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GENETIC DIVERSITY, HERITABILITY AND GENETIC ADVANCE IN OKRA [*Abelmoschus esculentus* (L.) Moench]

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ABSTRACT

Ten okra genotypes were evaluated at the Teaching and Research Farm, University of Maiduguri, Nigeria, during 2015 and 2016 dry seasons. The objective was to assess the degree of genetic diversity and heritability of different traits of okra. The combined analysis of variance revealed highly significant ($p<0.01$) differences among okra genotypes for plant height, days to 50% flowering, fresh pod length, fresh pod diameter and fresh weight per pod in both years. High heritability, genetic advance as percent of the mean and genotypic coefficient of variation were observed for all the studied characters except fresh pod diameter and days to 50% flowering. This indicated diverse genetic background and predominance of additive gene control for these characters, thereby providing a great scope for selection. Mahanalobis D^2 analysis allocated the 10 genotypes into four clusters. Cluster I was the highest cluster consisting four genotypes, followed by cluster II with three genotypes and cluster III two genotypes, while cluster IV was monogenotypic. Involvement of the highest yielding genotypes (Salkade, Y'ar gagure and Kwadag) in hybridization could increase novel recombinants to exploit transgressive segregates with high genetic yield potentials.

Keywords: *Abelmoschus esculentus*; variation; heritability; pod yield

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INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench] also known as Lady's finger, is of the family Malvaceae (*et al*Kishor *et al*., 2016). Okra is discovered to have originated in the Tropical Africa, and had extensively disseminated to Southern Europe, Asia, America and developing countries (Muhammad *et al*., 2013). According to FAO, the five highest okra producing countries in the year 2008 were Nigeria, Iraq, Côte d'Ivoire, India and Sudan (FAOSTAT, 2010). In Nigeria, okra ranks third among fruit vegetables according to production and consumption, following tomato and pepper (Ibeawuchi, 2007). The local cultivars differ in their growth habit such as leaf size and arrangement, branching, height, fruit characteristics and maturity period. Growth pattern of okra cultivars are similar during vegetative phase, although, the more vigorous ones have higher leaf area and dry matter accumulation (Akanbi *et al*., 2010).The immature fruits consumed as vegetables are used in soups, stews and salads, sliced, fried or boiled (Akanbi *et al*., 2010; Daniela *et al*., 2012). Okra fruit has easily digestible fibre content, fat free and low in calories (Kumar and Sreeparvathy, 2010; Reddy *et al*., 2013). Based on its tender

texture and mucilaginous, okra fruits can be utilized in soup thickening (Ijoyah and Dzer, 2012; Das *et al*., 2013). The edible portion of the fruit contains about 86.1% water, 9.7% carbohydrate, 1.0% fiber, 2.2 % protein, 0.8% ash and 0.2% fat (Saifullah and Rabbani, 2009). The green fruits are also rich sources of calcium, potassium, vitamins, and other minerals. Okra is also tolerant to a wide range of climatic conditions and cultivated in all agro–ecology of Nigeria.

The worth of germplasm collection depends on the number of accessions contained and their diversity, which are imperative for a reasonable utilization of plant genetic resources (Olaoye *et al*., 2009; AdeOluwa and Kehinde, 2011). Genetic diversity is the variability among different genotypes of a species (Bello *et al*., 2012ab). Genetic diversity plays a major role in crop improvement for identification of distinctive accessions vital for the curators of gene banks (Bello *et al*., 2011; Osekita and Akinyele, 2008). In any diversity studies, morphological characterization is been recommended as the first step to be taken before in–depth molecular and biochemical analyses are employed (Akash *et al*., 2013). Several researchers observed high degree of morphological variation among the West African okra accessions (Adeniji, *et al*., 2007; Akanbi *et al*., 2010; AdeOluwa and Kehinde, 2011). The success of any progress in a breeding programme however, is dependent not only on the magnitude of genetic variability present in that population, but also on the extent to which its desirable characters are heritable (Olawuyi *et al*., 2015, Bello *et al*., 2014ab). The variability available in a population can be partitioned into heritable and non-heritable components with aid of genetic parameters, such as, genotypic coefficient of variation, heritability and genetic advance, which also serve as a basis for selection (Muluken *et al*., 2016; Seth *et al*., 2016). Selection methods and the expected genetic response to selection in crops are determined by the magnitude of heritability estimate of the character for which selection is to be made. Cluster analysis is also a powerful tool to measure genetic divergence among genotypes in any crop. As okra production exhibit a major economy role of a nation, selection of high yielding edible fruit cultivars is very important. This study was conducted to assess the degree of genetic diversity, heritability and genetic advance of different traits of okra cultivars in the non–stress irrigation environments of Sudan savannah of Nigeria, with the view to formulating a breeding plan for selection and improvement.

MATERIALS AND METHODS

Experiment site and collection of planting materials

Field irrigation experiments were conducted at the Teaching and Research Farm, University of Maiduguri (11^0 53′N, 16′E) in the Sudan savannah of Nigeria, during 2015 and 2016 dry seasons. Ten okra cultivars of which four (Kwalpuku, Kwadag, Mola kwadag and Composite) were obtained from Borno State Agricultural Programme, Maiduguri, Nigeria and six cultivars (Yar'duwi, Salkade, Yar'gagure, Y'ar kwami. Kwadam and Lai-lai) sourced from Gagure Gulani Local Government Area of Yobe State, Nigeria. The morphological descriptions and the ten okra cultivars are shown in Table 1.

Experimental Layout and Cultural Practices

The field experiment was laid out in Randomized Complete Block Design with three replications. The plot was $216m^2$, divided into 33 plots of 2m x 2m with 1m spacing between replications, and 0.5m between treatments. Weeding was carried out manually at 3, 6, and 9 weeks after sowing (WAS). A compound fertilizer, N.P.K. 15:15:15 was

applied at the rate of 60kg N/ha in two doses, first at three weeks after planting and then at flowering. Two millilitres of Ultracide 40EC insecticide in 15 litres was applied fortnightly to control insect pests. Light watering was applied using a watering can at every morning and afternoon. This was continued for a week for rapid and well establishment of the germinated seedlings.

Table 1. The ten okra cultivars and morphological descriptions

	Cultivars	Morphological descriptions of okra plant
1	Y'ar duwi	It has short pale green stem, few flowers, finger leaves and small slim fruit with no spine.
2	Salkade	It is a tall cultivar with broad leaves, red stem and few flowers, long fruit with small diameter. The fruit is long, white and smooth with small diameter.
3	Y'ar gagure	It has a pale green spiny fruit, broad diameter and long stem. It also has red and sparsely flowers.
4	Composite	It has dark green fruit of medium size with medium diameter. It also has green stem and broad leaves with many flowers.
5	Kwalpuku	It has short stem, small leaves with many flowers and spiny fruits.
6	Kwadag	It has long stem with few flowers, big pods with spine and red stem.
7	Mola kwadag	It has short green stem with small finger–like leaves. It also has many flowers with big pods.
8	Y'ar kwami	It has dark green fruit with many flowers and big pods with spines.
9	Kwadam	This cultivar has short and white stem, medium leaves and spiny pods.
10	Lai-lai	It is runner–like, short, dark green with medium pod diameter. It also has white stem and small leaves with many flowers.

Data collection

Six (6) plants were randomly selected from each plot for the assessment of the okra quantitative characters. Data were recorded on days to 50% flowering, number of primary branches per plant, number of pods per plant, fresh pod length, fresh pod diameter (cm), plant height, fresh weight per pod (g) and fresh pod yield per plant (g).

Data analysis

Data collected in respect of each character were first computed with analysis of variance (ANOVA) separately before a combined ANOVA across the two-year growing seasons, using PROC GLM model of SAS (SAS Institute, 2011) to determine mean squares for each character. The SAS GLM procedure used for the ANOVA was mixed model. Replication was treated as a random effect, while cultivars as fixed effects. The degree of variation was determined using % coefficient of variation $P< 0.05$. Differences in character means were also measured using Least Significant Difference (LSD). Genotypic and phenotypic variances were estimated as suggested by Johnson *et al.* (1955). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and were determined following the formula suggested by Burton (1952). The heritability in broad sense was estimated as suggested by Johnson *et al*. (1955). The expected genetic advance estimate for the characters under selection was calculated as suggested by Allard (1960). Genetic advance in percentage of mean was calculated as suggested by Comstock and Robinson (1952). Mahalanobis' D^2 statistics ((Mahalanobis 1936)) and its auxiliary analysis were used to assess genetic divergences among the okra genotypes, as suggested by Rao (1952).

RESULTS AND DISCUSSION

The combined analysis of variance exhibited highly significant ($p<0.01$) differences among okra genotypes for plant height, days to 50% flowering, fresh pod length, fresh pod diameter and fresh weight per pod in both years (Table 2). This is in conformity with

the findings of Nwangburuka *et al*. (2012). The very large means squares recorded for these characters is an indication that the genetic components of the material are quite distinct, and any improvement sort could be directed to these characters. This is supported by the findings of several researchers (Akinyele and Osekita, 2006; Nwangburuka *et al*., 2012; AdeOluwa and Kehinde, 2013; Muluken *et al*. (2016).fresh weight per pod Furthermore, the genotypes revealed significant (P<0.05) differences for number of pods per plant and fresh pod yield per plant. However, non-significant differences among the genotypes for number of primary branches per plant showed that the genetic components of the parental material are intact. The analysis of variance indicated the presence of variability among the okra genotypes for most of the characters studied. This variability can therefore be exploited through selection to improve the crop for the desired characters. This result is in agreement with these workers (Salesh *et al*., 2010, Nwangburuka *et al*., 2012; Hazem *et al*., 2013; Amoatey *et al*., 2015). The sources of variation however, were non-significant for all the characters across years. The first order interaction of genotype × year was significant for all the characters. This implied that environment in the utilization of natural phenomenal was expected to necessitate the wide variation in these characters, which are regarded as the main components of crop yield. The yield potential of okra is to produce more pods per plant, and this can be realized by timely harvest of the fresh fruits to allow for more branches to be developed. This will invariably, enhance the crop yield. This is in accordance with the findings of Akinyele and Osekita (2006).

Mean performance of pod yield and yield contributing characters

Different okra genotypes were significantly differed for days to flowering (Table 3). The highest days to 50% flowering (50.69 days) was observed in Y'ar gagure, while the lowest (42 days) was recorded in Kwadam. The mean days to 50% flowering were 46.82 days, and 50% genotypes produced more than the mean days to anthesis. It indicated that the examined genotypes were morphologically different from each other in flower bearing habit as earlier reported by Muluken *et al*. (2016) . Different genotypes of okra exhibited statistically significant variation for plant height. The tallest status was attained in Kwadag and the shortest in Composite genotype. The mean plant height was 1.25m with Y'ar gagure and Kwadag only accomplishing more than the mean height. This also implied that the genotypes were phenotypically dissimilar as previously observed by Nwangburuka *et al*. (2012Number of primary branches per plant also varied decidedly among genotypes with Salkade having the highest number and Kwadam the least. Consequently, Salkade had the highest number of primary branches followed by Kwadag, Y'ar gagure and Y'ar kwami, which were above the mean of 2.92.

In most cases, the number of primary branches had shown markedly difference at early stage of okra growth as earlier noted by Jagan *et al*. (2013). The mean number of pods per plant was 28.03, and 50% of the genotypes achieved more than the mean. Y'ar gagure was superior with the highest number of pods per plant, followed by Kwadag, Salkade and Lai–lai in that order. Maximum number of fresh pod length was achieved in Salkade, whereas Kwalpuku had the least. This difference could be the variation in the plant height and number of bearing internodes in the genotypes. The mean number of fresh pod length was 13.08 and about fifty percent okra genotypes produced the longest pods more than the mean length.

Table 2. Mean squares from combined ANOVA for fresh pod yield and other related characters of okra genotypes under irrigation between 2015 and 2016 dry seasons in Maiduguri (Nigeria)

Sources of variation	Plant height (m)	Days to 50% flowering	Primary branches per plant (no.)	Pods per plant (no.)	Fresh pod length (cm)	Fresh pod diameter (cm)	Fresh weight per pod(g)	Fresh pod yield per plant (g).
Year (Y)	6.61	8.22	22.88	11.54	20.92	6.25	6.63	9.67
Rep (Year)	4.44	192.27**	187.63**	4.867*	6.54*	145.74**	79.22**	1221.63**
Genotypes	4286.82**	862.29**	174.11**	39.19**	5.85**	67.66**	65.44**	2376.11**
Genotype × Year	72.97*	63.82*	54.65*	41.53*	34.74*	38.37*	38.45*	45,53
Error	8.28	24.59	4.15	1.14	0.34	4.11	7.21	5.89

*,**, significant at P< 0.05 and P< 0.01 respectively

Table 3. Combined mean performance of ten okra genotypes for fresh pod yield and other related characters under irrigation between 2015 and 2016 dry seasons in Maiduguri (Nigeria)

Genotypes	Days to 50% flowering	Plant height at harvest (m)	Number of primary branches per plant (no.)	Number of pods per plant (no)	Fresh pod length (cm)	Fresh pod diameter (cm)	Fresh weight per pod(g)	Fresh pod yield per plant (g).
Y'ar duwi	43.11	1.14	2.84	25.34	12.34	1.56	15.96	479.38
Salkade	50.33	1.44	4.23	33.75	14.88	1.22	16.23	598.65
Y'ar gagure	50.75	1.39	3.51	34.45	14.73	1.83	16.56	616.97
Composite	44.23	1.11	1.89	22.54	12.52	1.48	14.73	428.62
Kwalpuku	43.00	1.18	3.18	23.92	11.49	1.51	13.14	488.38
Kwadag	49.31	1.49	3.75	34.35	14.37	1.84	16.83	622.67
Mola kwadag	49.11	1.21	2.66	24.88	12.84	1.48	14.64	457.92
Y'ar kwami	45.34	1.18	3.33	25.18	13.37	1.52	14.34	431.63
Kwadam	45.11	1.22	1.67	28.23	13.64	1.44	15.11	580.38
Lai–lai	47.93	1.16	2.12	28.64	11.59	1.52	14.98	532.85
Mean	46.82	1.25	2.92	28.03	13.08	1.54	15.25	523.75
Range	7.33	0.38	2.56	11.91	3.39	0.62	3.68	194.05
SE±	11.849	6.111	2.759	6.654	6.149	11.234	10.171	11.73
LSD α 0.05	2.23*	1.11*	1.45*	4.62**	2.14*	1.01*	1.43*	3.57
CV%	4.36	7.82	6.39	4.92	10.52	7.45	7.18	6.83

This parameter has been discovered to be significantly differed from accessions to accessions, as it also expresses their separate identity (Nwangburuka *et al*., 2012; Hazem *et al*., 2013; Amoatey *et al*., 2015). The mean fresh pod diameter was 1.54 cm with only Kwadag, Y'ar gagure and Y'ar duwi had more than that mean. Based on the differences in plant height, fruit length fruit and other morphological structure of the genotypes, fresh weight per pod varied from one another among the genotypes. With the mean of 15.25 for fresh pod weight, 40% of the genotypes produced more than the mean. The pod length of okra that varied from genotype to genotype possibly due to variation in days to anthesis and other morphological behaviour. The mean fresh pod yield per plant was 523.75gand Salkade, Y'ar gagure and Kwadag produced yield more than the mean pod yield. The variation was noticed probably due to variation in the yield contributing characters of the okra genotypes.

Estimates of variability components

Estimated variability components viz. Phenotypic, genotypic and environmental variances, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as percent of means (GA%) for 8 okra characters are presented in (Table 4).

Phenotypic and genetic variances

Large magnitudes of phenotypic variance were calculated for days to 50% flowering (233.7), followed by plant height (72.8) and fresh pod yield per plant (14.8), while the least value (0.2) was realized for fresh pod diameter (Table 4). The genotypic variance ranged between 0.02 and 36.0 in fresh pod diameter and plant height, respectively. The highest environmental variance of 49.9 was obtained for plant height, whereas fresh pod diameter (0.2) had the lowest. This environmental variance influenced the development of pod on plants, their numbers per plant as well as the ultimate pod yield per plant in this study. Interaction of phenotypic and genotypic variances revealed the greatest value for days to anthesis (220.4), while number of pods per plant (0.2) had the lowest. Phenotypic variances were higher than genotypic variances revealing the countenance of environmental factors for these characters. This trend of variation is in conformity with the findings of Ehab *et al*. (2013) and Magar and Madrap (2009).

High value of PCV and GCV with low level of deviation between the two genetic components showed less influence of environment on the phenotypic expression (Table 4). This inference is supported by Muluken *et al*., (2016). The phenotypic (PCV) and genotypic coefficient of variation (GCV) ranged from 2.4%-48.5% and 1.1-33.3% respectively, for fresh pod diameter and fresh pod yield. Many researchers discovered that genotypes and the corresponding variation not only owing to genotypes, but also to the environmental effects (Thirupathi *et al*., 2012; AdeOluwa and Kehinde, 2013; Ehab *et al*., 2013; Adekoya *et al*., 2014). According to Sivasubramaniah and Meron (1973), GCV and PCV values less than 10% are regarded to be low, values from 10% to 20% are medium, while values higher than 20% are considered as high, Regarding the degenotypeation of GCV and PCV obtained in this research, fresh pod diameter and number of

primary branches had the least values of less than 10% for both GCV and PCV. This showed a narrow range of variation and impeding scope for selection for these characters. This observation is also an indication of a measure of crop productivity, and numerical classifications of the genotypes were expected to be discriminated. Many researchers had similar findings for West African okra accessions (Nwangburuka *et al*., 2012; AdeOluwa and Kehinde, 2013; Adekoya *et al*., 2014). Low GCV and PCV value of characters on the other hand suggested the greater environmental impact on these characters thus; selection on account of phenotypic source would not be valuable for the genetic improvement of crops (Chaurasia *et al*., 2011; Bharathiveeramani *et al*., 2012; Das *et al*., 2012; Sankara and Pinaki, 2012; Thirupathi *et al*., 2012; Ehab *et al*., 2013; Kishor *et al*., 2016]. Contrarily, days to 50% flowering only had medium values for both coefficients of variations (Chaurasia *et al*., 2011). This implied that these characters are influenced by genetic effects. Hence, these characters are amenable to selection for further crop improvement. However, plant height, fruit length, number of primary branches, number of pods per plant, fresh pod length, fresh weight per podand fresh pod yield per plant had high values greater than 20% at both coefficients of variations, with degree of difference between the two considerably low. This is in line with Ehab *et al*. (2013). Many researchers however, submitted that high PCV and GCV implied less manifestation of environmental effects on such characters, which possibly enhance higher prospect of improvement via selection breeding (Salesh *et al*., 2010; Bharathiveeramani *et al*., 2012; Nwangburuka *et al*., 2012; Swati *et al*., 2014; Kishor *et al*., 2016). Therefore, selections of desirable characters by exploiting high phenotypic and genotypic values were most likely useful in improving the characters in the hybridization programme.

Estimate of broad sense heritability

Estimate of heritability in broad sense ranged between 25.84% for number of pods per plant to 93.84% for fresh pod yield per plant (Table 4). According to (Robinson *et al*., 1955) heritability is classified as low (0-30%), moderate (31-60%) and high > 60**%.** In this study, heritability in broad sense was highest (>60%) for days to 50% flowering, plant height, pod length, pod weight, pod diameter and pod yield. These characters appeared to respond efficiently to selection pressure. When heritability is 80% or greater for a character, selection is fairly easy for that character. Therefore, selection for these characters could lead to appreciable increase in okra pod yield. A very high heritability also indicated high genetic base. A close relationship between the genotype and phenotype is probably based on small environmental effects (Jagan *et al*., 2013; Muluken *et al*., 2016). Moderate heritability value was recorded for number of primary branches. Low broad sense heritability estimate however, was observed for number of pods per plant. This suggested that these genotypes cannot be improved through direct selection for these characters. If a character has a range of medium to high heritability, selection owing to individual performance would permit rapid improvement. Moderate heritability suggested improvement through selection. Low heritability also suggested ineffective direct selection in improving the characters because of masking effect of the environment (Nwangburuka *et al*., 2012; Bello and Olawuyi, 2015; Muluken *et al*., 2016).

Table 4. Estimates of genotypic variance (δ^2g) genotype × year interaction (δ^2gy) variance, phenotypic variance (δ^2p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) for fresh pod yield and other variables in ten okra genotypes under irrigation between 2015 and 2016 dry seasons in Maiduguri (Nigeria)

Characters	δ^2p	δ^2g	δ^2e	δ^2gy	PCV (%)	GCV (%)	Heritability H^2(bs) (%)	Genetic Advance (GA)	Genetic Advance as % of mean
Days to 50% flowering	233.7±19.3	16.72±4.3	11.2±2.7	220.4±129.2	18.1	17.7	86.7	8.7	16.1
Plant height	72.8±29.5	36.0±31.1	49.9±12.5	122.2±38.1	24.2	18.9	72.54	20.8	24.3
Number of primary branches per plant	8.7±3.9	6.6±1.9	2.5±0.6	7.5±4.5	29.9	24.8	48.41	7.4	20.2
Number of pods per plant	0.8±0.4	0.7±0.1	0.3±0.1	0.2±0.1	27.3	21.9	25.84	18.6	28.7
Fresh pod length	3.8±2.3	3.6±0.1	0.9±0.2	0.70±0.1	22.5	20.7	79.98	6.8	37.5
Fresh pod diameter	0.2±0.1	0.2±0.1	0.2±0.1	27.5±2.8	2.4	1.1	84.54	7.4	6.9
Fresh weight per pod	2.5±1.4	1.6±0.9	8.8±2.2	34.1±2.6	22.5	20.9	71.30	16.1	41.6
Fresh pod yield per plant	14.8±2.4	12.1±2.1	13.4±2.2	73.9±5.2	48.5	33.3	93.84	103.3	51.8

Estimate of genetic advance and expected genetic advance

According to Johnson *et al*. (1955), genetic advance as percent mean was classified as low (0≤10%), moderate (10≤20%) and high (≥20%). According to this ranking, plant height, number of primary branches, number pods per plant, pod length, pod weight and pod yield per plant had genetic advance of ≥20% (Table 4). This showed the role of additive gene action for these characters. Days to 50% flowering and pod diameter revealed moderate and low genetic advance, respectively. Accordingly, the result in this study indicated that expected progress from selection of the genotypes ranged from 16.1% for days to 50% flowering to 51.8% for pod yield. This corroborates with studies of (Olawuyi *et al*., 2015; Hazem *et al*., 2013).

The proportion of heritable variation was not sufficient to ascertain the genotypic coefficient of variation alone, but with the assistance of heritability estimates and genetic advance expressed as percentage of mean. Both high heritability in conjunction with genetic advance estimates, not only provide adequate information on each parameter, but also depicted an expression of additive genetic effect as well as genotypic response to selection (Pradip *et al*., 2010; Sibsankar *et al*., 2012). High heritability coupled with genetic gain as percent of the mean were observed for all the studied characters except fresh pod diameter and days to 50% flowering. This indicated diverse genetic background thereby providing a great scope for selection. Again, this suggested the predominance of additive gene control for these characters of studied, rather than the environment. Therefore, selection could be based on the phenotypic expressions for okra yield improvement (Muluken *et al*., 2016). While moderate heritability in consonance with high genetic advance were discovered for number of primary branches, low heritability and high genetic advance values were noted for number of pods per plant. This is in line with the findings of Jagan *et al*. (2013). High heritability value detected for number of primary branches accompanied with moderate genetic advance showed no influence of environment on the expression of the character similar to the report of Bozokalfa *et al*. (2010) This may be on account of higher environmental impact on the expression of such characters. This could restrict the scope of improvement by selection, as a consequence of the occurrence of non-fixable or non-additive (epistatic and/or dominant) effects. A situation where the characters had both low heritability and genetic advance, special techniques including recurrent selection and hybridization should be followed (Jagan *et al*., 2013).

Genetic diversity

Table 5 shows the components of four different clusters with their consistent genotypes and numbers. Cluster I was the highest cluster consisting four genotypes, followed by cluster II with three genotypes and cluster III two genotypes, while cluster IV was monogenotypic. The most diverse genotypes Mola kwadag, Y'arkwami, Kwadam and Lai-lai were from cluster I. These clusters pattern revealed that geographic diversity had no direct relationship with genetic diversity. Genetic divergence in okra accessions using cluster analysis was earlier reported by researchers (Akotkar *et al*., 2010; Das *et al*., 2012; Umrao *et al*., 2014; Seth *et al*., 2016). Generally, the genotypes pattern of distribution

from different geographical zones into distinct clusters was random. This could be the frequent and free exchange of genetic makeup among the plant breeders and farmers of different agro-ecological regions. Besides, the differential selection pressure based on regional preference enhanced greater similarity in the genotypes. The absence of association between geographical distance and genetic diversity showed that forces including exchange of genetic stock, spontaneous mutation, genetic drift, natural and artificial selection were expected to be responsible for genetic diversity rather than geographical origin (Pradip *et al*., 2010; Seth *et al*., 2016). Thus, selection for hybridization of genotypes should be on account of genetic divergence rather than geographic diversity.

Table 5. Clustering pattern of 10 okra genotypes by Tocher's method

Cluster	Members	Okra genotypes
I	4	Mola kwadag, Y'arkwami, Kwadam and Lai-lai
II	3	Y'arduwi, Salkade and Y'argagure
III	2	Kwalpuku and Kwadag
IV	1	Composite

Figure 1 show widely differed inter-cluster distances among the four clusters of okra genotypes. The inter-cluster distances however, were greater than the intra cluster distances, implying wider genetic diversity in the genotypes of different groups. The intra-cluster distance among the 10 genotypes showed least value between Cluster IV and I (4.57) exhibiting close associations among the genotypes in these clusters (Table 8). The highest intra-cluster value was noted between cluster III and I (14.2) followed by 9.83 between Cluster IV and III, indicating that the genotypes in these clusters were of greatest divergence. Thus, cross breeding among the genotypes in these clusters might result to transgressive segregations in the generation progress as earlier suggested by Umrao *et al*. (2014) and Seth *et al*. (2016).

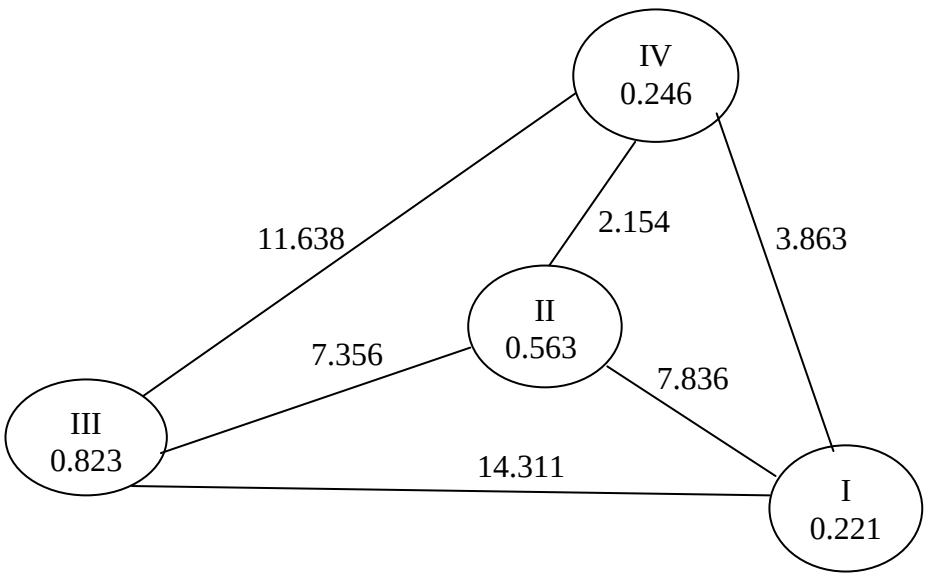

Figure 1. Inter and intra cluster distance in different clusters

The maximum inter-cluster distance between cluster III and I was 14.311, followed by cluster IV and III (Figure 1). Medium inter-cluster distance between cluster II and I was 7.836, followed by cluster III and II with 7.365. The least distance between cluster IV and I was 3.409, followed by cluster IV and II (2.154). The highest value of inter-cluster distance showed that the genotypes of cluster III was far apart from that of cluster I. The greater cluster distance between cluster IV and III also suggested that the genotypes of each pair of the clusters were highly diverse. The medium inter-cluster distance between cluster II and I, followed by cluster III and II however, revealed reasonable genetic divergence in the genotypes. The low inter-cluster distance between cluster IV and I, followed by cluster IV and II implied moderate genetic divergence in the genotypes (Figure 1). Larger intra and inter-cluster distances indicated greater genetic diversity among the genotypes, respectively within and between clusters. Consequently, the lowest intra and inter-cluster distances implied a very close of the two clusters as well as within the cluster of the genotypes (Pradip *et al*., 2010).

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