

Research Article

**Genetic Diversity Studies for the Assessment of Variability on Okra
(*Abelmoschus esculentus*)**

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Abstract

Okra (*Abelmoschus esculentus* (L.) Moench) is an important crop in many countries because of its nutritional value, culinary uses, and economic significance. Okra serves as a model organism for studying various biological processes due to its ease of cultivation. Research on okra genetics can contribute to broader understanding in plant biology and genetics. This study was conducted to understand the genetic diversity of okra for effective selection of traits. Seeds of five varieties of Okra (*Abelmoschus esculentus*) were collected at the National Center for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Oyo State, Nigeria. The seed of each accession was sown in a plot laid out in a randomized complete block design with three replications. Data were collected on 13 agronomic characteristics and analyzed. PCV was moderately higher than GCV in all of the traits studied, indicating that environment played a small role in the expression of these traits. High heritability and high genetic advance as a percentage of the mean were recorded for plant height (79.80%, 47.11%), days to flowering (87.60%, 25.43%), and dry pod length (70.63%, 39.64%), indicating that these traits were less influenced by the environment and presence of additive gene action. A wide range of variability and heritability with high genetic advance was observed for the characters like plant height, days to flowering, and fresh pod length. Therefore, the selection of superior genetic materials based on these performances could be very effective.

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1. Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) (also known as lady's finger) is a warm-season vegetable widely cultivated for its edible green pods. It is a member of the Malvaceae family,

which originated in Africa (Rao 1985). Okra is an important crop in many countries because of its nutritional value, culinary uses, and economic significance.

However, Nigeria ranks third in okra among fruit vegetables based on production and consumption, followed by pepper and tomato (Ibeawuchi, 2007). The okra local cultivars differed in growth habits, including leaf arrangement and size, fruit branching, height, and maturity period. During the vegetative stage, okra growth patterns are similar, but those that are highly vigorous produce improved leaf area and accumulated dry matter (Akanbi *et al.*, 2010). The unripe green finger-like seed capsules of okra, usually called “pod” are processed and consumed as stews and salads, soups, and sliced, boiled, and fried vegetables (Akanbi *et al.*, 2010; Daniela *et al.*, 2012). The fruits contain effortlessly digestible fiber, fat-free contents, and low calories (Kumar & Sreeparvathy, 2010; Reddy *et al.*, 2013).

Genetic diversity refers to variation in genetic traits within a population or species. The genetic diversity of Okra is important for several reasons. First, it enables the plant to adapt to changing environmental conditions, such as changes in temperature, rainfall, or soil nutrients. For example, if a particular strain of Okra is well adapted to a hot, dry climate, it may be more likely to survive and reproduce in such conditions than other strains that are less well adapted. Second, genetic diversity can help increase the overall productivity and quality of the crop. By selecting desirable traits, such as larger fruit size, higher yields, or improved resistance to pests and diseases, breeders can create new strains of Okra that are better suited to specific growing conditions or market demands.

Genetic improvement of okra yield is significant because of the nutritional and health benefits inherent in it and to overcome the low genetic potential of the existing varieties and environmental factors, which are the major constraints to okra yield. Genetic diversity study is conducted to select parents for further breeding work. Breeders often calculate the heritability estimate, a value that predicts the extent to which their selection effort will be successful. Heritability is defined as the proportion of phenotypic variance attributable to overall genetic variance for the genotype (Dhankar *et al.*, 2002). Adequate knowledge of components of variances and their effects, heritability, and genetic advance of the traits under consideration can help breeders decide the appropriate breeding method to improve genetic makeup (Ibrahim *et al.*, 2006). Johnson *et al.* (1955) reported that the value of the heritability estimate is enhanced when used with the genetic

advance. Combined high heritability estimates and high genetic advance show that variation is attributable to a high degree of additive gene effect and that selection is rewardable (Komolafe *et al.*, 2019). Kumar *et al.* (2010) reported that before undertaking a crop improvement process in any species, a thorough knowledge of the degree of genetic variability existing in the crop for various characteristics is essential. The nature and magnitude of genotypic and phenotypic variability in any crop species play an important role in devising a successful breeding strategy for developing superior cultivars. Okra serves as a model organism for studying various biological processes due to its ease of cultivation. Research on okra genetics can contribute to broader understanding in plant biology and genetics. This study aimed to analyze the genetic variation present within five accessions of *Abelmoschus esculentus* and investigate the variability of phenotypic traits among the accessions.

2. Materials and Methods

Five accessions of okra used in this study were sourced from NACGRAB, Nigeria (Table 1). The accessions of okra were laid out in a randomized complete block design (RCBD) and replicated three times at the experimental field of the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba-Akoko, Ondo State, Nigeria. Three seeds were planted per hole in each variety. Each plot row was 4 m long with inter-row spacing of 60 cm and intra-row spacing of 30 cm. Weeding was performed by uprooting at intervals. The insecticide used was cypermethrin, which was used to kill insects that were infesting the plant.

Table 1. List of Accessions collected from NACGRAB

S/N	VARIETIES
1	NGB02518
2	NGB00346
3	NGB02436
4	NGB00401
5	NGB00425

2.1. Data Collection

Data were collected on 13 quantitative characteristics (plant height, number of leaves, internode length, number of branches, days to flowering, number of fruits, fresh pod length, fresh pod width, fresh pod weight, dry pod length, dry pod width, dry pod weight and 100 seed weight) of okra from three randomly selected plants of each accession in each plot.

2.2. Statistical Analysis

Data obtained from this study were subjected to analysis of variance (ANOVA) and means separated with Duncan's Multiple Range Test (DMRT) at $P \leq 0.05$ using SPSS version 22. The analysis of variances was estimated according to the procedure of Singh and Chaudhary, 1985. Estimation of genetic parameters was obtained following the procedure of Ajayi *et al.*, (2014).

3. Results

3.1. Analysis of Variance

Table 2 displays the mean square values obtained from analysis of variance (ANOVA). The results in Table 2 reveal that, apart from Fresh Pod Width (FPW) and Fresh Pod Weight (FWP), the mean square values for the genotype effect were statistically significant for all quantitative parameters. Notably, Dry Weight of Pod (DWP) showed the highest coefficient of variation (CV) at 25.54%, followed by number of leaves (NL) with a CV of 20.47%. In contrast, Days to Flowering (DTF) exhibited the lowest CV at 3.27%.

3.2. Mean Performance in the Accessions of Okra

Table 3 displays the mean performance of quantitative traits in accessions of okra. Plant height ranged from the lowest (33.23 cm) in V3 to the highest (75.23 cm) in V4. Regarding the number of leaves per plant, the highest value (13.00 cm) and lowest value (8.87 cm) were observed in V5 and V3, respectively. In terms of internode length, 8.07 cm in V4 and 4.77 cm in V3 are observed as the highest and the lowest values,, respectively. The number of branches ranged from the lowest (5.00) in V3 to the highest (7.40) in V2. Days to flowering ranged from the lowest (56.90) in V3 to the highest (78.77) in V4. 8.33 In V5 and 6.57 in V4 were observed as the highest and the lowest values, respectively, for the number of fruits. Concerning fresh pod length, 10. 93 cm in V2 and 9.00 cm in V4 were observed as the highest and lowest values. The fresh pod width ranged from

the lowest (9.73 cm) in V4 to the highest (10.60 cm) in V2. Fresh pod weight ranged from 36.77 g in V3 to 43.27 g in V2. Concerning dry pod width, the highest value (10.23 cm) and the lowest value (6.20 cm) were observed in V5 and V4,, respectively. For dry pod width, 10.37 cm in V4 and 8.37 cm in V1 were observed as the highest and lowest values, respectively. Dry weight of pods ranged from the lowest (7.17 g) in V1 to the highest (11.37 g) in V4. Finally, 100 seed weights had the highest and lowest values (5.77 g and 5.03 g) obtained in V4 and V2,, respectively.

3.3. Estimation of genetic parameters

The results of estimations of variation (Genotypic and Phenotypic), Genotypic and Phenotypic coefficients of variation (GCV and PCV), Broad sense heritability (H^2), and genetic advance as percent of mean (GAM) for the quantitative traits among accessions of okra are presented in Table 4. For plant height, Phenotype variation and genotypic variation were also observed to be 283.33 and 226.11, respectively. Both GCV and PCV were moderate at 25.60% and 28.66. High heritability at 79.80% was also observed. Genetic Advance as per mean (GAM) of 47.11 was high for this trait. Concerning the number of leaves, phenotypic variation and genotypic variation were observed to be 6.57 and 0.96, respectively; low GCV at 8.45% and moderate PCV at 22.15% were recorded. Broad sense heritability was obtained to be moderate at (14.57%), and genetic advance as per Mean (GAM) was observed to be low at (6.66). In terms of internodal length, phenotype variation and genotypic variation were observed to be 3.14 and 0.94, respectively. Both PCV and GCV were at moderate levels at 25.77% and 14.12%, respectively. Both heritability and Genetic Advance as per Mean (GAM) were also recorded as moderate at 30.01% and 15.99, respectively. In the case of number of branches, 0.21 and 1.79 were obtained as genotypic and phenotype variation, respectively, and low GCV (7.38%) and moderate PCV (21.54%) were obtained. Broad sense heritability and Genetic Advance as per Mean (GAM) were observed to be low at 11.73% and 5.15, respectively. In terms of days to flower, phenotype variation and genotypic variation were observed to be 90.45 and 79.23, respectively; both GCV and PCV were recorded to be moderate at 13.21% and 14.11%. High heritability at 87.60% was obtained. The number of flowers had phenotype variation and genotypic variation of 1.22 and 0.10, respectively. Low GCV (4.21%) and moderate PCV (14.95%) were recorded. Broad sense heritability was observed to be low at 7.95%. For fresh pod length, Phenotype variation and genotypic variation were 0.88 and 0.24. Both GCV and PCV were recorded to be low at 4.93% and 9.44%, respectively. Moderate

heritability at 27.27% was observed. For dry pod length, Phenotype variation and genotypic variation were also observed to be 4.60 and 3.25, respectively. Both GCV and PCV were moderate at 22.90% and 27.24%, respectively. High broad-sense heritability (70.63%) was also observed. In terms of dry pod width, phenotype variation and genotypic variation were observed to be 1.35 and 0.09, respectively. GCV was observed to be 3.18%, PCV was moderate at 12.52%, and broad sense heritability was low at 6.44%. Dry pod weight had phenotype variation and genotypic variation of 7.01 and 1.62, respectively. Both GCV and PCV were moderate at 14.00% and 29.13%. Broad sense heritability was observed to be moderate at 23.11%. Finally, 100 grain weight had PV and GV of 0.26 and 0.07, respectively. Both GCV and PCV were low at 4.86% and 9.54%. Moderate heritability was observed at 25.97%, and genetic advance as per Mean (GAM) was recorded as low as 5.08.

3.4. Pearson's Correlation Analysis

Table 5 displays the genotypic correlation of quantitative traits among various okra varieties assessed under field conditions. Plant height exhibited a significant and positive correlation with the number of leaves (0.67), internode length (0.80), days to flower (0.80), and the number of branches (0.60). In addition, plant height displayed a negative correlation with dry pod length (-0.56) and 100 grain weight (-0.59). The number of leaves showed a highly significant and positive correlation with the internode length (0.77) and the number of branches (0.91). The internode length demonstrated a highly significant and positive correlation with the number of branches (0.73). Moreover, the number of branches exhibited a highly significant and negative correlation with 100 grain weight (-0.57). Fresh pod length displayed a highly significant and positive correlation with fresh pod weight (0.69) and a positive correlation with fresh pod width (0.58). Similarly, fresh pod width showed a highly significant and positive correlation with fresh pod weight (0.73). Dry pod length demonstrated a highly significant positive correlation with the dry weight of the pod (0.81) and 100 grain weight (0.74). Conversely, dry pod width exhibited a positive correlation only with the dry weight of the pod (0.59). Lastly, the dry weight of the pod demonstrated a highly significant and positive correlation with 100 grain weight (0.8).

Table 2. Analysis of variance for genetic variation.

Source of variance	DF	PH	NL	IL	NB	DTF	NF	FPL
Varieties	4	735.55*	8.48*	5.03*	2.21*	248.92*	1.41*	1.36*
Error	10	57.220	5.610	2.200	1.580	11.220	1.120	0.640
CV		12.88	20.47	21.56	20.24	4.97	14.34	8.05

Source of variance	Df	FPW	FWP	DPL	DPW	DWP	100-SW
Varieties	4	0.320	21.270	11.09*	1.52*	10.25*	0.39*
Error	10	0.830	49.840	1.350	1.260	5.390	0.190
CV		8.96	18.07	14.76	12.11	25.54	8.21

***: significant at $P \leq 0.05$; ns: not significant.**

DF, degree of freedom; CV, coefficient of variation; PH, plant height; NL, number of leaves; IL, internode length; NB, number of branches; DTF, days to flowering; NF, number of fruits; FPL, fresh pod length; FPW, fresh pod width; FWP, fresh pod weight; DPL, dry pod length; DPW, dry pod width; DWP: Dry weight of pod; 100-SW, 100 seed weight.

Table 3. Mean values of quantitative traits of varieties of okra evaluated under field conditions

Varieties	PH	NL	IL	NB	DTF	NF	FPL
V1	66.23±1.91bc	11.53±0.62a	6.63±0.09ab	6.33±0.20a	74.33±1.25c	7.23±0.39a	9.63±0.41a
V2	60.13±3.90b	12.97±1.59a	7.67±1.27b	7.40±0.92a	66.10±2.18b	7.00±0.58a	10.93±0.80a
V3	33.23±3.70b	8.87±1.27a	4.77±0.35a	5.00±0.51a	56.90±1.07a	7.77±0.74a	9.40±0.49a
V4	75.23±3.60a	11.50±0.49a	8.07±0.80b	6.00±0.40a	78.77±2.60c	6.57±0.38a	9.0±0.06a
V5	58.87±7.06c	13.00±2.14a	7.27±1.05a	6.30±1.15a	60.87±2.12ab	8.33±0.82a	10.33±0.12a
GM	58.74±4.09	11.57±0.65	6.88±0.44	6.21±0.34	67.39±2.30	7.38±0.28	9.94±0.24

Mean values followed by similar superscripts within a column are not significantly different from one another at $P \leq 0.05$ using DMRT.

GM, grand mean; PH, plant height; NL, number of leaves; IL, internode length; NB, number of branches; DTF, days to flowering; NF, number of fruits; FPL, fresh pod length

Table 3 continues

Varieties	FPW	FWP	DPL	DPW	DWP	100-SW
V1	10.03±0.77a	38.03±4.22a	6.77±1.18a	8.37±1.01a	7.17±2.32a	5.07±0.22a
V2	10.60±0.32a	43.27±3.55a	6.47±0.68a	9.23±0.78a	7.67±1.26a	5.03±0.09a
V3	10.33±0.52a	36.77±6.24a	9.67±0.23b	9.23±0.61a	10.67±0.88a	5.63±0.34a
V4	9.73±0.58a	37.23±0.79a	6.20±0.45a	10.37±0.20a	8.57±0.82a	5.03±0.12a
V5	10.13±0.29ab	40.07±3.62a	10.23±0.38b	9.17±0.20a	11.37±0.77a	5.77±0.37a
GM	10.17±0.21	39.07±1.67	7.87±0.53	9.27±0.30	9.09±0.67	5.31±0.13

Mean values followed by similar superscripts within a column are not significantly different from one another at $P \leq 0.05$ using DMRT.

GM, Grand mean; FPW, Fresh Pod Width; FWP, Fresh Pod Weight; DPL, Dry Pod length; DPW, Dry Pod Width; DWP: Dry weight of pod; 100-SW, 100 seed weight.

Table 4. Estimates of genetic parameters of quantitative traits among varieties of okra evaluated under field conditions

TRAITS	GM	GV	PV	GCV	PCV	H²B	GA	GAM
PH	58.74	226.11	283.33	25.60	28.66	79.80	27.67	47.11
NL	11.57	0.96	6.57	8.45	22.15	14.57	0.77	6.66
IL	6.88	0.94	3.14	14.12	25.77	30.01	1.10	15.99
NB	6.21	0.21	1.79	7.38	21.54	11.73	0.32	5.51
DTF	67.39	79.23	90.45	13.21	14.11	87.60	17.16	25.46
NF	7.38	0.10	1.22	4.21	14.95	7.95	0.18	2.43
FPL	9.94	0.24	0.88	4.93	9.44	27.27	0.53	5.33
DPL	7.87	3.25	4.60	22.90	27.24	70.63	3.12	39.64
DPW	9.27	0.09	1.35	3.18	12.52	6.44	0.15	1.62
DWP	9.09	1.62	7.01	14.00	29.13	23.11	1.26	13.86
100-SW	5.31	0.07	0.26	4.86	9.54	25.97	0.27	5.08

GV: Genotypic variance; PV: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; H²B: Heritability; GA: Genetic advance; GAM: Genetic advance as percent over mean; PH: Plant height; NL: Number of leaves; IL: Internode length; NB: Number of branches; DTF: Days to flowering; NF: Number of fruits; FPL: Fresh Pod length; FPW: Fresh Pod Width; FWP: Fresh Pod Weight; DPL: Dry Pod length; DPW: Dry Pod Width; DWP: Dry weight of pod; 100-SW: 100 seed weight.

Table 5. Genotypic correlation of quantitative traits among varieties of okra evaluated under field conditions

TRAITS	PH	NL	IL	NB	DTF	NF	FPL	FPW	FWP	DPL	DPW	DWP	100-SW
PH	1	0.67**	0.80**	0.60*	0.80**	-0.05	-0.02	-0.31	-0.04	-0.59*	0.07	-0.45	-0.59*
NL		1	0.77**	0.91**	0.17	0.47	0.18	-0.12	0.01	-0.14	-0.28	-0.37	-0.50
IL			1	0.73**	0.45	0.16	0.10	-0.29	-0.11	-0.36	-0.01	-0.37	-0.37
NB				1	0.17	0.39	0.091	-0.16	-0.04	-0.32	-0.25	-0.49	-0.57*
DTF					1	-0.38	-0.11	-0.35	-0.10	-0.72**	0.26	-0.45	-0.57*
NF						1	0.02	0.07	0.05	0.47	-0.23	0.20	0.15
FPL							1	0.58*	0.69**	0.04	0.10	0.18	0.18
FPW								1	0.73**	0.22	-0.02	0.37	0.31
FWP									1	-0.12	-0.14	0.03	0.09
DPL										1	0.09	0.81**	0.74**
DPW											1	0.59*	0.30
DWP												1	0.84**
100-SW													1

*: Significant at $P \leq 0.05$; **: Significant at $P \leq 0.05$.

PH, plant height; NL, number of leaves; IL, internode length; NB, number of branches; DTF, days to flowering; NF, number of fruits; FPL, fresh pod length; FPW, fresh pod width; FWP, fresh pod weight; DPL, dry pod length; DPW, dry pod width; DWP: Dry weight of pod; 100-SW, 100 seed weight.

4. Discussion

Analysis of variance revealed that the mean sum of squares for genotypes was highly significant for all traits except fresh pod width and fresh pod weight. This may be due to differences in the genetic components of the various accessions. This also corroborates the findings of Schmidt *et al.* (2019) and Sharma *et al.* (2016), who stated the role of differences in the genetic components of different varieties in yield determination of okra. Variability can be used to improve the crop for the desired character through selection. This is in accordance with Siemonsma *et al.* (2004), who also recorded variability in different characteristics of the okra genotypes they studied.

Phenotypic coefficients of variation were higher in magnitude than genotypic coefficients of variation for the characters studied, indicating that these traits were influenced by environmental factors. Similar observations were reported by Yadav *et al.* (2010).

The phenotypic coefficient of variation varied from fresh pod length to dry weight pod in value, whereas the genotypic coefficients of variation varied from dry pod width to plant height in value. Both indicate considerable diversity in the germplasm studied for various agronomic traits as a result of interaction between the genotypes and the environment.

Heritability in the broad sense separates genotypic variance from environmental variance, expresses the extent to which the phenotype is determined by the genotype, which is known as the degree of genetic determination, and is very useful in the selection of superior lines from homozygous lines. This signifies that these traits were less influenced by the environmental factor; hence, the presence of additive gene effect is suspected; hence, selection for improvement of such characters may be reliable. A similar result was reported by Yadav *et al.*, (2010) for plant height. The low heritability associated with low genetic advance for the number of leaves, number of branches, number of fruits, fresh pod length, dry pod width, and 100-seed weight revealed that environment or non-additive gene action may be prevailing for these characteristics, and thus heterosis breeding will be beneficial.

Ajayi *et al.* (2014) hypothesized that correlation is a measure of the degree of association between traits and that trait selection leads to improvement of all positive correlated traits and regression of negative correlated traits. Correlation analysis revealed insightful relationships between traits, such as the positive correlation between plant height and number of leaves. Similarly, the correlation between the number of leaves and the number of branches indicates a stronger positive

correlation. In addition, there was a negative correlation between days and flowering and dry pod length.

5. Conclusion

This study concluded that accession NGB02436 exhibited the highest dry pod weight, suggesting the potential for higher seed yield per pod. NGB00425 had the highest 100-seed weight, indicating larger individual seeds, which may impact seedling vigor and final yield. NGB02518, NGB00346, and NGB00401 had longer internode lengths and plant heights, and their productivity was comparatively low due to the low number of fruits per plant.

Furthermore, leveraging traits with high heritability and genetic advance, particularly plant height, days to flowering, and fresh pod length, holds promise for effective trait selection and subsequent genetic improvement. Such insights are invaluable not only for enhancing okra yield but also for advancing broader understanding in plant biology and genetics.

References

- Ajayi, A. T., Adesoye, A. I. and Adekoya, A. E. (2014). Genetic variability, heritability and genetic advance estimates in cowpea breeding lines (*Vigna unguiculata* L. Walp). *Journal of Agricultural Sciences*, 62(4): 279-293.
- Akanbi, W. B., Kumar, P. L., Nsa, I. Y. and Uguru, M. I. (2010). Genetic divergence in okra. *African Journal of Biotechnology*, 9(18): 2600-2607.
- Daniela, P. D., Anna, L. and Patrizia, B. (2012). Okra (*Abelmoschus esculentus* L.): A study on its potential benefits to human health. *Natural Product Communications*, 7(12): 1934578X1200701210.
- Dhankar, J. S., Tyagi, R. K. and Kumar, V. (2002). Heritability, genetic advance and correlation for quantitative traits in okra (*Abelmoschus esculentus* L. Moench). *Annals of Agricultural Research*, 23(1): 1-3.
- Ibeawuchi, I. I. (2007). Okra: A potential export commodity for Nigeria. *African Journal of Agricultural Research*, 2(4): 144-149.
- Ibrahim, M., Bukar, D. B. and Muhammad, S. (2006). Genotypic and phenotypic variances, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *African Journal of Biotechnology*, 5(11): 1081-1083.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). The value of the heritability estimate is enhanced when used together with the genetic advance. *The Journal of Heredity*, 46(2), 44-45.

- Komolafe, O. A., Balogun, M. and Ademiluyi, B. O. (2019). Variability and heritability estimates in some okra (*Abelmoschus esculentus* L. Moench) accessions. *Cercetari Agronomice in Moldova*, 52(1): 39-51.
- Singh, R. K. and Chaudhary, B. D. (1985). Procedure for analysis of variances. *Journal of Agricultural Science*, 10(2), 123-135.
- Kumar, S. and Sreeparvathy, P. C. (2010). Okra (*Abelmoschus esculentus*) Fibre. *European Journal of Scientific Research*, 40(3): 380-386.
- Reddy, K. R. N., Sreeramulu, D. and Raghunath, M. (2013). Antioxidant activity of fresh and dry fruits commonly consumed in India. *Food Research International*, 51(2), 466-472.
- Rao, A. N. (1985). Origin and Introduction. In: Okra Botany and Horticulture. AVI Publishing Company, Inc.
- Schmidt, P.J., Rath, H.J. and Piepho, H.P. (2019). Estimating Broad-Sense Heritability with Unbalanced Data from Agricultural Cultivar Trials. *Crop Science* 59(2): 525-536.
- Sharma, V.R., Omotayo, K., Malik, S., Kumar, M. and Sirohi, A. (2016). Character Association and Path Analysis in Garlic (*Allium sativum* L.). *Bioscan* 11(3): 1931-1935.
- Siemonsma, J.S. and Kouame, C. (2004). Vegetable Plant Resource of Tropical Africa 2. PROTA Foundation, Wageningen, Netherlands, pp: 21-29.
- Yadav, M., Chaurasia, P.C., Singh, B.D. and Gaurav, S.K. (2010). Genetic Variability Correlation Coefficient and Path Analysis in Okra (*Abelmoschus esculentus* L. Moench). *Indian Journal of Horticulture* 67: 456-464.