

## Evaluation of Genetic Variation, Heritability and Genetic Advance for Various Traits in Okra [*Abelmoschus esculentus* (L.) Moench] under north Gangetic Plains of Uttar Pradesh

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### Abstract

An experiment was undertaken on twenty genotypes and fifteen characters of Okra [*Abelmoschus esculentus* (L.) Moench] to evaluate variability, genotypic coefficient of variation (GCV), phenotypic coefficients of variation (PCV), heritability and genetic advance in all genotypes. The wide range of variability was observed among fifteen characters of all genotypes. The (PCV) were generally higher than their respective genotypic coefficient of variance, thus revealing the role of environmental factors. High PCV was exhibited by plant height (14.92 %), first branching node (37.38 %), number of branches per plant (36.06 %), number of seeds per fruit (22.43 %), first fruiting node (19.07 %), first flowering node (18.03 %) and yield (16.65 %) per hectare. High GCV were observed for number of branches per plant (29.80 %), first branching node (29.75 %), number of seeds per fruit (17.30 %), first fruiting node (15.27 %) and plant height (14.51 %). High heritability coupled with high genetic advance was observed for plant height (94.0 and 29.05 %), stem diameter (94.0 and 27.81 %), fruit weight (94.0 and 21.64 %), number of branches per plant (68.0 and 50.74) and first branching node (63.0 and 48.76 %).

### Highlights

- Highest PCV was exhibited by first branching node followed by number of branches of per plant, number of seeds per fruit, first fruiting node and first flowering node.
- Highest GCV was exhibited by number of branches of per plant, first branching node, number of seeds per fruit, first fruiting node and plant height.
- High heritability was found for plant height, stem diameter, fruit weight and fruit length.
- High heritability coupled with high genetic advance was observed for plant height, stem diameter, fruit weight, number of branches per plant and first branching node.

**Keywords:** Okra, variability, coefficient of variation, heritability and genetic advance

Okra [*Abelmoschus esculentus* (L.) Moench] is commonly known as Lady's Finger in England, Gumbo in the USA and Bhindi in India. It is a member of Mallow or Malvaceae family. It is one of the important vegetable, which is growing throughout the tropical, sub-tropical and warmer temperate part of the world. Being a multipurpose,

okra is valued for its tender delicious fruits. Its dry seed are a rich source of iodine, carbohydrate, protein, oil and vegetable curd. Seeds are also used as coffee additive or substitute. Its dry seeds contain 13-22% edible and 20-24% crude protein (Thamburaj and Singh, 2004). In India, Okra cultivated around the year in one or other region due to wide range of

climatic condition in different parts of the country. The all India area, production and productivity of okra in year 2012-13 is 0.53 Mha, 6.35 Mt and 12.0 t/ha respectively (Anon, 2013). The plant offers several features like erect growing habit, short life span, large showy flower and adaptability to wide range of climatic conditions which have a great value to the breeders in achieving quick genetic result. The prospect and possibilities for increase in quality and production of okra need genetic improvement for short plant with more number of nodes, short internodes, optimum seed viability, harvest index, suitability for processing, tolerant to biotic and abiotic stresses. For any breeding programme, some biometrical techniques like variability, heritability and genetic advance, correlation are prime importance to provide information about the relative contribution of various growths and yield related traits. (Vijay and Manohar, 1990) stated that characteristics which showed high range of variation in okra genotypes should be given priority in the selection. Since in breeding program, variability among the population is pre-requisite, high variability observed in respect of the traits under study implies that there is scope for making effective improvement of these traits. A survey of genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding program (Mishra *et al.* 2015). Thus, these biometrical techniques (variability, heritability and genetic advance) help in selection of superior plant genotypes for further breeding programme. Therefore this study was carried out to evaluate the genetic variation, heritability and genetic advance for various traits of Okra genotypes.

## Materials and methods

The present investigation was conducted at Vegetable Research Farm, Department of Horticulture, IAS, BHU, Varanasi, during the rainy season of 2013. Geographically, Varanasi is situated in eastern part of UP and subtropical track of north India between latitude 25° 15' north and longitude 83° 03' east and is located on an elevation of about 128.93 meters above mean sea level in north gangatic plains. The experiment was laid out in a Randomized Complete Block Design with three replications. The promising experimental material in form of seed was obtained

from IIVR, Varanasi. The 20 germplasm of okra were used in this investigation are BO-2, DOV-91-4, Larma 1, VRO-6, HRB-9-2, EC-169366, Bhindi Vaphy, D-1-87-5, HRB-55, P-7, Arka Abhay, VRO-5, VRO-3, EMS-8-1, Pusa Mukhmal, Punjab Padmani, Pusa Sawani, Arka Anamika, No. 315, VRO-4. The plant height was recorded when last fruit picking was done from respective plants with the help of measuring scale. The diameter of plant stem (cm) was recorded with use of vernier caliper and also the length (cm) and diameter (cm) of fruit was recorded same. Observations like number of nodes per plant as well as on the main stem, first branching nodes, number of branches per plant, Days taken to first flowering, first flowering node, first fruiting node, number of flowers per plant, number of fruits per plant, number of seeds per fruit was recorded manually. Weight of fruit (g) was noted by using weighing balance. Yield calculated (q/ha) for all treatment. Phenotypic and genotypic variability were calculated as per method proposed by Burton (1952). Heritability was calculated the formula suggested by Burton and De vane (1953). Genetic advance was worked out by using the formula suggested by Johnson *et al.* (1955).

## Results and discussion

### Genetic variation

Genetic variability considered as important aspect which taken into account before planning for any breeding programme. The success of any selection programme depends largely upon the magnitude of genetic variability present in the population. Thus, variability must be present in the population for getting desired success. Therefore, the traits showing wide range of variation in the present study (Figure 1) viz., plant height (64.03-124.33 cm), stem diameter (1.63-2.67 cm), number of nodes on the main stem (17.33-23.33), first branching node (1.00-3.67), number of branches per plant (2.33-7.33), days taken to first flowering (42.00-55.33), first flowering node (5.00-7.67), first fruiting node (5.33-9.67), number of flowers per plant (31.33-48.33), number of fruits per plant (28.67-46.00), fruit diameter (1.11-1.75 cm), fruit length (6.99-9.45 cm), fruit weight (7.35-10.84 gm), number of seeds per fruit (38.33-77.67) and yield (96.51-148.48 q/ha) are having the maximum scope for giving positive response to selection scheme. (Nanohar *et al.* 1986)

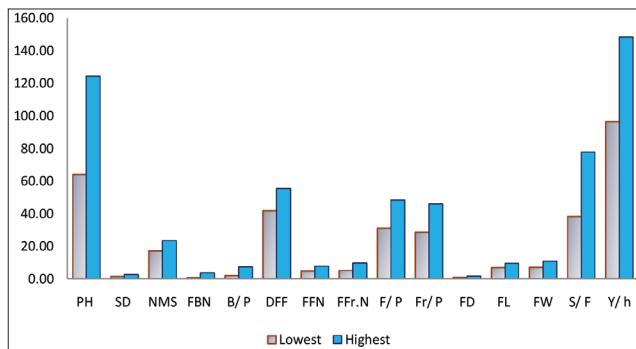


Fig. 1: Graphically representation of range for different characters

Plant height (PH), Stem diameter (SD), No. of nodes on the main Stem (NMS), First branching node (FBN), No. of branches per plant (B/P), Days taken to first flowering (DFF), First flowering node (FFN), First fruiting node (FFr.N), No. of flowers per plant (F/P), No. of fruits per plant (Fr/P), Fruit diameter (FD), Fruit length (FL), Fruit weight (FW), No. of seeds per fruit (S/F), Yield/ha (Y/h).

Table 1: GCV, PCV, heritability (bs) and Genetic advance as % of mean 5% for different characters in okra

| Characters                    | GCV   | PCV   | h <sup>2</sup> (bs) | GAM   |
|-------------------------------|-------|-------|---------------------|-------|
| Plant height                  | 14.51 | 14.92 | 0.94                | 29.05 |
| Stem diameter                 | 13.92 | 14.35 | 0.94                | 27.81 |
| No. of nodes on the main Stem | 7.09  | 9.41  | 0.57                | 11.02 |
| First branching node          | 29.75 | 37.38 | 0.63                | 48.76 |
| No. of branches per plant     | 29.80 | 36.06 | 0.68                | 50.74 |
| Days taken to first flowering | 7.15  | 9.67  | 0.55                | 10.90 |
| First flowering node          | 11.73 | 18.03 | 0.42                | 15.72 |
| First fruiting node           | 15.27 | 19.07 | 0.64                | 25.19 |
| No. of flowers per plant      | 10.31 | 13.86 | 0.55                | 15.80 |
| No. of fruits per plant       | 11.08 | 15.03 | 0.54                | 16.83 |
| Fruit diameter                | 9.46  | 12.03 | 0.62                | 15.32 |
| Fruit length                  | 10.53 | 11.48 | 0.84                | 19.90 |
| Fruit weight                  | 10.83 | 11.17 | 0.94                | 21.64 |
| No. of seeds per fruit        | 17.30 | 22.43 | 0.60                | 27.50 |
| Yield                         | 12.95 | 16.65 | 0.60                | 20.75 |

observed a wide range of variability in fruit weight among 13 ber genotypes in their study. (Saran *et al.* 2007) also observed the highest range of variation for fruit yield per plant and fruit weight. This observation suggests about the good scope of carrying out selection for these traits. While

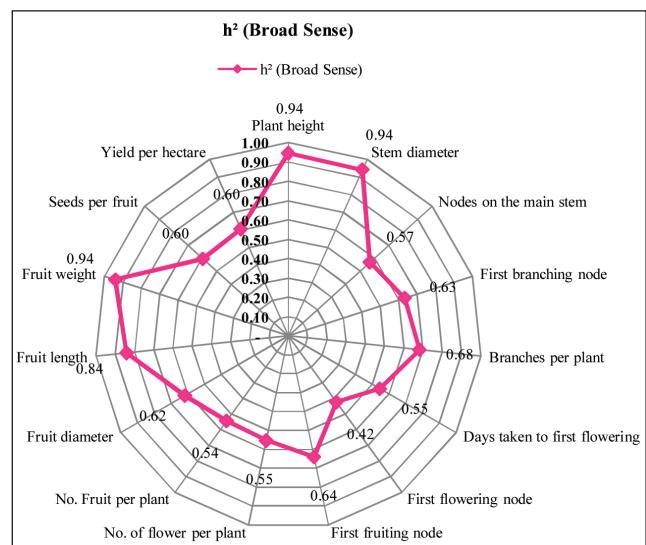


Fig. 2: Graphically representation of heritability for different characters

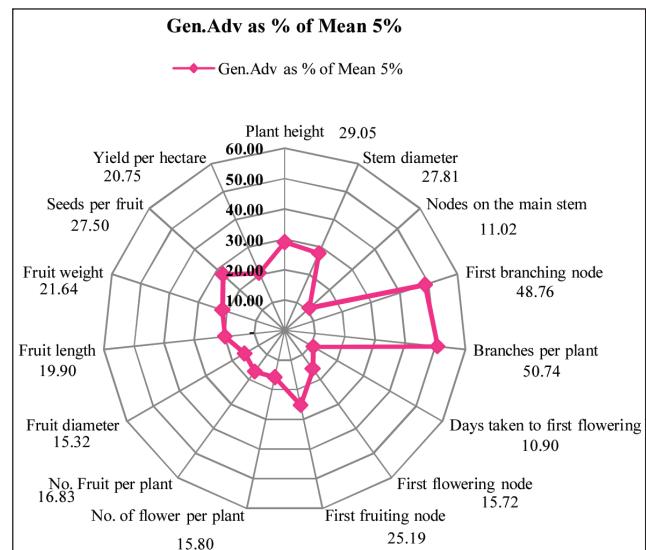


Fig. 3: Graphically representation of genetic advancement as percentage of mean 5%

dealing with variability an insight in to genotypic and phenotypic components of variability proves to be useful. Findings of most of the characters in the present study was supported by Alam and Hossain (2006), Chaudhary *et al.* (2009), Sengupta and Verma (2009) and Ahiakpa *et al.* (2013). The variance gives

a measure of variation within a particular trait but it fails to provide a real measure for comparison of variances among the different traits. So, the genotypic and phenotypic co-efficient of variations (GCV and PCV) are used to measures of variability among the genotypes under study. Table 1 reflected the highest phenotypic coefficient of variation was exhibited by plant height (14.92 %), first branching node (37.38 %), number of branches per plant (36.06 %), number of seeds per fruit (22.43 %), first fruiting node (19.07 %), first flowering node (18.03 %) and yield (16.65 %) per hectare. Thus, the characters showing maximum phenotypic coefficient of variation would be consider while making selection in spite of influence of environment to a certain extent. The result of high phenotypic coefficient of variation was in agreement with the findings of Adeoluwa and Kehinde (2011), Morey *et al.* (2012) and Das *et al.* (2012).

As far as genotypic coefficient of variation was concerned number of branches per plant, first branching node, number of seeds per fruit, first fruiting node and plant height have the maximum GCV, which are (29.80 %), (29.75 %), (17.30 %), (15.27 %) and (14.51 %) respectively. Results showed similarity with the findings of Jindal *et al.* (2010), Prakash and Pitchaimuthu (2010), Prakash *et al.* (2011), Kumar *et al.* (2012) and Shaikh *et al.* (2013). The minimum value of genotypic coefficient of variation was observed for number of nodes on the main stem (7.09 %), days taken to first flowering (7.15 %) and fruit diameter (9.46 %). Thus, the traits with high GCV are important to be considered while going for selection.

The GCV provides a measure for comparison of variability among different traits and sometimes gives some indication regarding validity of traits for selection. However, it does not provide clear picture of the extent of genetic gain to be expected from selection of phenotypic traits, unless heritable fraction of variation (heritability) was known (Burton, 1952). Heritability in broad sense according to Lush (1949) is the ratio of total genotypic variance to phenotypic variance, generally expressed in percentage. For making effective improvement in a trait under selection, heritability has been adopted by the large number of workers as a reliable indicator. The estimates of heritability are more advantageous when expressed in terms of genetic

advance. In the present experiment, heritability and genetic advance have been calculated for all the 15 characters. Higher estimate of heritability (0.94) were recorded for plant height, stem diameter and fruit weight followed by fruit length (0.84), number of branches per plant (0.68) with minimum for first flowering node (0.42). The findings are in accordance with Hazra and Basu (2000), Singh *et al.* (2006), Mager and Madrap (2009), Ramanjinappa *et al.* (2011) and Goswami *et al.* (2012).

### ***Heritability and Genetic Advance***

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 (Johnson *et al.* 1955), 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 (Johnson *et al.* 1955). Since heritability includes additive and non-additive gene effects, a breeder should take care of this fact while going for selection based on heritability. Data illustrated in Figure 2 clearly indicated that high heritability coupled with high genetic advance was observed for plant height (94.0 and 29.05 %), stem diameter (94.0 and 27.81 %), fruit weight (94.0 and 21.64 %), number of branches per plant (68.0 and 50.74) and first branching node (63.0 and 48.76 %). High heritability coupled with moderate level of genetic advance was estimated for fruit length (84.0 and 19.90 %). These results show similarity with the findings of Mehta *et al.* (2006), Dakahe *et al.* (2007), Adiger *et al.* (2011) and Duggi *et al.* (2013). However, some characters like days taken to first flowering (55.0 and 10.90 %) and number of nodes on the main stem (57.0 and 11.02 %) possessed low genetic advance along with low level of heritability suggesting the presence of non-additive gene action governing the inheritance of these traits. High heritability in these traits was observed mainly due to favourable environment rather than their genotype and the selection for these characters may not be rewarding. Lowest heritability was reported in case of first flowering node and number of fruits per plant.

## Conclusion

Results from present investigation clearly indicated that greater variability exist among all the characters of a selected genotypes. The trend of PCV was almost similar to GCV with higher values for most of the characters studied. Highest PCV was exhibited by first branching node followed by number of branches of per plant, number of seeds per fruit, first fruiting node and first flowering node. Highest GCV was exhibited by number of branches of per plant, first branching node, number of seeds per fruit, first fruiting node and plant height. Nodes on the main stem followed by days taken to first flowering showed lowest GCV and PCV. All other characters showed medium GCV and PCV value. High heritability was found for plant height, stem diameter, fruit weight and fruit length, while low heritability observed for first flowering node, fruit per plant, days taken to first flowering and nodes on the main stem. High heritability coupled with high genetic advance was observed for plant height, stem diameter, fruit weight, number of branches per plant and first branching node.

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