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Research Article

Morphological Characterization of Accessions of Okra (*Abelmoschus Spp* L.)

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ABSTRACT

Morphological markers are the traditionally proven and accepted tools as a first step, among a host of other techniques, for characterization of plant germplasm. The technique remains useful as a highly recommended first step to be undertaken prior to more in depth biochemical or molecular studies in okra germplasm. Ten parental accessions and 51 Fl progenies of A. esculentus and A. caillei evaluated for 15 qualitative and eight quantitative traits exhibited significant variations in all quantitative traits studied. Clustering pattern based on quantitative traits largely revealed no duplicates and clustering pattern especially among parental accessions, appears to reflect relationship based upon speciation as parental accessions belonging to A. caillei are clustered towards one end of the dendrogram, while members belonging to A. esculentus clustered towards the opposite end. Contributions of three principal components were 45.98 %, 23.31 %, and 14.46% for the first (PC1), second (PC2) and third (PC3) respectively, with corresponding Eigen values of 3.21837, 1.63171 and 1.01212 respectively, cumulating into maximum of 83.75 % of total variance. These results demonstrate possibility of producing superior hybrids of okra through artificial cross-pollination.

Key words: *Okra, Accessions, Morphological, Characterization, Hybridization.*

INTRODUCTION

Characterization and identification of genetic variability within germplasm collections are a preliminary requirement for the exploitation of useful traits in plant breeding[1,2]. The key objectives of okra germplasm characterization have generally been to identify high yielding genotypes with resistance to yellow vein mosaic virus (YVMV), fruit borer (*Spodoptera spp*.), jassid (*Cicadellidae*) and higher vitamin C content in the species that can be utilized for the improvement of a crop[3,4]. According to Beeching[5] one important aspect of crop improvement is assessment of genetic diversity of desirable characteristics such as increased yield, wide adaptability, pests and diseases resistance among other traits which exist within populations of crop species.

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Germplasm characterization also plays a key role in investigations of genetic diversity patterns and identification of duplicates within crop collections. It also facilitates studies of correlation among characteristics of agronomic importance[6]. The efficacy of the method deployed for the characterization process largely determines the potential genetic value of a particular germplasm[7]. Generally, characterization and genetic assessment is centered on use of genetic markers that are capable of detecting variation in either a protein or DNA sequence to identify the characteristics of a genetic material[7].

Morphological markers have traditionally been useful tools for preliminary characterization of plant germplasm. Despite the challenge of their ambiguity due to contribution of multiple genes and modifications or interactions with the environment, morphological markers still remain very useful primary methods for germplasm characterization[8]. They constitute the most readily available technique, thus published descriptor lists are readily available for most major crop species including okra. Characterization based on phenotypic traits is not easily reproducible, particularly, since they are affected by environmental variations[8]. In addition, it requires a large tract of land or greenhouse space to grow large populations of plants; it is labour intensive and difficult to manage[9]. However, the technique require little skills and are relatively inexpensive to carry out[10]. Morphological characterization of crops is facilitated by the use of standard descriptors, which provide an international format for producing a universally understood data for plant genetic resources[7].

Notwithstanding, the technique remains useful as a highly recommended first step to be undertaken prior to more in depth biochemical or molecular studies in okra germplasm[11,12]. A number of morphological, biochemical and molecular (DNA) markers have been developed and widely used to investigate diversity in plant genetic resources. However, resolution of diversity using biochemical analyses has received little attention due to their reliance on proteins/enzymes which are usually limited for most traits in plant germplasm[7]. On the contrary, molecular techniques which comprise a large variety of DNA-based markers are very efficient for analysis of variation in germplasm collections due to their ability to detect or amplify anonymous loci (expressed or non-expressed sequences). However, due to requirement of high expertise and sophisticated facilities, molecular techniques are very expensive to carry out[13].

The main objective of this study was to morphologically characterize ten local landraces of okra (*Abelmoschus esculentus* and *caillei)* and their 51 F1 offspring obtained from both intra-specific and inter-specific hybridization in order to ascertain differences in characteristics to aid the identification of promising genotypes for selection.

MATERIAL AND METHODS

Experimental site, edaphic and weather conditions

The work was carried out at the research farm of the Biotechnology and Nuclear Agriculture Research Institute (BNARI) of the Ghana Atomic Energy Commission (GAEC), Kwabenya, near Accra. The experimental site is located 05º 40' N and longitude 0º13'W at an elevation of 76 m above sea level within the coastal savannah agroecological zone of Ghana. The soil type is the Nyigbenya-Haatso series, which is typically well-drained savanna Ochrosol (Ferric Acrisol), derived from quartzite and Schist[14]. The maximum and minimum average temperatures are 30.10^{o}C and 23.20^{o}C, respectively. The mean annual rainfall was 220 mm. Average relative humidity, sunshine and wind speed were 42.00, 195.35 w/m2 and 742.72 m/s, respectively.

Experimental design, seed sowing and field management practices

The Randomized Complete Block Design was used with four replications. Ten parents and 51 F1s of okra accessions were planted on an 85.4 m x 25 m size of field. No fertilizer was applied, but weeds were controlled and other agronomic and management practices were carried out. Seeds of the ten parental accessions (Table 1) and F1s were sown after a heavy rainfall and that the rate of germination.

The seeds were sown at a depth of 2 cm at a spacing of 0.70 m x 0.50 m between and within rows with four seeds per hill and thinned to two per hill after germination.

Table 1: Okra parental accessions used in the study

Accession code	Origin	Accession name	Accession owner
T1 *(A. esculentus)*	Upper East region	Yire marna 1	Amitaaba
T2 *(A. esculentus)*	Upper East region	Yire marna 2	Amitaaba
T3 *(A. esculentus)*	Upper East region	Yire marna 3	Amitaaba
T4 *(A. caillei)*	Upper East region	Yire marna 4	Amitaaba
AM *(A. caillei)*	Eastern region	Amanfrom	Ahiakpa
VT *(A. esculentus)*	Volta region	Volta	Ahiakpa
ID *(A. esculentus)*	Greater Accra region	Indiana	Ahiakpa
AG *(A. esculentus)*	Ashanti region	Agric Short	Ahiakpa
YL *(A. caillei)*	Brong-Ahafo region	Yeji Local	Ahiakpa
KB *(A. caillei)*	Ashanti region	Kortebotor pink	Ahiakpa

Data collection

Data was collected using the International Plant Genetic Resources Institute[15] Descriptor List for okra. Data was taken on 23 characters, which include the following parameters and were grouped into four growth stages of the plant;

(a) Vegetative characters: general aspect of the plant, branching type (BRT), stem pubescence, stem colour, leaf shape and leaf colour. Data was taken on these characters prior to first fruiting of all accessions.

(b) Inflorescence characters: number of epicalyx segments (NES), shape of epicalyx segments (SES), persistence of epicalyx segments (PES), petal colour, and colouration of petal base.

(c) Reproductive characters: days to 50% germination (DG), maximum plant height (cm) (PHAFF).

(d) Fruit characters: position of fruit on main stem (PFMS), fruit colour, fruit length at maturity, length of peduncle, fruit shape, number of ridges per fruit (NRPP), fruit pubescence and number of days to 50% fruiting (DG). Position of fruit on main stem was determined on five data plants prior to harvesting of fruits. Number of ridges was recorded by counting the quantity of ridgeline or natural striations through the fruit and then coded accordingly. This was done on five pods of each accession. Data on fruit pubescence was taken by visual assessment of hairiness or smoothness of pods and a practical hand 'feel' on harvested fresh fruits.

Data analysis

Qualitative data was evaluated based on the morphological descriptors to identify the extent of variation within the parents and F1 populations for the selected qualitative traits. The quantitative data was subjected to Analysis of variance (ANOVA) to determine the level of significance of variability for the various parameters. A p-value of 0.05 or less was considered statistically significant. Duncan's multiple range test was deployed to determine differences among means. Cluster analysis based on similarity matrices was performed to generate a dendrogram in order to determine genetic relationships among the genotypes. Correlation analysis was also carried out to determine degree of association between the quantitative agro-morphological traits. Contribution of each trait to total genetic diversity within the populations studied was determined through principal component analysis based on correlation matrix of agro-morphological variables. Statsgraphics Centurion software (version 16.1) and Microsoft Excel Software (2010 edition) were used for Data analyses.

RESULTS

Variation in eight quantitative traits among 33 accessions of okra *(Abelmoschus esculentus)* including F1 offspring

Table 2 shows data on comparative performance of 33 okra genotypes comprising six parents and 27 F1s. The phenotypic characteristics of the six parental accessions growing on the field are shown in Figure 1.

Table 2: Variability in Eight Quantitative Traits among Six Accessions and 33 hybrids of okra obtained from intra-specific hybridization

ACCESS	LOF	LOPE	NSPP	FFW	DF	DOP	PHAFF	DG
T1	14.83±1.61^{hijk}	3.53±0.06^{g}	48.00±1.73^{jklm}	39.67±0.90^{mn}	41.33±0.58^{jk}	3.13±0.15^{jklm}	34.73±1.12^{defgh}	4.33±0.58^{jk}
T2 X T1	16.70±0.96^{imnop}	4.23±0.26^{hi}	49.33±6.03^{jklm}	41.30±0.92^{no}	35.33±0.58^{cde}	2.63±0.78^{defgh}	35.47±1.11^{efghi}	4.67±0.58^{cde}
T3 X T1	15.47±1.72^{ijklm}	3.33±0.15^{dfg}	43.67±2.08^{ghijk}	36.78±1.35^{ijk}	39.33±2.52^{ghij}	2.47±0.21^{bcdef}	30.03±1.00^{abcd}	7.67±0.58^{ghij}
VT X T1	14.13±1.10^{ghij}	3.43±0.31^{efg}	46.67±1.53^{ijkl}	40.00±1.67^{mno}	38.33±2.08^{fghi}	2.80±0.27^{fghijk}	41.83±0.76^{klmno}	4.33±0.58^{fghi}
AG X T1	11.07±1.69^{bcd}	2.80±0.10^{b}	45.33±0.58^{hijk}	31.19±0.28^{fg}	41.33±1.53^{jk}	2.10±0.10^{ab}	44.30±1.35^{mno}	6.67±0.58^{jk}
T1 X T2	13.53±1.56^{gh}	3.30±0.26^{defg}	42.67±1.52^{fghij}	39.36±1.40^{lmn}	37.33±2.08^{efg}	3.00±0.10^{hijklm}	44.83±3.75^{o}	5.33±0.58^{efg}
T2	15.63±1.03^{jklmn}	39.33±2.08^{efgh}	36.35±0.99^{ijk}	37.67±1.15^{efgh}	3.07±0.31^{ijklm}	30.60±1.04^{acbd}	4.77±0.25^{j}	3.33±0.58^{efgh}
T3 X T2	13.23±0.85^{fgh}	3.17±0.06^{bcdefg}	40.00±2.00^{efghi}	38.25±0.82^{klm}	38.33±1.15^{fghi}	2.67±0.31^{defgh}	33.90±1.75^{cdef}	4.33±0.58^{fghi}
ID X T2	10.03±0.55^{b}	4.50±0.17^{hij}	28.00±3.00^{ab}	32.66±0.78^{gh}	32.67±1.15^{ab}	2.67±0.15^{defgh}	29.30±0.61^{abc}	3.67±0.58^{ab}
VT X T2	18.33±2.52^{op}	3.50±0.27^{fg}	48.00±2.00^{jklm}	40.29±1.58^{mno}	37.00±1.73^{defg}	2.50±0.10^{cdef}	32.57±1.50^{abcde}	4.67±0.58^{defg}
AG X T2	10.67±0.61^{bc}	2.83±0.10^{bc}	45.67±1.53^{hijk}	29.47±1.55^{cdef}	40.67±1.15^{ij}	3.07±0.12^{ijklm}	41.87±2.01^{klmno}	5.67±0.58^{ij}
T1 X T3	11.23±0.97^{bcd}	3.03±0.06^{bcde}	37.33±0.58^{defg}	37.37±2.23^{ijkl}	37.67±0.58^{efgh}	2.77±0.31^{efghij}	30.47±1.50^{abcd}	4.33±0.58^{efgh}
T2 X T3	17.07±0.21^{mnop}	4.40±0.20^{hij}	42.67±1.53^{fghij}	30.75±0.76^{efg}	35.67±0.58^{cbe}	3.33±0.22^{m}	43.27±1.62^{lmno}	6.67±0.58^{cde}
T3	16.40±0.66^{klmno}	3.47±0.31^{fg}	25.00±1.00^{a}	40.90±0.86^{no}	43.67±2.31^{kl}	3.23±0.25^{lm}	28.17±0.76^{ab}	3.33±0.58^{kl}
VT X T3	16.40±0.66^{ghij}	3.43±0.06^{efg}	40.33±4.51^{efhi}	30.44±0.97^{def}	40.67±0.58^{ij}	3.10±0.20^{ijklm}	42.67±2.39^{klmno}	4.00±0.00^{ij}
AG X T3	11.30±0.80^{bcde}	3.10±0.27^{bcdf}	35.67±5.03^{cdef}	27.33±0.47^{bc}	43.67±1.53^{kl}	2.13±0.15^{abc}	44.57±2.38^{no}	5.67±0.58^{kl}
T1 X ID	12.93±1.01^{efg}	3.23±0.15^{cdefg}	39.33±4.51^{efgh}	34.51±0.80^{hi}	38.67±1.15^{fghi}	2.03±0.06^{a}	34.50±9.26^{defg}	3.33±0.58^{fghi}
T2 X ID	16.33±0.65^{klmno}	4.23±0.49^{hi}	31.33±3.21^{abcd}	24.81±1.44^{a}	34.00±1.73^{bc}	3.17±0.21^{klm}	32.83±3.82^{bcde}	5.67±0.58^{bc}
ID	14.03±0.71^{ghij}	2.83±0.06^{bc}	32.00±1.00^{bcd}	28.35±1.20^{bcd}	31.70±0.58^{a}	2.97±0.15^{hijklm}	27.77±1.45^{a}	4.33±0.58^{a}
VT X ID	13.10±0.79^{fg}	3.13±0.06^{bcdefg}	33.67±0.58^{bcde}	27.57±1.06^{bc}	36.33±1.53^{cdef}	2.67±0.21^{defgh}	35.47±5.50^{efghi}	3.67±0.58^{cdef}
AG X ID	10.97±0.85^{bcd}	2.83±0.12^{bc}	40.33±4.51^{efghi}	26.68±0.73^{ab}	39.00±1.00^{ghij}	2.33±0.21^{abcd}	38.83±1.56^{ghijkl}	4.67±0.58^{ghij}
T1 X VT	13.50±0.50^{gh}	3.13±0.12^{bcdefg}	40.33±3.51^{efghi}	37.00±1.00^{defg}	2.63±0.12d^{efgh}	39.57±3.17^{hijklm}	35.61±0.75^{ij}	4.67±0.58^{defg}
T2 X VT	2.60±1.06^{defg}	4.60±0.26^{ij}	44.67±4.51^{hijk}	32.85±2.55^{gh}	35.33±0.58^{cde}	2.90±0.20^{ghijkl}	41.60±3.50^{klmno}	7.67±0.58^{cde}
T3 X VT	17.20±0.53^{nop}	3.43±0.06^{efg}	42.67±6.66^{fghij}	42.06±1.60^{o}	37.00±1.00^{defg}	3.13±0.21^{jklm}	38.00±2.00^{fghijk}	4.33±0.58^{defg}
ID X VT	12.60±0.46^{befg}	2.93±0.06^{bcd}	50.33±5.51^{klm}	27.56±0.71^{bc}	34.67±0.58^{bcd}	2.90±0.10^{ghijkl}	38.97±3.41^{ghijkl}	3.33±0.58^{bcd}
VT	11.77±1.44^{cdef}	3.33±0.32^{defg}	66.33±2.08^{o}	40.36±1.14^{mno}	38.67±1.53^{fghi}	2.77±0.25^{efghij}	40.37±1.42^{jklmno}	5.33±0.58^{fghi}
AG X VT	10.33±1.53^{bc}	2.83±0.22^{bc}	45.00±1.00^{hijk}	28.74±0.42^{bcde}	38.33±0.58^{fghi}	2.13±0.12^{abc}	39.90±4.55^{ijklmn}	6.67±0.58^{fghi}
T1 X AG	11.27±0.87^{bcd}	3.03±0.06^{bcde}	53.00±8.00^{lmn}	41.18±1.60^{no}	46.33±0.58^{m}	2.73±0.25^{efghi}	38.50±2.50^{fghijk}	7.67±0.58^{m}
T2 X AG	13.97±1.11^{ghi}	4.13±0.32^{h}	53.67±4.16^{mn}	27.46±1.09^{bc}	36.33±2.08^{cdef}	2.83±0.06^{fghijk}	32.47±3.44^{abcde}	6.33±0.58^{cdef}
T3 X AG	15.33±0.72^{ijkl}	3.40±0.30^{efg}	30.00±2.00^{abc}	41.52±1.50^{no}	41.33±1.53^{ij}	2.80±0.20^{fghijk}	36.03±2.51^{efghij}	4.67±0.58^{jk}
ID X AG	11.07±0.86^{bcd}	2.97±0.21^{bcd}	29.00±1.00^{abc}	29.59±0.80^{cdef}	37.33±1.15^{efg}	2.53±0.31^{defg}	29.60±2.25^{abc}	6.33±0.58^{efg}
VT X AG	11.93±0.95^{p}	3.10±0.10^{bcdef}	43.67±3.06^{ghijk}	40.44±1.34^{mno}	40.00±1.00^{hij}	2.47±0.06^{bcdef}	34.50±4.27^{defg}	6.00±0.00^{hij}
AG	6.57±1.01^{a}	2.20±0.30^{a}	57.00±7.21^{n}	30.25±0.39^{def}	45.33±0.58^{lm}	2.40±0.20^{abcde}	41.87±1.03^{klmno}	8.33±0.58^{lm}
Mean	13.12±2.52	3.40±0.63	42.12±9.25	34.29±5.60	38.42±3.50	2.73±0.39	36.65±5.70	5.20±1.48
CV%	19.18%	18.32%	21.97%	16.32%	9.12%	14.41%	15.56%	28.40%

LOF (Length of pod); LOPE (Length of petiole); NSPP (Number of seeds per plant); FFW (Fresh Fruit weight); DF (Days to 50% flowering); DOF (Diameter of fruits); PHAFF (Plant height at 50% flowering); DG (Days to 50% germination)

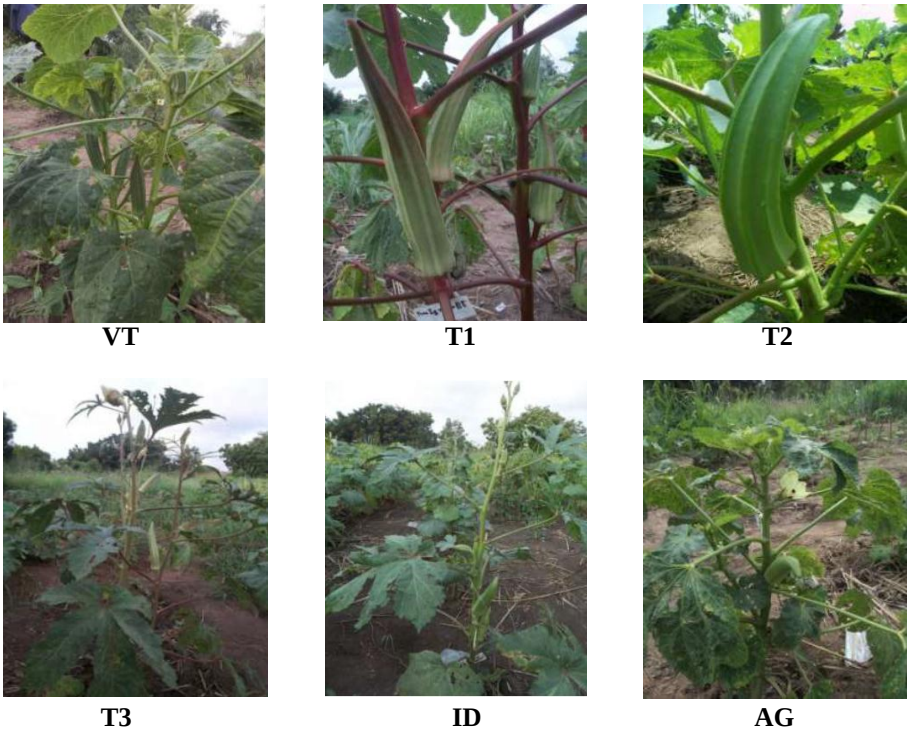

Figure 1: Parental accessions with fruits on the experimental field

The analysis of variance revealed that the differences among the selected genotypes were very highly significant for all the characters investigated, indicating the presence of

variability among them. There were very highly significant differences ($p<0.001$) in the mean number of days taken for seedlings of the 33 accessions of okra to emerge. Genotype AG took the longest mean number of 8.33 days to emerge while the crosses ID X VT, T3 X T3 and T2 X T2 recorded the shortest mean number of 3.33 days. Growth parameters differed significantly among the okra accessions. The tallest plants at 50% flowering were recorded for the cross AG X T1 with a mean value of 44.57. This was closely followed by those of T1 X T2 and AG X T3 with mean heights of 44.30 cm and 41.83 cm respectively. The least value was recorded for ID a parental generation with a mean value of 27.77 cm. Mean square estimates for plant height at flowering showed very highly significant ($p<0.001$) differences amongst the 33 parents and their offspring. Number of days to 50% flowering differed very highly significantly ($p<0.001$) among the parents and F1 varieties of okra evaluated. The cross T1 X AG recorded the highest mean number of days to flower with a value of 46.33 days and accession ID had the least mean value of 31.70 days. With respect to pod length, it differed very highly significantly ($p<0.001$) among the 33 okra varieties. Pods of VT X T2 gave the highest mean value of 18.33 cm, while AG had the least mean value of 6.57 cm. There were also very highly significant ($p<0.001$) differences in the average number of seeds per pod among the 33 accessions of okra evaluated. The crosses VT X VT and ID X AG the highest and least mean values of 66.33 and 29.00 respectively.

Variation in seven quantitative traits among 28 inter specific accessions of okra *(Abelmoschus caillei)* including F1 offspring

The variation in seven quantitative agro-morphological traits of four accessions of okra and 24 F1 offspring obtained from inter-specific hybridization among the accessions is presented in Table 3.

Table 3: Variability in Seven Quantitative Traits among Six Accessions and 28 hybrids of okra obtained from inter-specific hybridization

ACCES	LOF	DG	DF	NOB	NSPP	FFW	PHAFF
AM	12.43±0.45^{fgh}	8.67±0.58^{h}	65.33±2.52^{j}	23.00±2.00^{de}	59.67±1.53^{ij}	38.83±1.23^{jkl}	119.67±4.5^{1h}
T1XAM	13.33±0.42^{hijk}	5.33±0.58^{de}	46.33±4.04^{de}	13.33±2.52^{abcd}	52.33±2.08^{gh}	40.12±1.24^{jkl}	95.90±13.67^{g}
T2XAM	12.60±.36^{gh}	3.67±0.58^{abc}	53.00±5.29^{abc}	10.33±2.52^{ab}	35.33±2.52^{abc}	34.93±2.30^{fghi}	60.50±6.38^{bcde}
T3XAM	14.53±0.35^{lmn}	3.33±0.58^{ab}	42.00±3.00^{abcde}	16.00±4.00^{bcd}	34.00±3.61^{ab}	40.70±1.40^{kl}	76.33±25.11^{efg}
IDXAM	11.40±0.40^{def}	3.33±0.58^{ab}	46.67±6.66^{de}	7.67±2.52^{ab}	39.00±3.61^{bcd}	27.58±0.58^{ab}	51.63±2.97^{abcd}
VTXAM	13.80±0.26^{ijklm}	4.67±0.58^{cd}	43.67±3.51^{bcde}	13.00±2.65^{abcd}	65.67±5.13^{jk}	39.39±1.11^{jkl}	51.33±9.02^{abcd}
AGXAM	9.63±0.47^{b}	6.67±0.58^{f}	39.00±2.00^{ab}	8.67±1.53^{ab}	69.67±1.53^{kl}	33.27±3.01^{defg}	60.67±13.80^{bcde}
T4	14.50±0.50^{lmn}	7.67±0.58^{g}	44.67±2.08^{cde}	6.33±1.53^{ab}	47.67±2.52^{efg}	40.80±2.17^{l}	60.33±5.51^{bcde}
T1XT4	15.03±0.61^{no}	3.67±0.58^{abc}	40.33±1.53^{abc}	7.00±2.00^{ab}	54.67±1.53^{ghi}	39.35±1.19^{jkl}	47.63±4.25^{abcd}
T2XT4	12.80±0.20^{ghij}	4.67±0.58^{cd}	38.67±1.53^{ab}	8.00±2.00^{ab}	51.67±4.51^{fgh}	36.48±0.58^{ghij}	44.67±3.51^{abc}
T3XT4	15.93±1.22^{o}	3.00±0.00^{a}	37.00±2.00^{a}	4.67±1.53^{ab}	45.00±5.00^{def}	39.71±1.07^{jkl}	53.33±6.11^{abcd}
IDXT4	11.77±0.25^{efg}	3.33±0.58^{ab}	36.67±1.15^{a}	1.67±1.53^{a}	37.33±4.51^{bc}	26.82±0.85^{a}	42.00±2.65^{abc}
VTXT4	13.83±0.21^{jklm}	4.67±0.58^{cd}	43.33±1.53^{bcde}	6.33±27.78^{de}	65.00±3.61^{jk}	38.36±1.58^{ijkl}	40.63±1.18^{abc}
AGXT4	10.90±0.60^{cde}	5.33±0.58^{de}	45.33±1.15^{cde}	7.67±1.15^{ab}	58.00±6.00^{hi}	32.85±1.00^{def}	35.00±19.47^{a}
KB	11.50±0.50^{def}	10.33±0.58^{i}	75.33±3.51^{k}	30.00±2.00^{e}	69.33±2.08^{kl}	37.10±2.78^{hijk}	177.67±3.21^{i}
T1XKB	14.60±0.36^{mn}	4.30±0.58^{bcd}	47.33±2.08^{e}	12.00±3.61^{abcd}	41.67±3.79^{cde}	39.65±1.13^{jkl}	52.10±16.23^{abcd}
T2XKB	14.53±0.57^{lmn}	3.67±0.58^{abc}	52.00±2.65^{f}	12.67±1.53^{abcd}	54.67±5.03^{ghi}	36.65±2.90^{ghij}	53.00±4.00^{abcd}
T3XKB	14.10±0.66^{klmn}	4.00±0.00^{abc}	63.33±2.52^{ij}	11.00±2.65^{abc}	30.00±3.61^{a}	38.99±1.34^{ijk}	54.00±5.57^{abcd}
IDXKB	13.47±0.76^{hijk}	3.67±0.58^{abc}	37.00±2.00^{a}	4.67±2.52^{ab}	38.33±6.51^{bcd}	31.90±2.94^{cdef}	47.67±2.52^{abcd}
VTXKB	12.73±0.85^{ghi}	4.67±0.58^{cd}	41.67±2.08^{abcd}	13.00±4.58^{abcd}	70.00±2.00^{kl}	39.81±0.78^{ijk}	77.07±16.49^{efg}
AGXKB	10.03±0.15^{bc}	6.33±0.58^{ef}	46.33±1.53^{de}	9.00±2.02^{ab}	67.67±2.08^{kl}	31.37±1.69^{cde}	57.00±6.56^{bcde}
YL	6.53±0.50^{a}	9.00±1.00^{h}	77.00±2.00^{k}	22.00±1.73^{cde}	38.00±3.00^{bcd}	27.44±1.44^{ab}	134.67±5.51^{h}
T1XYL	11.10±0.80^{de}	6.00±0.00^{ef}	61.33±2.08^{hij}	13.33±4.16^{abcd}	55.00±5.00^{ghi}	29.24±1.55^{abc}	92.50±7.37^{g}
T2XYL	10.63±0.51^{bcd}	5.33±0.58^{de}	60.67±2.52^{hij}	14.33±2.08^{bcd}	38.33±2.53^{bcd}	36.91±1.44^{hij}	85.67±11.68^{fg}
T3XYL	13.40±0.80^{hijk}	4.00±1.00^{abc}	58.00±2.65^{gh}	11.00±2.65^{abc}	34.33±4.51^{abc}	30.69±1.01^{bcde}	66.57±14.65^{def}
IDXYL	11.47±0.93^{def}	4.00±0.00^{abc}	46.33±3.06^{de}	9.00±2.65^{ab}	35.33±4.51^{abc}	29.75±1.18^{abcd}	56.60±11.57^{bcde}
VTXYL	11.53±0.45^{def}	5.33±0.58^{de}	53.67±3.51^{fg}	8.00±2.65^{ab}	73.00±6.25^{l}	39.72±1.73^{jkl}	68.87±21.84^{def}
AGXYL	9.93±0.67^{bc}	6.33±0.58^{ef}	59.67±1.53^{hi}	12.33±2.52^{abcd}	47.67±4.16^{efg}	33.71±5.10^{efgh}	63.63±4.41^{cde}
Mean	12.43±2.07	5.18±1.91	50.01±11.32	11.88±7.84	50.30±13.62	35.44±4.77	68.81±32.35
CV%	16.678%	36.9758%	22.6119%	65.9567%	27.0706%	13.452%	47.0216%

LOF (Length of pod); LOPE (Length of petiole); NSPP (Number of seeds per plant); FFW (Fresh Fruit weight); DF (Days to 50% flowering); DOF (Diameter of fruits); PHAFF (Plant height at 50% flowering); DG (Days to 50% germination)

Very highly significant variations ($p \leq 0.001$) were observed among the accessions for all seven quantitative traits. Generally, values for days to first flowering (DF), number of branches per plant (NBPP), plant height at 50% flowering (PHAFF) and Days to 50% germination (DG), recorded for parental accessions were higher than those recorded for

the F1 offspring. However, for fresh fruit weight (FFW), length of pod (LOF) and number of seeds per plant (NSPP) values obtained for the F1 offspring were comparatively higher than those of parental accessions. Overall, T4, VT X YL, YL, T3XT4, recorded highest values for (FFW, NSPP, DF, and LOF) respectively, while KB gave the highest values for (PHAFF, NOB and DG) respectively. On the contrary, AG X T4, ID X T4, T3 X KB, T3 X T4 and YL recorded lowest values for PHAFF, FFW, and NSPP, (DG and LOF) respectively. Similarly, ID X T4 registered the lowest values for (NOB and DF).

Variation in qualitative traits among ten accessions of okra (A. *esculentus* and *caillei*) and their F1 offspring

Variability of qualitative traits among ten local accessions of okra (A. *esculentus* and *caillei*) and 51 F1 offspring obtained from different cross combinations were observed (Data not shown). The accessions showed greatest variability with respect to fruit colour. In general, five groups of colour namely; red, green, deep green, green with red patches and yellowish were recorded across both parents and hybrids. Petal colour gave the least variation with two categories either yellow or cream but majority (66.67 %) expressed cream. Regarding leaf colour, a greater number of the parents and F1s were green with 21% showing green with red patches. Expression of pubescence on leaf and stem varied from glabrous, to conspicuous pubescence. However, most of the accessions produced slight pubescence. For stem pubescence, 50% produced slight pubescence with the least (13.33%) being downy and rest prickly. Pod length was categorized into very long, long, medium and small. 50 % of the F1 offspring produced very long or long, followed by medium with 30% and 20% recording small.

Clustering pattern of ten local accessions of okra and their 24 intra-specific F1 offspring

Analysis of a furthest neighbour dendrogram showing genetic relatedness of ten local accessions of okra and 24 F1 offspring obtained from inter-specific hybridization among the accessions was undertaken. Figure 2 shows the genetic relationship among ten local accessions and 24 F1 offspring obtained from their inter-specific crosses, based on furthest neighbour method (Euclidean).

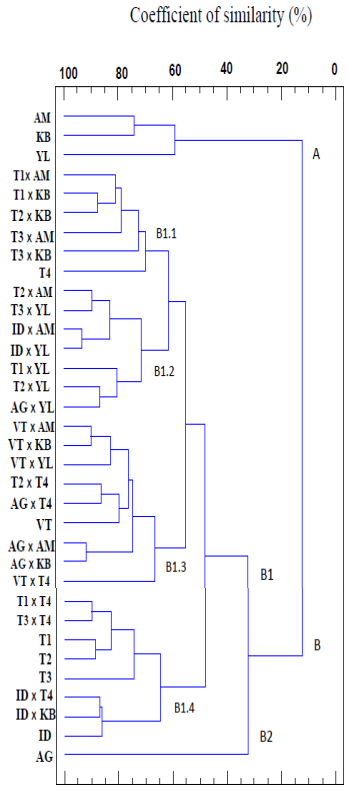

Figure 2: Dendrogram showing relatedness of ten accessions of okra and 24 F1 offspring

The accessions were separated into two clusters (A and B) at a genetic distance of 12.33%. Cluster A contains three accessions, made up of parental accessions AM, KB and YL. Cluster B on the other hand subdivided repeatedly into two sub-clusters of B1 and B2 with B2 containing a single parental accessions, AG which is most distantly related to AM. However, B1 again separated into sub-sub-clusters (B1.1, B1.2, B1.3 and B1.4). The analysis revealed no duplicates and clustering pattern especially among parental accession, appears to reflect relationship based upon speciation as parental accessions (AM, KB, YL and T4) and their hybrids belonging to *A. caillei* are clustered towards one end of the dendrogram while members belonging to *A. esculentus* and their hybrids also clustered towards the opposite end.

Principal Components Analysis (PCA)

Table 4 displays factor scores of seven quantitative traits for three principal components accounting for variability among 10 local accessions of okra (*A. caillei*) and 24 F1 offspring obtained from inter-specific hybridization among the accessions as well as contributions and eigen values of each principal component. Contributions of the three principal components were 45.98 %, 23.31 %, and 14.46% for the first (PC1), second (PC2) and third (PC3) respectively, with corresponding eigen values of 3.21837, 1.63171 and 1.01212 respectively, cumulating into maximum of 83.75 % of total variance.

Table 4: Association of seven quantitative traits with three principal components accounting for total variability among 10 accessions of okra and their F1 offspring

	Principal Component (PC)		
	PC1	PC2	PC3
LOF	**0.342138**	**0.481271**	-0.353075
DG	-0.491386	0.0818066	**0.200812**
DF	-0.462612	-0.104235	-0.369037
NOB	-0.396005	**0.275532**	-0.234668
PHAFF	-0.488485	0.0830871	-0.19164
NSPP	-0.16779	**0.40132**	**0.76343**
FFW	0.0622948	**0.711999**	-0.155574
Eigen value	3.22*	1.63	1.01
% variance	45.98*	23.31	14.45
Cumulative % variance	45.98	69.29	**83.75***

Bolded values represent variables which made significant contribution to total variance in respective axes. Maximum eigen value and percent variance are asterisked (*); minimum eigen value and percent variance are underlined. Maximum cumulative percent variance of the 3 principal components is bolded and asterisked.

The first component is far more important than the other two, since it accounts for 45.98% of the variation in the data. There appears to be a contrast between LOF and FFW on one hand and DG, DF, NOB, PHAFF and NSPP on the other, as the latter set all have negative values. Factor scores of the variables indicate that length of fruit and fresh fruit weight exhibited significant positive association with PC1 indicating that breeding in this component will lead to increased fruit length and fresh fruit weight. The same effect will on the other hand, lead to reduction in days to 50% germination, days to 50% flowering, number of branches per plant, number of seeds per pod and plant height at first fruiting. Regarding PC2, the significant variables were length of pod, fresh fruit weight, number of seeds per fruit and number of branches per plant. This indicates increased values when breeding in component two while earliness could be achieved, since the value for earliness is negative in this component. Again, number of days to 50% germination and number of seeds per pod made significant positive contribution to the genetic variance in PC3.

Correlation studies among seven quantitative traits of okra

The levels of association among seven quantitative traits of ten accessions of Okra and their inter-specific F1 hybrids are shown in Table 5. Length of pod was very highly correlated with fruit weight with a correlation coefficient r = 0.5504. Again, fresh fruit weight was also significant and positively correlated with number of seeds per pod. However, fresh fruit weight and length of pod are significant but negatively correlated with days to 50% flowering. This indicates that, selection for pod length will also lead to increased fresh fruit weight.

Table 5: Correlation matrix for seven quantitative traits of okra (*A. esculentus* and *A. caillei*)

	LOF	DG	DF	NOB	PHAFF	NSPP	FFW
LOF							
DG	-0.5286***						
	0.0000						
DF	-0.3163**	0.4630***					
	0.0040	**0.0000**					
NOB	-0.1248^{ns}	0.4178***	0.6332***				
	0.2555	**0.0001**	**0.0000**				
PHAFF	-0.2947**	0.5061***	0.5995***	0.6066***			
	0.0073	**0.0000**	**0.0000**	**0.0000**			
NSPP	-0.1651^{ns}	0.4798***	-0.0608^{ns}	0.1256^{ns}	0.0861^{ns}		
	0.1326	**0.0000**	0.5798	0.2524	0.4330		
FFW	0.5804***	0.0154^{ns}	-0.0915^{ns}	0.1610^{ns}	0.0749^{ns}	0.2452*	
	0.0000	0.8886	0.4047	0.1424	0.4948	**0.0255**	

LOF = Length of pod; DG= Days to 50% germination; DF= days to 50% flowering; NOB =Number of branches per plant; PHAFF = Plant height at first fruiting; NSPP = Number of seeds per plant; FFW = Fresh fruit weight. Below each correlation coefficient (**bolded)** is P-value (underlined). *, **, *** = significant at P ≤ 0.05, 0.01, 0.001 respectively; Ns = not significant at P ≤ 0.05.

It was observed that accessions with low plant height matured early and produced large fruits. This is reflective of the values obtained from the correlation matrixes as pod length is significant but negatively correlated with days to 50% germination and days to 50% flowering with r = 0.5286 and – 0.3163 respectively. It is also noteworthy that tall plants with lots of branches, produced many smaller fruits. This is shown in the significant but positive correlation between plant height and number of branches per plant with a correlation coefficient r = 0.6066.

DISCUSSIONS

Variations in qualitative and quantitative agro-morphological traits of 10 accessions of okra (*A. esculentus* and *A. caillei*) and their intra-specific and interspecific F1 offspring

The results indicate that all the 61 accessions (ten parents and 51 F1s) of okra exhibited significant variation in morphological traits but minimal variation in qualitative traits. This is consistent with the findings of Omalsaad[16]. This observation implies that the latter traits are not useful for studying genetic diversity of okra germplasm. The significant differences among the quantitative traits is an indication that genetic diversity exists among the accessions as well as hybrids and thus provides a basis for selection. This is in consonance with what has been reported earlier by Ahiakpa[17] and Aladele[18], where it was demonstrated that such genetic variability exist amongst okra varieties evaluated in the respective studies.

It was found that the accessions differed significantly in the number of days to 50% flowering. It has been demonstrated that on a general basis, early flowering is detrimental for overall productivity in okra as the source to sink ratio will be potentially limited for effective photosynthesis[20].

Earliness in okra is determined by the number of days from sowing to 50% full-bloom. Differences in flowering periods among the varieties imply that their maturity periods vary. Depending on the desire of the breeder or farmer, appropriate selection can thus be made for either early or late maturing plants. Early maturing plant types for instance could be selected for areas with short rainy seasons in rain fed ecologies. Such genotypes will also be suitable for areas where farmers grow a second crop to take advantage of residual moisture after harvesting the early crop. This is supported by results obtained by Nwangburuka[3] and Oppong-Sekyere[20]. Plant height of the accessions evaluated was also significantly different. The height of the plant can potentially affect yield as those that are taller are usually more prone to wind damage in the event of heavy rainfall. Height at flowering and fruiting are of particular interest for breeding programmes because tall, thin stems increase rate of lodging near harvesting time[21] and this could culminate in loss of dry matter and a subsequent decrease in fruit yield. Similar reports have been presented by Doku[21] in rice and okra by Akinyele and Oseikita[22] and Myanmar[23].

Number of days to 50% flowering and plant height at maturity, among other agronomic characters, are some of the most variable traits that are necessary for selection aimed at improving desirable traits in okra[22]. It is suggestive from this that number of days to 50% flowering and plant height at flowering are controlled by the same genetic variables[24]. Consequently, selection for dwarf stature plants may thus be made on the F1 hybrids as they were shorter than most parental varieties evaluated in the current study. Generally, okra accessions exhibited varying degrees of fruit pubescence spanning from prickly, slightly rough (smooth), downy to little hairs on fruits but with the majority having slight pubescence. This is in contrast with the findings of Bisht[25], who found downy type of fruit pubescence to be the most pronounced followed by slightly rough while prickly fruits were the least in the okra accessions studied. This could be an indication of preference of Ghanaian farmers' for smooth fruit types and thus, disselecting the hairy types[11].

Petal colour among the accessions was either cream or yellow. This is contrary to observation made by Myanmar[23] who found petal colour to be 100% yellow for all 40 okra accessions examined. Akinyele and Akinlosotu[26] also found similar results in the okra accessions they studied. Variations were also conspicuously observed for position of fruit on main stem. The position of fruits was mainly erect, horizontal or pendulous. Most of the accessions had their fruits in the erect position on main stem as against pendulous and horizontal positioning of fruits on main stem of the accessions. This is because different genotypes have the tendency of exhibiting different growth habits, whether as a result of selection or a natural adaption mechanism. This is similar to observations made by Hanson[27] in tomato. Yellowish green was the most predominant fruit colour while green and green with red patches were least observed among the accessions. These results are similar to those found by Oppong-Sekyere[11] and Myanmar[23] in okra. Ariyo[28] indicated that the pattern of genetic variation observed in characters studied in West African okra suggests a lot of outcrossing among the taxon.

The considerable morphological variation observed in the characters of the accessions studied could perhaps, be attributed to the preponderance of out-crossing among these different accessions[11]. There were also intense variation in number of branches per plant, number of seeds per pod (fruit), stem pubescence, fruit shape, type of pod axis, branching type, fruit peduncle and fruit length. These are consistent with results reported in okra morphological diversity studies by Amoatey[29].

Genetic relationship among ten local accessions of okra and their intra-specific F1 hybrids based on cluster analysis

Variations among genotypes do not only indicate their genetic constitution but also their interactions with the environment. Hence

combining qualitative and quantitative traits gives more desirable results in cluster analysis[30]. The pattern of clustering from the cluster analysis based on both quantitative and qualitative traits, generally reflected variability in terms of genus characteristics, as all entries of cluster A are accessions of *A. caillei* and take a long time to mature and also are taller compared to those of cluster B. Separation of the entries into sub-clusters also reflected similarity based on parents and their offspring, since members of sub-subclusters were composed of parents and their offspring. Any pair of genotypes which share genetic similarity of above 95% may be considered identical[31]. By applying this criterion to the results of the correlation analysis, no pair of entries is possible duplicates.

Contribution of seven quantitative traits to total variability via principal components analysis (PCA)

The main aim for undertaking principal component analysis in genetic diversity studies is to identify variables which contribute most to genetic variability to be selected for characterizing genotypes[32]. Results of the principal component analysis showed that 83.75 % of the total variability among the okra accessions evaluated in this study was accounted for by the first three principal components thus, greater percentage of the total variance was explained by these components. This compares with 82.97 % and 75.77 % reported by earlier researchers, Ahiakpa[17] and Torres-Morán[33] who also evaluated 30 accessions of okra (*Abelmoschus* spp L.) in Ghana and 12 local cultivars of roselle cultivated in Mexico respectively. Fruit length and fresh fruit weight shared significant positive association with the first principal axes (PC1) which contributed most (45.98%) to the total genetic variance. This implies that genes controlling the inheritance of these traits accounted for most of the genetic divergence as pointed out by Adeniji and Aremu[34]. Therefore, it provides good basis for their selection for future investigations pertaining to genetic diversity of okra germplasm.

Correlation analysis of seven quantitative agro-morphological traits of okra

Fruit traits are perhaps the most important traits in okra and their improvement is of particular interest in okra breeding programmes. Results of the correlation analysis reveal strong positive association between length of pod and days to 50% germination compared with fresh fruit weight. This implies that component breeding would lead to significant increase in fresh fruit weight if these traits are considered, since they are positively correlated as pointed out by Hazra and Basu[35]. Improvement of fresh fruit weight could also be accomplished indirectly through selection for number of seeds per pods and length of pod since both traits shared strong positive association with fresh fruit weight. However, in breeding for fresh fruit weight; plant height, number of branches per plant, days to 50% germination and days to flowering would have negative effect since there is negative association with these traits. Days to first flowering was positively correlated with plant height at 50% flowering, number of branches, length of fruit and days to 50% germination Hence, breeding for earliness would have significant effect on these traits of importance.

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REFERENCES

1. Oseikita, O. S., Akinyele, B. O., Genetic analysis of quantitative traits in ten cultivars of okra. *Asian J of Plant Science.***7:** 510 – 513 (2008).
2. Oka, H. I., Distribution of genes in rice population. In: rice germplasm: Collecting, Preservation and Use.

Proceedings of the Third International Workshop, Manila, 10-12 May, 1990. IRRI, Los Baños, Philippines, pp. 41-45 (1991).

3. Nwangburuka, C. C., Kehinde, O. B., Ojo, D. K., Denton, O. A., Popoola, A. R., Morphological classification of genetic diversity in cultivated okra, *Abelmoschus esculentus* (L) Moench using principal component analysis (PCA) and single linkage cluster analysis (SLCA). *African J of Biotechnology*. **10(54):** 11165-11172 (2011).
4. Bisht, I. S., Bhat, K. V., Okra, (*Abelmoschus spp.*). In: Ram, J. Singh (Editors), CRC Press. Genetic Resources, chromosome engineering, and crop improvement, *vegetable crops*, **3:** 147-183 (2006).
5. Beeching, R. J., Marmey, P., Gavalda, M., Noirot, M., Hayson, R. H., Hughes, A. M. and Charrier, A., An assessment of genetic diversity within a collection of cassava (*Manihot esculanta* Crantz) germplasm using molecular markers. *Annals of Botany*. **72:** 515 – 520 (1993).
6. CIAT, Germplasm characterization. In: Pineda B. and Hidalgo R. Multi-Institutional distance learning course on the ex-situ conservation of plant genetic resources. (eds). 171 – 184 (2007).
7. De Vicente, M. C., Guzmán, F. A., Engels, J., Ramanatha, R. V., Genetic characterization and its use in decision making for the conservation of crop germplasm: The Role of Biotechnology; Villa Gualino, Turin, Italy – 5-7. 57pp March, (2005).
8. Staub, J. E., Serquen, J. C., Gupta, M., Selection for multiple lateral determinate cucumber genotypes. *Cucurbit Gen. Coop. Rpt*. **18:** 5-6 (1996).
9. Vogel, J. M., Rafalski, A., Powell, W., Morgante, M., Andre, C., Hanafey, M., Tingey, S. V., Application of genetic diagnostics to plant genome analysis and plant breeding. *Horticultural Sci*ence **31:** 165-167 (1996).
10. Hoogendijk, M., Williams, D., Characterizing genetic diversity of home garden crop species; some examples from the Americas. In proceedings of the second International, home Gardens Worship. 17 – 19. July 2001. Witzenhansen, Federal Republic of Germany Home gardens and in site conservation of plant genetic resources in farming systems. Eds, J. W., Watson and P. B., Eyzaguirre. pp. 34 – 40 (2001).
11. Oppong-Sekyere, D., Assessment of genetic diversity in a collection of Ghanaian Okra germplasm *(Abelmoschus spp L.)* using morphological markers. Thesis (MSc.), Department of Crop Science, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana. pp. 42-60 (2011).
12. Smith, J. S. C., Smith, O. S., Finger printing crop varieties. *Advance Agronomy* **47:** 85 – 140 (1992).
13. Soni, K., Rawat, S., Gupta, A., Yangyom, K., Pundit, S., Naik, P. K., Singh, H., Genetic characterization of *Rhodiola rosea* Using Gene Specific SSR and CAPS Molecular Markers. *J of Genetic Engineering and Biotech*. **11:** 1 – 10 (2010).
14. FAO/ UNESCO, Soil map of the world, revised legend, World Resources Report 60. FAO, Rome. pp. 146 (1994).
15. IPGRI, Okra Descriptor list. International Crop Network Series 5 International Board for Plant Genetic Resources (IBPGR), Rome, Italy (1991).
16. Omalsaad, A. K. M., Aminul I., Murshida A. J., Zahira, Y., Mohamad, O., Genetic relationship between roselle (*Hibiscus sabdariffa* L.) and kenaf (*Hibiscus cannabinus* L.) accessions through optimization of PCR based RAPD method. *Journal of Food and Agriculture*. **26(3):** 247 – 258 (2014).
17. Ahiakpa, J. K., Kaledzi, P. D., Adi, E. B., Peprah, S., Dapaah, H. K., "Genetic diversity, correlation and path analyses of okra (*Abelmoschus* spp. Moench) germplasm collected in Ghana". *Inter. J of*

Development and Sustainability. **2(2):** 1396 – 1415 (2013).

18. Aladele, S. E., Ariyo, O. J., De Lapena, R., Genetic relationship among West African okra (Abelmoshcus caillei) and Asian genotypes (*Abelmoschus esculentus*) using RAPD. *Afrian J of Biotechnology* **7:** 1426-1431 (2008).
19. Aboagye, L. M., Isoda, A., Nyima, H., Takasaki, Y., Yoshimura, T., *et al*., Plant type and dry matter production in peanut (Arachis hypogea L.) cultivars: varietal differences in dry matter production. *Japanese J of Crop Science* **63:** 289-297 (1994).
20. Oppong-Sekyere, D., Akromah, R., Nyamah, E. Y., Brenya, E., Yeboah, S., Evaluation of some okra (*Abelmoschus spp* L.) germplasm in Ghana. *African Journal of Plant Science,* **6(5):** 166-178 (2012).
21. Doku, A. H., Characterization of 18 African rice (*Oryza glaberrima*) in Ghana. An (MPhil.) thesis, Department of Nuclear Agriculture and Radiation Processing, University of Ghana. (unpublished) Pp. 87-102 (2011).
22. Akinyele, B. O., Oseikita, O. S., "Correlation and path coefficient analyses of seed yield attributes in okra (*Abelmoschus esculentus* Moench)". *African J of Biotechnology*. **14:** 1330 – 1336 (2006).
23. Myanmar, A. K., Evaluation of Okra Germplasm. ARC-AVRDC Training Report, pp. 55-76 (1995).
24. Hussain, S., Muhammad, Noor, S., Shah, A., Iqbal, Z., Response of okra (*Abelmoschus esculentus*) cultivars to different sowing times. *Journal of Agricultural and Biological Science* **01:** 55-59 (2006).
25. Bisht, I. S., Mahajan, R. K., Rana, R. S., Genetic diversity in South Asia okra. (*A. esculentus*) germplasm collection. *Annual Applied Biology*. **126:** 539-550 (1995).
26. Akinyele, I. O., Akinlosotu, A., "Effect of germination on the oligosaccharide and nutrient content of cowpea". *Journal of Food Chemistry*, **(39):** 157-165 (1991).
27. Hanson, S., Nairot, M., Some proposed procedures for obtaining a core collection using quantitative plant characterization. International Workshop on Okra genetic resources held at NBPGR. *Inter. Crop Network Series*. **5:** 89 – 94 (1991).
28. Ariyo, O. J., Genetic diversity in West African Okra (*Abelmoschus caillei* (A. Chev.) Stevels) – Multivariate analysis of morphological and agronomic characteristics. *Genetic Resources and Crop Evolution*. **40:** 125-132 (1993).
29. Amoatey, H. M., Klu, G. Y. P., Quartey, E. K., Doku, H. A., Sossah, F. L., Segbefia, M. M., Ahiakpa, J. K., Genetic Diversity Studies in 29 Accessions of Okra (*Abelmoschus spp* L.) Using 13 Quantitative Traits. *American J of Experimental Agriculture* **5(3):** 217-225 (2015).
30. Dixon, A. G. O., Nukenine, E. N., Genotype environment interaction and optimum resource allocation for yield and yield components of cassava. *African Crop Science Journal*. **8:** 1 – 10 (2000).
31. Andersson, M. S., Schultze-Kraft, R., Peters, M., Duque, M. C. and Gallego, G., "Extent and structure of genetic diversity in a collection of the tropical multipurpose shrub legume *Cratylia argentea* (Desv.) O. Kuntze as revealed by RAPD markers". *Electronic J of Biotechnology*. **10(3):** 1 – 9 (2007).
32. Johnson, R. A., Wichern, D. W., Applied Multivariate Statistical Analysis, 3rd ed. Prentice-Hall Incorporated, New Jersey (1992).
33. Torres-Morán, M. I., Escoto-Delgadillo, M., Ron-Parra, J., Parra-Tovar, G., Mena-Munguía, S., Rodríguez-García, A., Rodríguez-Sahagún, A., Castellanos-Hernández, O., Relationships among twelve genotypes of roselle (*Hibiscus sabdariffa* L.) cultivated in western Mexico. *Industrial Crops and Products*. **34:** 1079 – 1083 (2011).

34. Adeniji, O. T., Aremu, C. O., Interrelationships among characters and path analysis for pod yield components in West African okro (*Abelmoschus caillei* (A. chev) stevels). *J of Agronomy*. **6(1):** 162 – 166 (2007).

35. Hazra, P., Basu, D., "Genetic variability, correlation and path analysis in okra". *Annual Agricultural Resources.* **3:** 452 – 453 (2000).