-pollinated crop, with insect-mediated out-crossing reported up to 20 per cent, which contributes significantly to genetic variability within the crop (Patil, 1995). It is one of the most preferred fruit vegetables and is widely cultivated in tropical, subtropical and warm temperate regions across the world. The tender green fruits are mainly consumed as a vegetable in various culinary preparations such as slicing and frying. In addition, okra leaves are occasionally used as cattle feed, while the mature seeds are roasted, ground and used as a coffee substitute. Nutritionally, okra is rich, containing 86.10 per cent water, 2.20 per cent protein, 0.02 per cent fat, 9.70 per cent carbohydrates, 1.0 per cent fibre and 0.80 per cent ash (Saifullah and Rabbani, 2009). It is also a good source of vitamin C (30 mg/100 g), calcium (90 mg/100 g) and iron (1.5 mg/100 g) (Pal *et al.*, 1952).

Genetic variability within a population is a fundamental requirement for the success of any plant breeding programme. The differences, whether latent or expressed, among genotypes of a species constitute genetic diversity. Variability refers only to the observable phenotypic differences, which may arise due to genetic factors, environmental influences, or their interaction. A higher degree of variability enhances the probability of identifying and selecting superior genotypes. Moreover, the division of total variability into heritable and non-heritable components provides insight into the efficiency of selection procedures (Fisher, 1918).

Heritability, which reflects the extent to which a trait is transmitted from parents to their progeny, serves as an important parameter for assessing the proportion of genetic variance in relation to total phenotypic variance. However, heritability alone does not fully predict the potential genetic improvement achievable in future generations. Genetic advance, on the other hand, estimates the expected progress under a given selection intensity. The combined consideration of heritability and genetic advance offers a more reliable indication of selection response, as an increase in heritability along with phenotypic variability generally results in greater genetic advance.

Therefore, comprehensive knowledge of genetic advance and the direct and indirect effects of various traits on yield is essential for plant breeders. Improvement in yield and quality of okra is typically accomplished through the selection of genotypes possessing desirable trait combinations present in natural populations or through hybridization. In view of these considerations, the present study was undertaken to evaluate genetic variability in okra germplasm.

Materials and Methods

The present experiment was carried out at the department of horticulture, college of agriculture, Vasanthrao Naik Marathwada Krishi Vidyapeetth, Parbhani, during summer, 2024. The list of the evaluated genotypes along with their sources was illustrated in Table 1. Each genotypes was sown at 45 × 30 cm spacing, accommodating 15 plants in each plot with two replications. The observations were recorded from five selected plants from both replication on nineteen parameters viz., plant height (cm), number of primary branches per plant, inter nodal length (cm), number of leaves per plant, node at which first flower appears, days to 50% flowering, days to first picking, fruit length (cm), fruit weight (g), fruit diameter (cm), number of locules per fruit, number of seeds per fruit, 100/ seed weight, number of fruits per plant, fruit yield per plant (g), fruit yield per plot (Kg), yellow vein mosaic virus, enation leaf curl virus and fruit and shoot borer.

The data was then analyzed using the mean values by following methods suggested by Cochran and Cox (1957).

Table.1 List of genotypes under study

S.No.	Germplasm Accessions	Source
T_1	IC-3759	NBPGR, Regional Station, New Delhi
T_2	IC-7433	NBPGR, Regional Station, New Delhi
T_3	EC-305766	NBPGR, Regional Station, New Delhi
T_4	IC-9327	NBPGR, Regional Station, New Delhi
T_5	IC-3302	NBPGR, Regional Station, New Delhi
T_6	IC-637613	NBPGR, Regional Station, New Delhi
T_7	EC-329369	NBPGR, Regional Station, New Delhi
T_8	IC-8991	NBPGR, Regional Station, New Delhi
T_9	EC-305664	NBPGR, Regional Station, New Delhi
T_{10}	EC-305653	NBPGR, Regional Station, New Delhi
T_{11}	IC-10252	NBPGR, Regional Station, New Delhi
T_{12}	EC-305612	NBPGR, Regional Station, New Delhi
T_{13}	EC-305714	NBPGR, Regional Station, New Delhi
T_{14}	EC-305741	NBPGR, Regional Station, New Delhi
T_{15}	IC-293530	NBPGR, Regional Station, New Delhi
T_{16}	EC-305672	NBPGR, Regional Station, New Delhi
T_{17}	IC-42450	NBPGR, Regional Station, New Delhi
T_{18}	IC-42483	NBPGR, Regional Station, New Delhi
T_{19}	EC-329361	NBPGR, Regional Station, New Delhi
T_{20}	EC-391363	NBPGR, Regional Station, New Delhi
T_{21}	EC-391124	NBPGR, Regional Station, New Delhi
T_{22}	IC-329367	NBPGR, Regional Station, New Delhi
T_{23}	IC-329421	NBPGR, Regional Station, New Delhi
T_{24}	EC-305643	NBPGR, Regional Station, New Delhi

T_{25}	IC-305715	NBPGR, Regional Station, New Delhi
T_{26}	EC-329544	NBPGR, Regional Station, New Delhi
T_{27}	EC-329366	NBPGR, Regional Station, New Delhi
T_{28}	IC-33812	NBPGR, Regional Station, New Delhi
T_{29}	IC-30853	NBPGR, Regional Station, New Delhi
T_{30}	EC-429364	NBPGR, Regional Station, New Delhi
T_{31}	IC-429314	NBPGR, Regional Station, New Delhi
T_{32}	EC-329360	NBPGR, Regional Station, New Delhi
T_{33}	EC-329370	NBPGR, Regional Station, New Delhi
T_{34}	IC-42460	NBPGR, Regional Station, New Delhi
T_{35}	Arka Anamika	IIHR, Bangalore
T_{36}	Parbhani kranthi	MPKV, Rahuri Maharastra

Results and Discussion

From the analysis of variance for yield and yield attributing characters it was observed that, the mean sum of squares for treatments was found to be significant for all the characters except number of leaves per plant, fruit diameter and 100/ seed weight (Table 2). The 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 3). Sivasubramaniam and Madhava Menon (1973) suggested that the values greater than 20 per cent indicate the high phenotypic and genotypic coefficients of variation, the values ranged between 10 to 20 per cent indicate the moderate phenotypic and genotypic coefficients of variation, while the values less than 10 per cent indicate the low phenotypic and genotypic coefficients of variation. Higher amount of variation was observed for number of leaves per plant, fruit yield per plot, incidence of yellow vein mosaic virus, enation leaf curl virus and fruit and shoot borer indicating the existence of wider genetic variability. The higher magnitude of PCV compared to GCV indicates the influence of environmental factors on the expression of the trait.Hence, phenotypic selection alone may not very effective.

Johnson *et al.,* (1955a) 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.

Graph.1 Graph showing the estimation of genetic variability

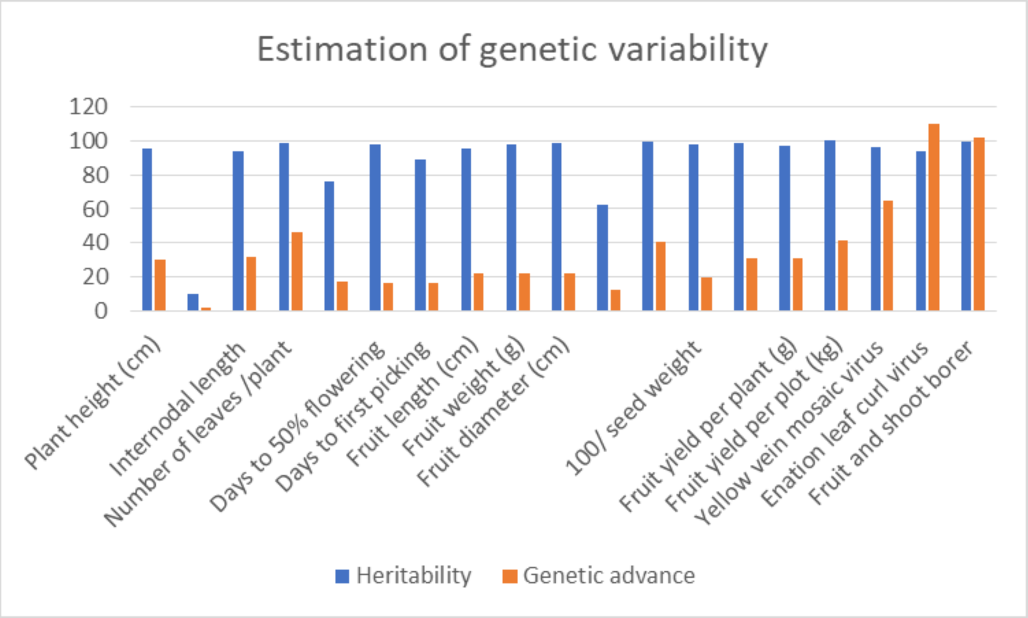


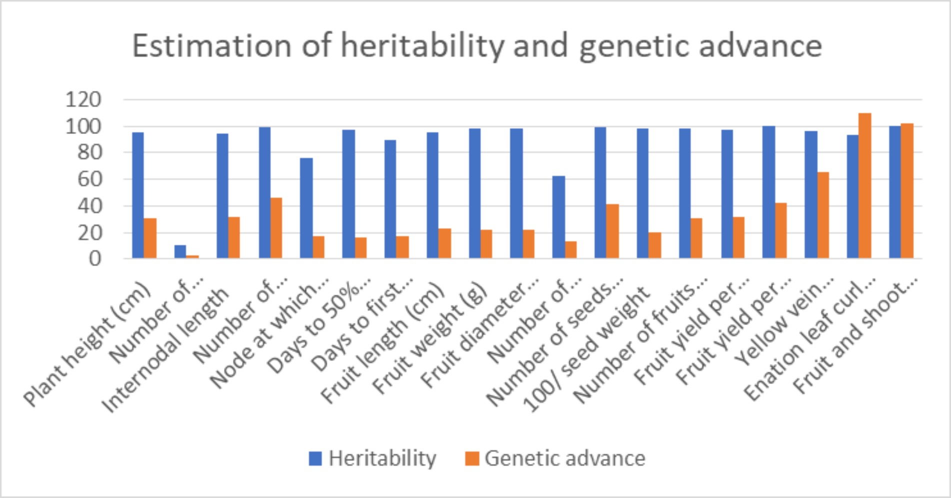
Table.2 Analysis of variance for yield and yield attributing characters in okra

S.No.	Characters	Mean sum of squares		
		Replication	Treatment	Error
1	Plant height (cm)	6.462	334.780 ***	7.864
2	Number of branches per plant	0.002	0.019 *	0.0159
3	Internodal length	0.023	2.317***	0.072
4	Number of leaves /plant	0.211	19.728	0.112
5	Node at which first flower appears	0.013	0.266 ***	0.036
6	Days to 50% flowering	0.190	27.426***	0.332
7	Days to first picking	0.142	37.153***	2.114
8	Fruit length (cm)	0.011	2.559 ***	0.058
9	Fruit weight (g)	0.006	2.582***	0.030
10	Fruit diameter (cm)	0.003	0.063	0.005
11	Number of locules per fruit	0.000	0.203 *	0.000
12	Number of seeds per fruit	1.534	163.810 ***	0.573
13	100/ seed weight	0.027	0.826	0.007
14	Number of fruits per plant	0.035	10.240***	0.0824
15	Fruit yield per plant (g)	0.013	0.069***	0.013
16	Fruit yield per plot (kg)	2.625	1843.630***	1.665
17	Yellow vein mosaic virus	1.175	8.182***	0.174
18	Enation leaf curl virus	0.720	8.908***	0.289
19	Fruit and shoot borer	0.018	11.939***	0.017

Table.3 Estimation of genetic variability, heritability and genetic advance as per of mean in okra

S.No.	Characters	Variance		GCV (%)	PCV (%)	h^2b (%)	GA as %of mean
		Genotypic	Phenotypic				
1	Plant height (cm)	163.45	171.32	15.00	15.36	95.41	30.20
2	Number of branches per plant	0.002	0.01	3.32	10.42	10.20	2.19
3	Internodal length	1.12	16.02	16.53	1.19	93.96	32.00
4	Number of leaves /plant	9.80	9.92	22.71	22.84	98.87	46.52
5	Node at which first flower appears	0.11	0.15	9.69	11.11	76.15	17.42
6	Days to 50% flowering	13.54	13.88	8.11	8.21	97.60	16.51
7	Days to first picking	17.51	19.63	8.67	9.18	89.23	16.87
8	Fruit length (cm)	1.25	1.30	11.23	11.49	95.50	22.61
9	Fruit weight (g)	1.27	1.30	10.90	11.03	97.68	22.20
10	Fruit diameter (cm)	0.03	0.03	10.96	11.06	98.30	22.40
11	Number of locules per fruit	0.10	0.10	6.236	6.23	62.30	12.84
12	Number of seeds per fruit	81.62	82.19	19.90	19.97	99.30	40.85
13	100/ seed weight	0.40	0.41	9.58	9.67	98.09	19.55
14	Number of fruits per plant	5.08	5.16	15.12	15.24	98.40	30.90
15	Fruit yield per plant (g)	0.04	0.05	15.37	15.63	96.72	31.15
16	Fruit yield per plot (kg)	920.98	922.64	20.26	20.28	99.82	41.71
17	Yellow vein mosaic virus	4.00	4.17	32.18	32.88	95.83	64.90
18	Enation leaf curl virus	4.30	4.59	54.92	56.74	93.71	109.53
19	Fruit and shoot borer	5.96	5.97	49.51	49.58	99.70	101.84

Graph.2 Graph showing the estimation of heritability and genetic advance



The estimates of heritability in broad sense were high for all characters. In the present study high genetic advance was observed for the characters plant height, internodal length, number of leaves per plant, fruit length, fruit weight, fruit diameter, number of seeds per fruit, number of fruits per plant, fruit yield per plant, fruit yield per plot, yellow vein mosaic virus, enation leaf curl virus and fruit and shoot borer. Moderate genetic advance was observed for node at which first flower appears, days to 50% flowering, days to first picking, number of locules per fruit, 100/ seed weight and low estimates of genetic advance was observed for number of branches per plant.Similar observations have been reported by Patil *et al.,* (1996), Panda and Singh (1997), Dhankar and Dhankar (2002) and Mehta *et al.,* (2006).

According to Panse (1957), a character with high heritability coupled with high genetic advance (in % mean) is an indication of expression of additive gene action. Characters without such combination appear generally because of non-additive gene action (Liang and Walter, 1968). High genetic advance couple with high heritability was observed for plant height, internodal length, number of leaves per plant, fruit length, fruit weight, fruit diameter, number of seeds per fruit, number of fruits per plant, fruit yield per plant, fruit yield per plot, yellow vein mosaic virus, enation leaf curl virus and fruit and shoot borer are likely to be operated by additive genes. Improvement in these characters would be effective by selection on the basis of phenotype. These results are in consonance with the earlier reports of Adiger *et al.,* (2011) and alam *et al.,* (2010).

In conclusion, the presence of substantial genetic variability, high heritability and high genetic advance for key economic traits suggests ample scope for improvement through selection in the studied okra genotypes.

Data availability

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

Author contributions

Akhila Srinidhi Pendyala: Investigation, analysis, S. J. Shinde: writing original draft, D. K. Zate: Methodology, investigation, V. S. Khandare: Conceptualization, methodology, writing, A.T. Daunde: Investigation, analysis, P. R. Zanwar: writing-reviewing and Manisha Kharat: acquisition protocol validation.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

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