

Original Research Article

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## Assessment of Genetic Diversity in Elite Genotypes of Okra [*Abelmoschus esculentus* (L.) Moench]

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### ABSTRACT

An attempt was made to assess the genetic variability, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench] using 31 diverse genotypes; were grown in randomized block design with three replications during *kharif* 2018 at college farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat (India). Observations were recorded on ten characters showing considerable variability. Mean values were used to determine characters' phenotypic and genotypic variances, phenotypic and genotypic coefficients of variation, broad sense heritability and genetic advance as percentage of mean. Significant variation existed in all the characters. The phenotypic coefficient of variations was found slightly higher than the genotypic coefficient of variations for all characters studied, indicating that the apparent variation is not only genetic but also influenced by the growing environment in the expression of the traits. The moderate magnitude of PCV and GCV was observed for internodal length and number of fruits per plant. High heritability coupled with high genetic advance as per cent of mean was observed for internodal length and number of fruits per plant revealing the importance of additive gene action in the inheritance of these characters and suggested reliable okra improvement through selection of the traits.

#### Keywords

Genetic variation,  
Genotype,  
Phenotype,  
Heritability,  
Genetic advance

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### Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] is commonly known as Lady's Finger in England, Gumbo in the USA and Bhindi in India. It is ancient and economically important vegetable crop cultivated throughout the world and is a native of tropical Africa. Okra is an annual vegetable crop propagated by seeds in

tropical and subtropical region of the world like India, Africa, Turkey and other neighbouring countries. Its tender fruits are used as a vegetable and are generally marketed in fresh state, but sometimes in canned or dehydrated form. In India, okra is one of the most important vegetable crops grown for its tender green fruits during summer and rainy seasons. It is a member of

Mallow or Malvaceae family with  $2n=8x=72$  to 144 chromosomes and is polyploid in nature. There are 30 species under genus *Abelmoschus* in the old world and four in the new world (Joshi and Hardas, 1956). Out of them, *Abelmoschus esculentus* ( $2n=130$ ) is the only species known to be cultivated extensively. Okra is a self-pollinated crop, however occurrence of out crossing to an extent of 4 to 19 per cent (Choudhury and Choonsai, 1970) by insects has been reported which renders considerable genetic diversity.

Creation and utilization of variability using proper breeding procedure is a pre-requisite for the genetic improvement of any crop. Generally, amount of variability is more in the early segregating generations as compared to later generations. The phenotypic expression of the plant character is mainly controlled by the genetic makeup of the plant and the environment in which it is growing. Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean.

Genetic improvement of a crop is pivoted on the strength of genetic diversity within the crop species. Adequate variability provides options from which selections are made for improvement and possible hybridization. Heritability assumes that individuals more closely related are more likely to resemble one another than distant ones (Falconer). Estimate of heritability assists breeders to allocate resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources. There are different ways to calculate heritability. It may be estimated as broad-sense or narrow-sense, on single plant, individual plot or mean of entry. Genetic advance explains the degree of gain obtained in a character under a particular

selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. It also indicates the presence of additive genes in the trait and further suggest reliable crop improvement through selection of such traits. Estimates of heritability with genetic advance are more reliable and meaningful than individual consideration of the parameters.

Continuous improvement of okra is imperative which can be achieved through effective selection of suitable parent materials of significant genetic variability. The objective of the present study was to estimate the genetic variation, heritability and expected genetic advance in the elite okra genotypes and to evaluate suitable selection criteria for further breeding.

## **Materials and Methods**

Diverse genotypes of okra totalling 31 (Table 1), were obtained from different research stations for the study were grown in randomized block design with three replications. Each entry was presented by a single-row plot of ten plants, spaced at 60 x 30 cm. The present experiment was carried out in *kharif* 2018 at college farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat. All recommended horticultural package of practices were applied for field maintenance and harvesting.

Data was recorded on ten parameters *viz.*, days to 50 % flowering, internodal length, number of branches per plant, plant height, number of fruits per plant, fruit length, fruit diameter, fruit weight, fruit yield per plant and fiber content. The GCV and PCV were determined according to Cockerham (1963). Heritability in broad sense was calculated using formula proposed by Allard (1960) and expressed in percentage. Genetic advance for each character was predicted by the formula given

by Johnson *et al.*, (1955). Mean values were used to determine characters' variances, coefficients of variation, broad sense heritability and genetic advance percentage of mean.

## Results and Discussion

The genotypic variance followed the trend of phenotypic variance and was greater than environmental variance for all the characters. This implied that phenotypic variability might be considered as a reliable measure of genotypic variability. In the present study, the phenotypic and genotypic variances were greater than the environmental variance for all the character under study except number of branches per plant and fruit yield per plant where genotypic variance is lower than environmental variances. Similar results were obtained by Kumar *et al.*, (2019) for number of branches per plant and by Bello *et al.*, (2015) for fruit yield per plant, which indicated that influence of environment on expression of traits was lower or negligible, hence selection would be effective (Table 2).

With view to compare different quantitative characters in respect of phenotypic and genotypic variability, phenotypic coefficient of variation and genotypic coefficient of variation were calculated. The genotypic coefficient of variation measures the range of inherent variation present in a character and helps to compare the variability present in different characters. The PCV and GCV measure the extent of variation present in the population in the particular character. In the present investigation, PCV was higher than the respective GCV for all the traits studied, revealing that the environment had an important role to play in influencing the expression of these characters which is in accordance with findings of Sundaram and Rajkumar (2015), Khajuria *et al.*, (2015), Kandasamy *et al.*, (2015), Jadhav *et al.*,

(2016), patil *et al.*, (2017), Singh *et al.*, (2017), Niraja *et al.*, (2018) and Priyanka *et al.*, (2018).

The moderate magnitude of GCV and PCV was observed for internodal length and number of fruits per plant. This is in relation with the earlier reports of Akotkar *et al.*, (2010), Ramanjinappa *et al.*, (2011), Chandra *et al.*, (2014), Mallesh *et al.*, (2015), Chandramouli *et al.*, (2016), Mohammad and marker (2017a) and Ullangula (2017) for internodal length and with Adiger *et al.*, (2011), Prakash *et al.*, (2011a), Ramanjinappa *et al.*, (2011), Pooja *et al.*, (2011), Chandra *et al.*, (2014), Kumar and Kumar *et al.*, (2014), Sundaram and Rajkumar (2015), Chandramouli *et al.*, (2016), Shivaramgowda *et al.*, (2016), Yadav *et al.*, (2016), Meenakshi *et al.*, (2017) and Singh *et al.*, (2017) for number of fruits per plant.

However, low magnitudes of GCV and PCV were recorded for days to 50 % flowering, average fruit length, average fruit diameter, average fruit weight and fiber content, among which the average fruit weight has the lowest GCV and PCV. The most probable reason could be the phenotypic plasticity occurring in these traits is the main source of variation than the genetic variance. Such result also indicated that selection is not effective for these traits because of the narrow genetic base (Vishwas 2019). Lower magnitude of GCV and PCV were also reported by Pooja *et al.*, (2011), Jagan *et al.*, (2013), Archana *et al.*, (2015), Chandramouli *et al.*, (2016), Patil *et al.*, (2017), Niraja *et al.*, (2018), Priyanka *et al.*, (2018) and Kumar *et al.*, (2019) for days to 50 % flowering; Patel *et al.*, (2014), Jadhav *et al.*, (2016), Sharma *et al.*, (2016), Meenakshi *et al.*, (2017), Priyanka *et al.*, (2018) and Kumar *et al.*, (2019) for average fruit length; Adiger *et al.*, (2011), Chandra *et al.*, (2014), Archana *et al.*, (2015), Khajuria *et al.*, (2015), Sharma and Prasad (2015), Jadhav *et al.*, (2016),

Shivaramgowda *et al.*, (2016), Mohammad and marker (2017a), Ullangula (2017), Niraja *et al.*, (2018), Vrunda *et al.*, (2018) and Kumar *et al.*, (2019) for average diameter; Ramanjinappa *et al.*, (2011), Rekha *et al.*, (2015), Chandramouli *et al.*, (2016), Sharma *et al.*, (2016), Singh *et al.*, (2017) and Priyanka *et al.*, (2018) for average fruit weight.

The low magnitudes of GCV and moderate magnitudes of PCV respectively, was observed for number of branches per plant, plant height and fruits yield per plant. This is in relation with the earlier reports of Akotkar *et al.*, (2010), Mallesh *et al.*, (2015), Rekha *et al.*, (2015), Sundaram and Rajkumar (2015) and Kumar *et al.*, (2019) for number of branches per plant; Archana *et al.*, (2015), Rekha *et al.*, (2015) and Chandramouli *et al.*, (2016) for plant height and Jagan *et al.*, (2013) and Kumar *et al.*, (2019) for fruits yield per plant.

In the present study, the difference between PCV and GCV were lower for most of the characters except number of branches per plant which suggesting negligible role of environment in the expression of traits, so improvement in these traits is easily possible by phenotypic selection.

Heritability is important genetic parameter, which serves as an index of transmissibility of the character in the next generation. Heritability estimates show the amount of heritable and non heritable components of variation exhibited by the individual trait.

The genetic advance is the improvement in the characters of selected population over the base population. Heritability, however indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with

genetic gains are more effective and reliable in predicting the improvement through selection (Johnson *et al.*, 1955).

In the present study, high heritability coupled with high genetic advance as per cent of mean was observed for internodal length and number of fruits per plant revealing the importance of additive gene action in the inheritance of these characters. Similar results were reported for internodal length by Phanikrishna *et al.*, (2015), Sundaram and Rajkumar (2015), Chandramouli *et al.*, (2016), Mohammad and marker (2017a), Patil *et al.*, (2017), Singh *et al.*, (2017) and Ullangula (2017) and for number of fruits per plant by Shivaramgowda *et al.*, (2016), Badiger *et al.*, (2017), Meenakshi *et al.*, (2017), Mohammad and marker (2017a), Patil *et al.*, (2017), Singh *et al.*, (2017), Ullangula (2017) and Vrunda *et al.*, (2018).

In the present study, high heritability coupled with moderate genetic advance was recorded for plant height, average fruit length and fiber content.

The result was in agreement with the finding of Kumar and Kumar (2014), Patel *et al.*, (2014) and Pachiyappan and Saravannan (2016) for plant height and Pachiyappan and Saravannan (2016), Shivaramgowda *et al.*, (2016), Meenakshi *et al.*, (2017), Mohammad and marker (2017a), Patil *et al.*, (2017), Singh *et al.*, (2017) and Priyanka *et al.*, (2018) for average fruit length.

The high heritability coupled with low genetic advance was recorded for days to 50 % flowering and average fruit diameter. It infers that this character was regulated by non-additive gene action. The heritability is being exhibited due to the low influence of environment over the genotype and simple selection will not be rewarding due to the predominance of non-additive genes.

**Table.1** List of okra genotypes used in experiment

Sr. No.	Genotypes	Sources
1.	Parbhani Kranti	MKV, Parbhani
2.	Arka Abhay	IIHR, Bangalore
3.	Arka Anamika	IIHR, Bangalore
4.	Kashi kranti	IIVR, Varanasi
5.	Pusa Sawani	IARI, New Delhi
6.	VRO-6	IIVR, Varanasi
7.	HRB-55	HAU, Hissar
8.	NOL-16-3	NAU, Navsari
9.	NOL-16-6	NAU, Navsari
10.	NOL-17-1	NAU, Navsari
11.	NOL-17-2	NAU, Navsari
12.	NOL-17-3	NAU, Navsari
13.	NOL-17-5	NAU, Navsari
14.	NOL-17-6	NAU, Navsari
15.	NOL-17-7	NAU, Navsari
16.	NOL-17-8	NAU, Navsari
17.	NOL-17-10	NAU, Navsari
18.	GAO-5	AAU, Anand
19.	AOL-09-2	AAU, Anand
20.	AOL-12-52	AAU, Anand
21.	AOL-13-73	AAU, Anand
22.	AOL-13-144	AAU, Anand
23.	AOL-14-32	AAU, Anand
24.	JOL-08-2	JAU, Junagadh
25.	JOL-08-4	JAU, Junagadh
26.	JOL-09-4	JAU, Junagadh
27.	JOL-09-5	JAU, Junagadh
28.	JOL-11-12	JAU, Junagadh
29.	JOL-13-05	JAU, Junagadh
30.	JOL-14-10	JAU, Junagadh
31.	JDNOL-11-12	JAU, Junagadh

**Table.2** Range, mean, GCV %, PCV %, heritability ( $h^2_{bs}$  %) and genetic advance as per cent of mean (GAM %) for various traits in okra genotypes

Sr. No	Character	Range	Mean	Component of variance			GCV %	PCV%	$h^2_{bs}$ %	GAM %
				$\sigma_e^2$	$\sigma_G^2$	$\sigma_p^2$				
1	Days to 50 % flowering	39.66 – 50.33	43.96	1.79	5.49	7.28	5.33	6.14	75.40	9.53
2	Internodal length (cm)	4.38 – 8.00	6.11	0.18	0.71	0.89	13.78	15.43	79.80	25.37
3	Number of branches per plant	2.00 – 3.30	2.67	0.17	0.04	0.21	7.56	17.44	18.80	6.75
4	Plant height (cm)	97.18 – 138.94	121.87	36.96	129.55	166.51	9.33	10.58	77.80	16.97
5	Number of fruits per plant	9.86 – 15.06	12.25	0.37	1.95	2.32	11.40	12.44	84.00	21.54
6	Average fruit length (cm)	9.54 – 12.07	11.06	0.13	0.41	0.55	5.84	6.70	76.00	10.48
7	Average fruit diameter (cm)	1.36 – 1.78	1.58	0.005	0.008	0.013	5.66	7.20	61.90	9.18
8	Average fruit weight (g)	11.90 – 14.20	13.47	0.28	0.23	0.51	3.56	5.34	44.40	4.88
9	Fruit yield per plant (g)	132.24 – 210.24	167.32	351.53	244.19	595.73	9.33	14.58	41.00	12.31
10	Fiber content (%)	3.73 – 5.27	4.71	0.05	0.10	0.16	6.99	8.58	66.40	11.73

However, these traits can be improved in heterosis breeding programme by development of hybrid and also by exploitation of transgressive segregants. The result was in agreement with the finding of Chandramouli *et al.*, (2016), Patil *et al.*, (2017) and Priyanka *et al.*, (2018) for days to 50 % flowering and for average fruit diameter by Chandra *et al.*, (2014), Bello *et al.*, (2015), Bello and Aminu (2017) and Patil *et al.*, (2017).

Moderate heritability in conjunction with moderate genetic advance was observed for fruit yield per plant which indicates the role of both additive and non-additive gene action governing the inheritance of this trait and offers the best possibility of improvement through progeny selection or any modified selection procedures aiming to exploit the additive gene effects. Similar results were reported by Archana *et al.*, (2015), Badiger *et al.*, (2017) and Priyanka *et al.*, (2018).

The moderate heritability coupled with low genetic advance was recorded for average fruit weight. Similar results were reported by Priyanka *et al.*, (2018). The low heritability coupled with low genetic advance was recorded for number of branches per plant indicating high influence of environment and consequently its selection may not be effective. The result was in agreement with the finding of Sharma and Prasad (2015), Pachiyappan and Saravannan (2016) and Badiger *et al.*, (2017).

The present results indicated that high heritability coupled with high genetic advance and moderate to high GCV and PCV were recorded for internodal length and number of fruits per plant indicating the role of additive gene action in the inheritance of these traits, hence further improvement in these characters would be achieved by selection in the present material.

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