

Genetic variability and correlation analysis in indigenous germplasm of okra (*Abelmoschus esculentus* L. Moench)

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ABSTRACT

An experiment was undertaken to evaluate the genetic variability, coefficient of variation, heritability, genetic advance and correlation coefficient among indigenous okra accessions based on morphological parameters. Ten okra accessions collected from different parts of Garo Hills regions of Meghalaya were planted during 2019 at NEHU Tura campus, Meghalaya in random block design with three replications. The Analysis of variance exhibited significant differences among the accession for different characters evaluated. The phenotypic coefficient of variance (PCV) was predominantly superior to their corresponding genotypic coefficient of variance resulting the role of environmental aspects. A high heritability in relation with high genetic advance as the percentage of mean value was observed for plant height. The Correlation studies between various quantitative characters exhibited significant association between parameters. Plant height, number of fruits per plant showed highly positive significant association with fruit yield per plant both at phenotypic and genotypic level. On the basis of mean performance for fruit yield and its component characters from the present investigation 5 superior okra germplasm lines namely T-4, T-6, T-7, T-8 and T-10 were selected as superior and most promising genotypes for the crop improvement programmed in okra.

Keywords: Okra, variability, coefficient of variation, heritability, genetic advance, correlation coefficient

INTRODUCTION

Okra (*Abelmoschus esculentus* (L) Monoech) primarily known as 'bhindi' or 'Lady's finger', and belongs to the Malvaceae family. The genus *Abelmoschus* comprises of nine species namely *A. esculentus*, *A. tuberculatus*, *A. angulosus*, *A. moschatus*, *A. ficulens*, *A. tetraphyllus*, *A. crinitus*, *A. callei*, *A. Manihot*. Out of these only *Abelmoschus esculentus* is cultivated species. It has a chromosome number of $2n=2x=130$ (Kumar *et al.* 2010). It is a versatile crop due to its use as buds, flowers, pods, and stems, dry stems, pods, fresh leaves and seeds (Pradip *et al.* 2010; Kabir and Pillu, 2011). It is grown commercially in India and widely accepted as a popular vegetable crop due to its high nutritional value and pleasant flavour (Emmanuel *et al.* 2014). A genotypes which are identified, differentiated according to their nature or quality are refers as characterization (Magar and Madrap, 2009). Characterization of crops is an initial step in any crop improvement programme. It provides information on diversity among the genotype

collections and enables the identification of unique accessions essential for gene bank and such characterization is essential both for breeding and for the purpose of germplasm conservation and crop improvement (Ivin and Anbuselvam, 2021). Availability of diverse germplasm, is the pre requisite for any crop breeding and successful crop improvement programme. Such diverse germplasm plays a crucial role in productivity, profitability, sustainability and strengthening the food and nutritional security of the population pressure. Hence, characterization, evaluation, utilization and Conservation of germplasm is very much necessary. There are a number of land races and indigenous germplasm of okra available in Garo Hills region of Meghalaya, but very less work has been conducted to characterize these okra germplasms scientifically. To explore the genetic potential of indigenous germplasm lines of okra from West Garo Hills, Meghalaya the present research work is formulated for the selection of superior genotypes in okra for crop improvement programme.

MATERIALS AND METHODS

The experimental material comprised of a total of 10 indigenous germplasm lines of okra (T1: Sangsanggre; T2: Marapara; T3: Chanmari; T4: Rongkhon; T5: Amingda rangsagre; T6: Dangsapara; T7: Dadenggre; T8: Rongram; T9: Damalgre; T10: Chibragre) collected from different parts of Garo Hills region of Meghalaya, India. Field experiment was conducted in randomized block design (RBD) with three replications. The okra seeds were sown in the month of April, 2019. The spacing between the rows was maintained at 45 cm while within the plants was maintained at 45 cm. Recommended cultural and agronomic practices were followed during the crop growth period. About 20-25 t/ha of FYM was mixed at the time of land preparation. N:P₂O₅:K₂O was applied at a dose of 100 kg, 60 kg and 50 kg per hectare respectively. Half dose of N and full dose of P and K were applied at the time of planting. The balance half of N was given 30 days after sowing. Five plants were randomly selected from each germplasm per replication to record

the data. The indigenous germplasm lines of okra were evaluated for twenty three horticultural traits. Among the twenty three horticultural traits, thirteen traits were quantitative (plant height, first flowering node, first fruit producing node, number of fruits per plant, fruit width, fruit length, days to 80% maturity, days to 50% flowering, number of seeds per fruit, number of nodes per plant, 100 seed weight, number of internodes per plant and fruit yield per plant). The observations were recorded according to NBPGR, New Delhi descriptors. The mean values were subjected to statistical analysis (ANOVA) as suggested by Panse and Sukatme (1954) using SAS version 9.2 (SAS, 2008). Phenotypic and genotypic coefficient of variation (PCV and GCV), heritability (h^2) in the broad sense and expected genetic advance as a percentage of mean (GAM) was determined by Genres software (GENRES, 1994) using the formula recommended by Burton and De Vane (1953). Correlation coefficient was analysed using SAS software among the quantitative characters.

Table 1: Analysis of variance for 13 quantitative horticultural characters in okra

Source of Variation	Degree of freedom	Mean square												
		D-50%F	FFN	FFPN	FL	FW	NFPP	PH	D-80%M	NSPF	100-SW	NNPP	NINPP	FYP
Replication	2	7.6	0.5	0.5	0.07	0.01	3.0	1.19	2.4	29.6	8.8	2.4	2.4	1812.0
Genotypes	9	397.0	4.4	4.4	16.9	0.1	53.1	2302.0	2.8	347.5	377.3	2.8	2.8	110195.3
F- value		7.42	3.6	3.6	37.8	6.0	37.8	1403.2	4.0	3.9	102.1	4.0	4.0	260.8

D-50%F- days to 50% flowering, FFN- first flowering node, FFNP- first fruit producing node, FL- fruit length (cm), FW- fruit width (cm), NFPP- number of fruits per plant, PH- plant height (cm), D-80%M- days to 80% maturity, NSPF- number of seeds per fruit, 100- SW- seed weight (g), NNPP- number of nodes per plant, NINPP- number of internodes per plant, FYP- Fruit yield per plant (g)

RESULTS AND DISCUSSION

Analysis of variance for thirteen quantitative traits of okra is presented in Table no 1. Significant differences were observed between the genotypes for all the parameters estimated. It is clearly indicated that there was a sufficient variability for each trait among the genotypes selected for the study. Mean values of different quantitative traits of 10 indigenous okra germplasm are presented in Table 2. It was found that the genotype T-2 had taken the maximum days to 50% flowering of 87.6 whereas the genotype T-7 had taken the minimum days to 50% flowering of 49.6 days. Earliness is a desirable character and tends to give early fruiting and early marketable yield in

okra (Singh *et al.* 2017). The genotype T-6 produced the first flowering node and first fruit producing node at the uppermost node of 8.6 whereas the genotype T-7 produced the first flowering node and first fruit producing node at the lowermost node of 5. Singh *et al.* (2006) reported the similar result. The genotype T-10 was having the highest fruit length of 22.03 cm whereas the genotype T-3 was having the lowest fruit length of 14.6 cm. Maximum fruit width was recorded in genotype T-6 of 2.53 cm whereas the genotypes T-8 showed the minimum of fruit width of 2 cm. The maximum number of fruits per plant was observed in genotypes T-8 of 24.6 whereas the genotype T-2 showed the minimum. The maximum plant height was observed in genotype T-10 of 148.9 cm whereas the

minimum plant height was recorded in genotype T-7 of 49.2 cm. Sachan (2006) and Guddamath *et al.* (2011) reported similar result in okra. Days to 80% maturity was maximum in genotype T- 3 of 103 days whereas the genotype T-7 showed the minimum number of days of 69.4. The number of seeds per fruit ranged from 61.3 (T7) to 99 (T4). Maximum value for 100 seed weight was recorded in genotype T-10 (66.5g) and minimum in genotype T-3 (29.26g). The variation for days to 80% maturity, number of seeds per fruit and 100 seed weight among the genotypes studied might be attributed by an environmental factors such as fluctuation in night and day temperature, humidity, rainfall and nutritional factors. The number of seeds per fruit ranged from 35.2 -100.6 (Singh *et al.* 2006).

Maximum number of nodes and internodes per plant was recorded in genotype T-5 and lowest in genotype T-6. Alam and Hossain (2008) reported moderate variations for number of nodes per plant. Considerable genetic variability among the genotypes for number of internodes per plant was observed by Kumar *et al.* (2011). Fruit yield per plant was found highest in genotype T-10 (855.9g) and lowest in genotype T-2 (290.5g). The grand mean for fruit yield per plant was found 526.3g. Fruit yield per plant depends upon the number of fruits per plant and individual fruit weight. Therefore, higher fruit yield might be associated to higher number of fruits per plant and higher individual fruit weight (Singh *et al.* 2007).

Table 2: Mean of 13 quantitative morphological traits of indigenous okra

Treatment	DAYS 50% F	FFN	FFPN	FL	FWTH	NFPP	PH	DAYS 80% M	NSPF	100-SW	NNPP	NINPP	FYP
1	77	8	8	19.8	2.1	14	92.4	90.8	78.6	37.9	11.6	10.6	385.0
2	87.6	6	6	19.8	2.3	11	71.1	98.6	81	62.4	12	11	290.5
3	85.3	8.3	8.3	14.6	2.1	15.3	61.3	103	75.3	29.2	11	10	475.6
4	71.6	6.6	6.6	17.5	2.1	16	98.3	85.6	99	47.9	11.6	10.6	651.8
5	63.3	6	6	19.3	2.1	13.3	81.1	84.3	93.6	51.2	14	13	397.8
6	84.3	8.6	8.6	17	2.5	20.6	70	102.3	80.6	44	10.3	9.3	571.0
7	49.6	5	5	16.1	1.6	21.6	49.2	69.4	61.3	51.2	11	10	537.3
8	73	7	7	15.3	2	24.6	103.0	97.0	84.6	57.0	12	11	783.2
9	74.6	7.3	7.3	16.3	2.4	17	84.1	100.3	71.3	56.2	11.6	10.6	317.8
10	81.3	8.3	8.3	22.03	2.2	19	148.9	101.1	87.3	66.5	11.3	10.3	855.9
CV	9.7	15.5	15.5	3.7	7.8	6.8	1.4	8.07	11.5	3.8	7.1	7.8	3.9
CD (5%)	12.5	1.9	1.9	1.1	0.2	2.0	2.1	12.8	16.0	3.2	1.4	1.4	35.2

The highest PCV and GCV was recorded for fruit yield per plant followed by plant height whereas the minimum value of phenotypic and genotypic coefficient of variation was obtained for number of nodes per plant (Table 3). In the present study, the estimated PCV values were found to be greater than their corresponding GCV values for most of the characters. Which indicated that the variation for these characters is not only due to genotypes but also due to the environmental factors. Hence, in selection for crop improvement PCV and GCV values plays an important role (Prakash and Pitchaimuthu, 2010; Umrao *et al.* 2014). Broad-sense heritability values (h^2_b) were ranged from medium to high with a value ranged from 46.4%

to 99.7%. Plant height (99.7%) was observed as the most heritable trait followed by fruit yield per plant (98.8%) and the least heritability value (46.4%) was observed for first flowering node and first fruit producing node. The genetic advance as a percent of mean ranged from 10.5% to 74.4%. Fruit yield per plant (74.4%) recorded the highest value for genetic advance as a percentage of mean followed by plant height (66.2%) and the minimum value (10.5%) for number of nodes per plant. High heritability coupled with high genetic advance and high genotypic coefficient of variation for a character are more authentic and highly selective factors for effective selection in crop improvement programme (Nasit *et al.* 2009).

First flowering node and first fruit producing showed highly significant positive association with fruit width (0.705), days to 80% maturity (0.875) and exhibited negative association with number of nodes per plant (-0.565) and number of internodes per plant (-0.565). Fruit length had highly significance positive association with plant height (0.604) and number of seeds per fruit (0.524). Fruit width exhibited strongly significant positive association with days to 80% maturity (0.911) and number of seeds per fruit (0.524). Number of fruits per plant showed strongly significant positive association with fruit yield per plant (0.711) and significant negative association with number of nodes per plant (-0.514) and number of internodes per plant (-0.514) respectively. Number of seeds per fruit (0.621), 100 seed weight (0.508) and fruit yield per plant (0.638) showed significant positive association with Plant height. Number of seeds per fruit exhibited

significant positive association with number of nodes per plant (0.594) and number of internodes per plant (0.594). Singh *et al.* (2006) also reported higher magnitude of genotypic correlations than the corresponding phenotypic correlations between yield and its attributing traits in okra.

It may be concluded from the results that the greater variability exist for economically important characters provide a good scope for the genetic improvement of crop. On the basis of mean performance for fruit yield and its component characters five superior okra germplasm lines namely T-4, T-6, T-7, T-8 and T-10 were selected as superior and most promising genotypes for the crop improve in okra. The diversity present among the genotypes can be used for enhancing desirable traits through selection and hybridization breeding programme.

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