Genetic Variability and Heritability Studies in West African Okra (*Abelmoschus caillei* (A. Chev. Stevels)

O. F. Adewusi[1*] and S. O. Adeweso[2]

[1]*Department of Crop, Soil and Pest Management, Federal University of Technology, Akure, Nigeria.*
[2]*Christ Apostolic Church Grammar, Olorunsogo, Ibadan, Oyo State, Nigeria.*

Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Genotypic and phenotypic variances, genotypic coefficient of variation and phenotypic coefficient of variation, heritability and genetic advance were estimated for twelve agronomic characters in ten West African okra, *Abelmoschus caillei*. The genotypic coefficient of variation ranged from 0.47 days to 50/% flowering to 41.43 for number of fruits per branch. Heritability estimate ranged from 32.00 days to 50% flowering to 98.14 for seed yield. Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were estimated for edible pod length, dry fruit weight, number of seeds per pod, number of fruit per plant, number of pod per branch and seed yield per plant indicating a good genetic variability in these characters in West African okra. Thus direct selection for these traits would be highly effective in West African okra. The relatively high magnitude of heritability along with high genetic advance recorded for edible pod length, number of branches per plant, dry fruit weight, number of seeds per pod, number of fruits per branch, number of fruit per plant and seed yield per plant were indicative of likely effectiveness of selection for these characters.

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*Corresponding author: E-mail: ofadewusi@gmail.com;

1. INTRODUCTION

West African okra, *Abelmoschus caillei* belongs to the family Malvaceae. It is a warm season crop that thrives well in a good loamy soil high in organic matter with good moisture retention capacity. It is a self pollinated - allopolyploid hybrid between *Abelmoschus esculentus* and *Abelmoschus manihot* [1]. It is an important vegetable crop in Nigeria and many tropical and sub-tropical countries. On a worldwide basis, okra production as fresh fruit vegetable was estimated at 4.8 million tonnes, but most of the production was in India (70%) followed by Nigeria (15%), Pakistan (2%), Ghana (2%) and Iraq (1.7%) [2].

According to [3], conventional okra account for 90-95% of the global production while West African okra contributes the remaining 5-10%. Also according to the estimates of the authors, okra production in West and Central Africa has reached about 500,000 – 600,000 tonnes annually with West African okra making up half of this amount. West African Okra is biennial, promising and essentially photoperiod sensitive being a short day plant [4]. It is tolerant of insect pests and diseases.

The potential of the seeds as a new source of plasma replacement or blood volume expender was emphasized by [5]. It is cultivated primarily for its fresh pods and leaves which are frequently eaten green as vegetable. The importance of this crop lies in the mucilaginous property of the fruit, which makes easy the consumption of bulky food. Okra pods at the edible stage contains 85mls water, 2.1 g protein, 0.2 gfat, 8 g carbohydrate, 367 calories, 1.7 g fiber, 175.20 mg minerals and 232.72 mg vitamins in 100 g of edible portion [6]. Progress in breeding for economic characters that are quantitative in inheritance and therefore subject to environmental variability are determined by the nature and magnitude of genetic variability.

In effecting improvement in yield, selection of superior genotype is based on the outward appearance (phenotype) which is prone to variation due to fluctuating environmental factors. Under similar environmental conditions, any progress in a breeding program depends on the magnitude of genetic variability in a population and the extent to which the desirable traits are heritable (heritability). Generally, the success of any crop improvement program largely depends on the magnitude of genetic variability and genetic advance. Genetic variability is a very important component of plant breeding which is a major tool being used to cope with the ever increasing pressure of an expanding world population on food production [7].

Information on genetic variability of different characters of a crop and about the useful genes in each accession which is properly evaluated to identify the potential accessions is necessary prior to breeding program for improvement in any crop. Hence, the need to partition overall variability into heritable and non - heritable components with the aid of genetic parameters such as genotypic and phenotypic coefficients of variation and heritability. Considerable variation has been reported in some West African okra characters by several other researchers [8,9], [10] and [11]. Heritability estimates have been observed for length and width of pods by [12] and for pod and seed yield by [13]. Genetic variability and heritability studies have been done in a wide range of crops such as conventional okra [14]. [15,16,17,18] and [19]. Determination of heritability estimates using different methods will provide information on the proportion of phenotypic variance that is due to genetic factors for different traits but heritability estimate alone is not a sufficient measure of the level of possible genetic progress that might arise not even when the most outstanding individuals are selected in a breeding program. The value of heritability estimate is enhanced when used together with the selection differential or genetic advance [20].

The present investigation is to assess the genetic variability, heritability and genetic advance from 12 characters contributing to yield in West African okra so as to assist the plant breeder to design testing procedure for identifying superior genotypes.

2. MATERIALS AND METHODS

The experimental materials for the present investigation consisted of ten accessions of West African okra as shown in Table 1. They were obtained from the germplasm collection of the National Centre for Genetic Resources and Biotechnology Moor plantation, Ibadan, Nigeria. These were grown at the Farm Centre of the Federal Polytechnic Ilaro, Ilaro Ogun State in

2008 and 2009 using Randomized Complete Bock Design with four replications. A single row of 10m in length was used for each accession. A spacing of 1m by 0.6m was adopted between rows and within rows, respectively. Two seeds were planted per hole to a depth of 1cm into the soil and later thinned to one stand per hill. Weeding was carried out manually at 3weeks after planting (3WAP) and as necessary to keep the plot weed free. Following thinning, fertilizer application of a compound fertilizer in the form of NPK 15:15:15 was applied by drilling at the recommended rate of 60kg/ha in two doses, first, at three weeks after planting and at flowering to enhance the growth of the crop. Cypermethrin at the rate of 50ml/10litres of water was applied from 4weeks after planting and forthnightly so as to reduce damage on the crop by insect pests.

Table 1. Names and source of Okra accessions, *Abelmoschus caillei*

Accession code	Accession name	Source
1	NGAE-9660	National Centre
2	NGAE-9661	for Genetic
3	NGAE-9663	Resources and
4	NGAE-9664	Biotechnology
5	NGAE-9666	(NACGRAB)
6	NGAE-9667	
7	NGAE-9669	
8	NGAE-96123	
9	CEN 010	
10	OWODE-5	

Data were collected on ten competitive plants of each accession in each replication. Data were collected on the following characters: - edible pod length (cm) (ten days after anthesis), maximum pod length (cm), number of branches per plant, days to50% flowering, dry fruit weight (g), number of ridges per pod, number of seeds per pod, number of fruit per branch, number of leaves per plant at flowering, maximum plant height (cm), number of fruits per plant and seed yield per plant (g).

Yield and yield component data were subjected to analysis of variance according to the procedure outlined by [21]. Genotypic and phenotypic variances were determined according to [22];

Genotypic variance $(\sigma 2\ g)\ = \dfrac{(MSG - MSE)}{r}$

Phenotypic variance $(\sigma 2\ p) = \dfrac{(MSG + MSE)}{r}$

Error variance $(\sigma^2\ e)\ = \dfrac{MSE}{r}$

where:

MSG = Genotype mean square
MSE = Error mean square
r = Number of replication

The variance components were used to compute the genotypic coefficient of variability, phenotypic coefficient of variability and heritability (in broad sense), according to [23] thus:

$$PCV\ (\%) = \dfrac{\sigma\ p}{X}\ x\ \ 100$$

$$GCV\ (\%) = \dfrac{\sigma\ g}{X}\ x\ \ 100$$

Where: $\sigma\ p$ = phenotypic standard deviation

$\sigma\ g$ = genotypic standard deviation

X = grand mean for the character under consideration.

Broad sense heritability and the genetic advance expected under selection, assuming a selection intensity of 5% were estimated according to the formula of [24] as follows:

Where

Heritability (broad-sense) = $\dfrac{\sigma^2\ g}{(\sigma^2\ g + \sigma^2\ e)}$

$\sigma^2\ g$ is the estimate of genotypic variance
$\sigma^2\ e$ is the estimate of environmental variance

where:

$(GA) = (K)\ x\ \sigma\ p\ x\ (H)$

GA = expected genetic advance

K = selection differential (2.06 at 5% selection intensity)

$\sigma\ p$ = phenotypic standard deviation.

H =Heritability in broad sense

The analysis of variance for the 12 characters considered showed significant differences among the accessions (Table 2). Very low to low character variation was observed as measured by coefficients of variation (CV). The CV values ranged from 1.38 for days to flowering to 33.14% for number of leaves per plant at flowering.

Table 2. Mean squares, analysis of variance of plot means and coefficient of variation (%CV) for 12 characters in West African okra,
Abelmoschus caillei

Source of variation	Df	EPL (cm)	MPL (cm)	NBP	DTF (d)	DFW (g)	NRP	NSP	NFB	NLP	PHT (cm)	NFP	Seed Yield (g)
Replication	3	4.494**	4.720**	14.580**	12.038**	652.8**	20.416**	1320.677**	0.080	36.117	31.437	0.328*	107.578**
Accession	9	11.757**	14.913**	20.853**	1.853	273.6**	9.972**	2005.369**	0.917**	70.115**	283.941**	1.207**	30.696**
Error	27	0.367	0.597	0.633	1.260	7.096	1.238	26.035	0.086	21.222	37.947	0.107	0.5701
CV%		13.65	9.29	9.76	1.38	10.78	16.06	9.15	26.71	33.14	8.44	14.11	8.89

*****Significant P ≤ 0.05; 0.01; DF = degree of freedom.*
EPL=Edible pod length; MPL= Maximum pod length; NBP=Number of branches per plant; DTF=Days to flowering; DFW=Dry fruit weight; NRP=Number of ridges per pod;
NSP=Number of seeds per pod; NFB=Number of fruits per plant; NLP=Number of leaves per plant at flowering; PHT=Plant height; NFP=Number of fruits per plant.
CV=Coefficient of variation

2.1 Cluster Analysis

The dendrogram resulting from the analysis is shown in Fig. 1. In this grouping based on measured traits, the SLCA classified the accessions into three distinct groups. Cluster 1 contains 20% of the accessions (NGAE-9612 and CEN 010), cluster 2 contains 40% of the accessions (NGAE-9666, NGAE-9660, NGAE-9667 and OWODE-5) while cluster 3 contains 40% of the accessions (NGAE-9663, NGAE-9669, NGAE-9661 and NGAE-9664). Accessions in cluster 1 recorded the highest seed weight values; accessions in cluster 2 recorded moderately high seed weight values while those in cluster 3 recorded the least seed weight values.

The means, genotypic and phenotypic variances (PCV & GCV) of all the characters studied are presented in Table 3. The accessions of West African okra showed significant variability for most of the characters. PCVs were higher than GCVs in all the characters. The PCV ranged from 0.23 for number of fruits per branch to 501.34 for number of seeds per pod while the GCV ranged from 0.15 for days to flowering to 494.83 for number of seeds per pod.

The phenotypic and genotypic coefficient of variation, broad sense heritability estimates and genetic advance of the 12 characters evaluated are presented in Table 4. The PCV estimates were higher than the GCV estimates for all the characters studied. The PCV ranged from 0.84% to 43.53% while the GCV ranged from 0.47 to 41.43 days to 50% flowering and number of fruits per branch, respectively. Heritability estimates ranged from 32.00% days to 50% flowering to 98.70% for number of seeds per pod. On an average, the heritability estimates were very high for most of the characters except days to 50% flowering and number of leaves per plant at flowering. The genetic advance ranged from 0.55 days to 50% flowering to 81.61 for number of seeds per pod. The highest genetic advance as percent of mean was recorded for number of seeds per pod (81.61) followed by number of fruits per branch (81.23); dry fruit weight (67.19) and seed yield per plant (66.01).

3. DISCUSSION

The significant variations among the 10 accessions of West African okra with respect to the 12 characters that were observed may be regarded as a reflection of their diverse eco-geographical backgrounds. This gives high possibility of improvement of these characters through selection either directly or following recombination through hybridization of desirable genotypes. The higher relative value of phenotypic variance to its genotypic counterpart implies environmental influences on the characters. This is consistent with report by [25] who were of the opinion that if environmental variability is negligible compared to genetic variability, selection will be effective in improving the character if such character has high genotypic variability and also easily measureable. Therefore character with moderate value of genotypic coefficient of variation such as edible pod length, dry fruit weight, number of seeds per pod, number of fruit per branch and seed yield might be further improved through varietal selection.
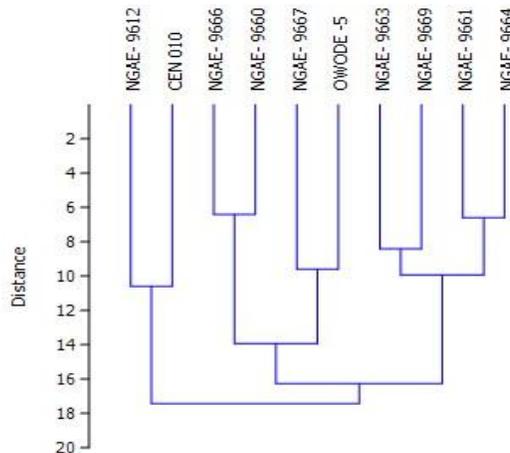

Fig. 1. Dendrogram showing genetic relationship among 10 accessions of West African Okra, *Abelmoschus caillei* using Single Linkage Cluster Analysis (SLCA)

Table 3. Mean, PCV & GCV (s) of 12 characters studied in West African okra, *Belmoschus caillei*

Character	Mean	PCV	GCV
EPL (cm)	5.33	2.94	2.81
MPL (cm)	8.31	3.73	3.58
NBP	8.15	5.21	5.06
DTF (d)	81.21	0.46	0.15
DFW (g)	24.70	68.40	66.63
NRP	6.93	2.49	2.18
NSP	55.79	501.34	494.83
NFB	1.10	0.23	0.21
NLP	13.90	17.53	12.22
PHT (cm)	72.99	70.99	61.50
NFP	2.32	0.30	0.28
Seed Yield (g)	8.48	7.67	7.53

EPL=Edible pod length; MPL= Maximum pod length ; NBP=Number of branches per plant; DTF=Days to flowering; DFW=Dry fruit weight; NRP=Number of ridges per pod; NSP=Number of seeds per pod; NFB=Number of fruits per plant; NLP=Number of leaves per plant at flowering; PHT=Plant height; NFP=Number of fruits per plant

Table 4. PCV, GCV, Broad-sense heritability (H^2) and Genetic Advance (GA %) for 12 characters in West African okra, *Abelmoschus caillei*

Charater	PCV (%)	GCV (%)	H^2 (%)	GA (%)
EPL (cm)	32.20	31.46	95.51	63.34
MPL (cm)	23.23	22.76	96.00	45.94
NBP	28.00	27.57	96.96	55.93
DTF (d)	0.84	0.47	32.00	0.55
DFW (g)	33.48	33.05	97.41	67.19
NRP	22.79	21.33	87.59	41.12
NSP	40.14	39.88	98.70	81.61
NFB	43.53	41.43	90.59	81.23
NLP	30.12	25.15	69.73	43.27
PHT(cm)	11.54	10.74	86.64	20. 60
NFP	23.67	22.60	91.14	44.44
Seed Yield (g)	32.35	32.35	98.14	66.01

EPL= Edible pod length; MPL-= Maximum pod length ; NBP= Number of branches per plant; DTF=Days to flowering; DFW= Dry fruit weight; NRP=Number of ridges per pod; NSP=Number of seeds per pod; NFB=Number of fruits per plant; NLP-Number of leaves per plant at flowering; PHT- Plant height; NFP-Number of fruits per plant. GCV – Genotypic coefficient of variation; PCV - Phenotypic coefficient of variation; H^2 – Heritability in broad sense; GA – Genetic advance

Different estimates of varietal variability have been reported in West African okra [26]. Although, GCV gave information on the genetic variability present in the various quantitative characters, it is not enough to determine the amount of genetic gain that is heritable. [27] described the heritable portion of the total phenotypic variability as the total heritability estimates. Heritability estimates alone indicate the extent with which selection of genotypes can be based on phenotypic appearance. However, [28] suggested that genotypic coefficient of variation together with heritability estimates would give the best picture of genetic advance to be expected from selection. In addition, [29]

reported that heritability estimates show only the extent with which selection of genotypes could be based on phenotypes but its utility increased when used along with estimates of genetic advance. High heritability values for most of the characters suggest effectiveness of direct selection for such characters.

According to [30] genotypic coefficient of variation along with heritability and genetic advance will provide better information than single parameter alone. The high heritability estimates together with high genotypic coefficient of variation and relatively high genetic advance for edible pod length, dry fruit weight, number of

seeds per pod, number of fruit per branch and seed yield per plant indicated that these characters are highly heritable. Therefore, selection for these characters on the basis of phenotypic performance is likely to be dependable and effective. This result is in agreement with previous studies of [31].

4. CONCLUSION

The understanding of genetic variability and heritability between characters in a cultivar is very significant in determining selection procedure and breeding method in any effort aimed at improving a particular trait of interest. Variability observed in this study for all traits were indicative of the differences in the genetic make-up of the cultivars considered thus offering better chances and large scope for selection. Phenotypic variances were generally higher than their respective genotypic variances thereby revealing the role of environmental factors on genotype expression of the various accessions. This gave rise to the variability observed for all traits of the accessions. High PCV and GCV values are necessary as a guide in selection and breeding programmes. However, the genetic advance for each of the traits should be considered in the course of breeding to ensure success in breeding and crop improvement.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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