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ASSESSMENT OF GENETIC DIVERGENCE IN KENAF (*Hibiscus cannabinus* L.) GENOTYPES USING AGRO-BOTANICAL CHARACTERISTICS AND MULTIVARIATE ANALYSIS

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SUMMARY

Agro-botanical characteristics of 33 kenaf genotypes were investigated for genetic divergence using agro-botanical and multivariate analyses. The genotypes were evaluated and data analyzed across two seasons in 2014. Multivariate analysis was used to identify the genetic variation among the genotypes and the extent of contribution of each factor to the variation. Wide variation observed in the genotypes' agro-botanical characteristics proved their genetic diversification. Stems and leaves of the plants were predominantly green. Leaves of most genotypes were palmate, deeply lobed and had serrate margin. First 6 principal component axes showed strong discriminating ability among the characters, and accounted for 81.5% of the total variance. Principal component axes (PCAs) I and II had eigen values greater than unity and the difference between the 2 axes were (1.526). The discriminating ability of PCA I was strongest but did not adequately distinguish the genotypes. It accounted for 26.7% due to basal, middle and top stem diameter. Principal component II which accounted for 16.5% described variation in the flowering pattern whereas PC III described variation due to yield components accounting for 13.0%. The basal, middle and top stem diameters, days to first, and 50%, flowering, bast and core dry weights respectively contributed large variability as 0.8832, 0.8866, 0.8963, 0.8413, 0.6761, 0.8063 and 0.8138 as eigen vectors. The genotypes were early maturing and plant height in four clusters ranged from 201.50 cm to 264.83 cm. Genotypes that clustered into groups I and II are good candidates for fibre production. PCAs I and II adequately distinguished 32 of the 33 genotypes suggesting a high level variability among the genotypes. Genotypes AU-24524[3], A-60-282-5[1], AC-31324[4], Tianung 2 and Ex-Shika loaded the first 3 principal axes. Genotypes 2QQ 1[3] and AU-60-282[6] were most distinct in all the 3 configurations.

Key words: Accessions discrimination, agro-botany, diversity, fibre, genoype, kenaf, principal component analysis

Key findings: Crop diversity represents a rich source of materials potentially useful in breeding. Knowledge of variability in genotypic characteristics of kenaf is important for effective breeding programme for commercial production and utilization of the crop. This study, therefore, investigated 33 kenaf genotypes for diversity using botanical characteristics, growth and flowering patterns as well as yields to identify, characterize and group distinct genotypes for selection for genetic and breeding programmes of kenaf.

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INTRODUCTION

Kenaf (*Hibiscus cannabinus* L. 2n = 36) is a short day annual herbaceous plant belonging to the Malvaceae which is a moderate size family with 50 genera and 1000 species. The family is notable for both its economic importance. Taxonomically, the crop is classified in the Furcaria section of Hibiscus containing 45 species that are morphologically related (Taylor, 1995; Su *et al*., 2004). The existence of semi-wild kenaf in Africa (especially Kenya and Tanzania) indicates that the crop originated from Africa. Kenaf is grown as a subsistence crop in Nigeria, but it is gradually becoming a major crop in the country for its numerous uses. The crop is currently gaining popularity as many farmers are increasingly aware of its economic potentials. CTA (1996) reported that it has provided raw materials for the manufacture of bags and as composites in making high quality paper and newspaper. The bast fibre is used for producing gunny bags, clothes, ropes, canvas and carpets whereas its core fibre is useful as building materials, soil modifiers, active carbon, absorbent and paper. Roots, leaves and seeds of kenaf are processed for livestock feed, human food, oil, medicine, fertilizers and dyeing materials (Liu, 2000; Webber and Bledsoe, 2002). Kenaf has also been examined for its possible uses in bio-energy sector (Alexopoulou *et al*., 2004).

Kenaf has round stem that is 1-2 cm in diameter and it grows between 2-4 m tall. The leaves may be lobed or un-lobed depending on the variety and position on the plant as well as age. It is a cleistogamous and monoecious plant (Mohamad *et al*., 2011), and its fruits occur in capsules of 2 cm diameter containing several seeds that take 45 days for ripening. Two kinds of fibres, namely the long fibre and short fibre, are obtainable from kenaf plants. The long fibre types are mainly in the thin bark (cortical layer) called bast fibre, whereas the short fibres are in the ligneous core (pith).

Multivariate statistical analysis and numerical taxonomy has been used in summarizing and describing the variability in germplasm collections in the Malvaceae family. Denton and Nwangburuka (2012) studied morphological diversity among *Corchorus olitorious*. Ariyo (1987); Nwangburuka *et al*. (2011) investigated okra accessions using principal components and single linkage cluster analyses. Ariyo (1993) used factor, principal component and canonical analyses to study the extent of genetic diversity among 30 accessions of West African okra. The author found large genetic variability among okra accessions. Genotype × traits which evaluates cultivars based on multiple traits and for identifying lines that are superior (Mishra *et al.*, 2015). Principal component analysis (PCA) is a descriptive method which shows the pattern of covariation of characters among the individual data by removing inter-correlation among variables and allows a multi-dimensional relationship to be plotted on two or three principal axes (Hair *et al*., 1998). PCA relies upon the eigen vector decomposition of the covariance or correlation matrix (Granati *et al*., 2003). In the eigen vector decomposition by correlation matrix, any trait that does not significantly correlate with the principal component scores is not considered to be vital in the classification process (Kamara *et al*., 2003). Cluster analyses are used to complement the results of multivariate analysis. Correlation analysis has been used to measure the degree of relationship between variables (Falconer, 1989) whereas path coefficient analysis measures the direct of one trait upon another trait and permits the separation of correlation coefficients into components of direct and indirect effects (Li, 1977). Akinyele and Osekita (2006) used correlation and path coefficient analyses to study seed yield attributes in okra (*Abelmoschus esculentus* L.) Moench. Ogunkanmi *et al.* (2010) demonstrated the presence of inter and intra genetic variability among 40 accessions each of *Corchorus incisifolus* and *Corchorus olitorius*, using molecular markers.

Identification and knowledge of similarity and dissimilarity among genetic resources is critical to find and select suitable resources adapted to specific environments for effective breeding programs. In the same vein, promotion and recommendation of crops to farmers for commercial cultivation is appropriate only after thorough research and information on the crops. Such information is obtained by evaluation of the available crops'

genotypes. However, the crop's genotypic characteristics of the crop is still poorly understood because information on this aspect is very limited. This has made the identification of the various genotypes of the crop difficult. It has also retarded effective conservation and utilization of the numerous varieties of the crops that are available for either breeding programs or cultivation for commercial purposes (Zhou *et al*., 2002). Therefore, this study attempted to evaluate kenaf genotypes in order to understand their genetic divergence using agro-botanical, agronomic, flowering and yield characteristics. The study also classified the genotypes for further selection and other useful kenaf breeding program in Nigeria.

MATERIALS AND METHODS

A total of 33 kenaf genotypes were obtained from Institute of Agricultural Research and Training, Nigeria. The genotypes comprised of 30 exotic lines obtained from different parts of the world, especially United States of America and Mexico, one indigenous line and two varieties developed by Institute of Agricultural Research and Training, Nigeria. The genotypes were evaluated in dry season (January to May) and rainy season (May to September), 2014. The dry season evaluation was done in a fadama environment under irrigation. Seeds of each genotype were planted in a two-row plot, 5 m each, at a spacing of 25 cm within row and 1 m between rows in the field in each of the 2 seasons. The experiment was laid out in randomized complete block design with three replications in each season. Four seeds were sowed per hill and thinned to 2 per stand to adjust the population density to 80,000 plants ha^{-1} at 3 weeks after planting. About 60 kg ha^{-1} NPK fertilizer was applied at four weeks after planting. The plots were kept weed free throughout the study. Each plot was divided into 2 halves; plants on one half was observed and harvested for fibre at 50% flowering stage whereas those on the second half were harvested for seed. Both the fibre and the seed were harvested and processed appropriately.

Plants of each accession were observed for 32 traits including qualitative botanical characteristics, flowering pattern (days to first, and 50%, flowering), quantitative growth such as plant height, stem diameter (basal, middle and apical), length of internode and number of nodes as well as yield including basal core diameter, and seed, core and fibre weights. Data were collected from 10 randomly selected plants from each plot. The qualitative botanical parameters were score by visual assessment. Plant height (PH) was measured from the ground level to the top (base of the apical leaves) of the plants. The stem diameter (BSD), middle stem diameter (MSD) and top stem diameter (TSD) were respectively measured by a venier callipers at 15 cm above the base, mid-length and top part of the plant. Days to first flowering (DTFF) and days to 50% flowering (D50%F) were number of days from planting to emergence of first flower and day when 50% of the plants per plot flowered. Other parameters taken were length of internode (LINT) as the distance between two consecutive internodes at the middle of the plant, number of nodes (NND) taken by counting the nodes on a plant. Leaf length (LLGT) and petiole length (PLGT) were respectively taken as distance from apex of a leaf to base of the leaf, and distance from base of the leaf to point of attachment of the leaf to the plant (node). Yield data such as basal core diameter (BCD) was obtained with vernier callipers at 15 cm up the base of the plant, seed weight (SWT), bast dry weight (BDWT) and core dry weight (CDWT) were collected by weighing. The growth data were taken when the crops were 80 days old.

Fibres were extracted from the plants by retting process after cutting at the ground level. The freshly cut kenaf bundles were assorted by plot, tagged and soaked in a running stream and allowed to float. The soaked kenaf were prevented from being washed away. The process was kept for 14 days after which the fibre was stripped from core manually and washed in clean water to ensure fibre quality. The fibre was dried by direct sunshine for 5 days. Fibre dryness was taken by hand feeling. Dry plants with the pods were cut just before the seeds shattered and threshed for seed recovery.

The data collected were subjected to multivariate analysis using the PAST: Palaeontological Statistics Software Package (2001) to identify genetic variation among the

genotypes, the extent of genetic variation and contribution of each factor and character to the variation. The variance was decomposed into principal component axes. Eigen-values and factor loadings obtained from the PCA were used to determine the relative discriminative power of the axes and their associated characters. Correlation matrix was used as the eigen vectors decomposition in the PCA in this study. The relationship between the first PC and each of the other three PCs were described with bi-plot procedure and the genotypes were subjected to cluster analysis to show their genetic relatedness with SAS (2004).

RESULTS

Botanical characterization

Wide variation observed in the kenaf genotypes is described in Table 1. Stems and leaves of the plants were predominantly green. However, a few genotypes had stem colors that were different from green. Also, few plants had leaves with red spots (12%). The frequency of the plants with different green color were in the order of greenish brown (8%), greater than light brown (5%), greater than purple (3%) and purple greater than dark brown. Leaf shape of most genotypes was palmate. Serrate leaf margin was common among the genotypes and most genotypes' leaves were deeply lobed. Only few genotypes had leaves that were either shallow (32%) or not lobed (32%). The lobed plants had seven leaf lobes. Other descriptions of the leaves of the genotypes were shown in Table 1.

Principal components analysis

Tables 2, 3 and 4 presented data on eigen values, percentage variance and eigen vectors loadings for each character and each genotype. Table 2 showed that only 6 principal axes had eigen values greater than one, and accounted for about 81.5% of the total variance. Only PCs I and II had eigen values greater than one and were 1.526 difference from one another.

Table 3 showed the eigen vectors loading for each character. PC I was loaded with BSD, MSD and TS whereas PC II was loaded with DTFF and D50%F; and BDWT and CDWT loaded PC III. Only LINT loaded PC VI. The PH loaded PC I and PC V (Table 3). Variation due to BCD and LLGT was explained across the six PCs. Genotype designation and associations between genotypes and each of the 6 axes that explained variance among the genotypes were presented in Table 4. PC I differentiated 30 of the 33 genotypes. AU-24524[3], A-60-282-5[1], AC-31324[4], Tianung 2 and Ex-Shika loaded the first three principal axes. Figures 1, 2 and 3 illustrated the configuration of the genotypes on principal axes. It is evident that the Genotypes 2 and 10 were most distinct in all the three configurations. But Genotypes 2, 7 and 10 appeared most distinct in plot of principal axes 1 and 2; Genotypes 2, 5 and 10 in plot of principal axis 1 against 3 whereas only Genotypes 2 and 10 were described as most in Figure 3.Genotype 2QQ 1[3] (2) was most distinct.

Cluster analysis

According to Table 5 and Figure 4, the kenaf genotypes clustered into four groups. There were 5, 6, 7 and 15 genotypes respectively in Cluster I, II, III and IV (Figure 4). Genotypes 1, 2, 8, 11 and 13 clustered into group I whereas Genotypes 5, 10, 12, 14, 16, 23 and 33 clustered into group III. Significant variation existed among the clusters in all the parameters studied. The standard error and CV were higher in cluster III and lowest in cluster IV in plant height whereas the SE and CV were higher in cluster II and least in cluster I in D50%F. Plant height in the clusters ranged from 201.50 to 264.83 cm with group III having the highest plant height and group II having the least. The genotypes that clustered into group I flowered earlier than those in other groups whereas those in group II flowered later. Seed weight was highest in group I. Bast weight was higher in genotypes that clustered into groups I and II than those in groups III and IV. Table 5 showed that SEs and CVs were variable among the clusters in SWT and BDWT. Variations in other attributes were shown in Table 5.

Table 1. Variation in botanical characteristics of the genotypes of kenaf studied.

Trait	Attribute of trait		
	Most frequent	% of most frequent in total sample	Other characters by rank
Stem colour	Green	72.0	Greenish brown > light brown > purple > dark brown
Leaf shape	Palmate	68.8	Reniform > hastate
Leaf margin	Serrate	66.8	Crenate > undulate. Rarely lancerate
Leaf colour	Green	88.0	Green with red spots
Leaf lobation	Deeply lobed	68.0	Shallow lobed > not lobed
Leaf apex shape	Acute	100.0	
Leaf base shape	Sagitate	75.2	Cordate
Leaf mid-rib colour	Green	76.5	Green with red spots
Leaf margin colour	Green	81.0	Green with red spots
No. of lobe per leaf	Seven	54.4	Almost equal number were one lobe per leaf
Shape of central leaf	Lanceolate	61.3	Elliptic-lanceolate > ovate
Distance between leaf lobes	Intermediate	55.5	Very distant > no measurable distant
Leaf density	High = Intermediate	44.7	Low (11.6%)
Petiole orientation	Horizontal	53.9	Inclined upward > inclined downward
Petiole colour	Greenish red	70.1	Green > purple
Flower colour	Cream	72.6	Purple
Branching habit	Medium	54.5	High > no branch

= indicates equal to; > indicates greater than

Table 2. Eigen values, percentage variance and cumulative percentage variance in characters of kenaf genotypes studied as decomposed into principal component axes.

Principal axis	Eigen value	Difference	Percentage variance	Cumulative percentage variance
1	4.001	1.526	26.7	26.7
2	2.475	0.530	16.5	43.2
3	1.944	0.436	13.0	56.1
4	1.508	0.265	10.1	66.2
5	1.243	0.188	08.3	74.5
6	1.055	0.214	07.0	81.5
7	0.841	0.148	05.6	87.1
8	0.693	0.213	04.6	91.7
9	0.480	0.144	03.2	94.3
10	0.335	0.065	02.2	97.2
11	0.271	0.149	01.8	99.0
12	0.122	0.093	0.8	99.8
13	0.029		0.2	99.9

Table 3. Eigen vectors loading for characters of kenaf genotypes studied as decomposed into first 6 principal component axes.

Character	Eigenvectors					
	PC I	PC II	PC III	PC IV	PC V	PC VI
Plant height	0.5336	0.1263	0.0044	0.0502	-0.5493	-0.0014
Basal stem diameter	0.8832	0.3320	-0.1903	0.2214	-0.0539	0.0640
Middle stem diameter	0.8866	0.3412	-0.1917	0.2090	-0.0456	0.0435
Top stem diameter	0.8936	0.3203	-0.2119	0.1880	-0.0425	0.0574
Day to first flowering	0.2690	-0.8413	0.1008	0.3242	0.1349	-0.0176
Day to 50 % flowering	0.4118	0.6761	0.2835	0.3787	0.1630	0.0681
Seed weight	-0.1795	0.2577	-0.0045	-0.4580	0.7077	-0.0876
Length of internode	-0.4015	-0.2185	0.2290	0.0918	-0.1037	0.7220
Number of node per plant	-0.5188	0.2584	-0.0331	0.6343	0.1995	-0.0753
Base core diameter	-0.3784	0.2385	0.3769	0.3665	-0.3024	-0.3843
Bast dry weight per plant	0.2407	0.3073	0.8063	-0.1516	0.0663	0.1767
Core dry weight per plant	0.3634	0.2828	0.8138	-0.0036	0.0437	0.1175
Width of middle leaf lobe	0.2659	-0.6239	0.1976	-0.0887	0.0464	-0.4083
Leaf length	-0.3138	-0.0485	-0.3991	0.2618	0.2655	0.3550
Petiole length	-0.3820	0.4009	0.1702	0.5218	0.4109	-0.1414

Table 4. Eigen vectors loading for genotypes of kenaf studied as decomposed into first 6 principal component axes.

Genotype	Genotype Designation	Eigen vectors					
		PC I	PC II	PC III	PC IV	PC V	PC IV
G45-2	1	0.2035	0.0378	-0.0135	0.0068	0.0087	0.0035
2QQ 1^{3}	2	0.3556	0.0525	0.0145	0.0141	0.0031	-0.0540
AU-75-41^{4}	3	0.0907	0.0443	-0.0465	-0.0168	-0.0518	0.0264
Ifeken 100	4	0.1032	-0.0031	0.0138	0.0510	0.0017	0.0137
AU-2452-4^{3}	5	-0.1817	0.1603	-0.1302	0.0109	-0.0008	-0.0123
Ex-Shika 24^{2}	6	-0.0084	-0.0228	-0.0039	0.0022	0.0216	0.0096
A-60-282-5^{1}	7	-0.0447	-0.0612	0.0345	0.0105	0.0137	0.0009
Cuba 19^{2}	8	0.2043	-0.0068	0.0188	0.0057	-0.0089	-0.0006
AU 2452^{4}	9	-0.0435	-0.0044	-0.0093	0.0344	-0.0273	0.0123
AU-60-282^{6}	10	-0.1470	0.2118	0.2311	-0.0145	-0.0025	0.0053
AU-72-4^{8}	11	0.1402	-0.0130	-0.0046	-0.0468	-0.0335	0.0040
2QQ 17^{3}	12	-0.1407	-0.0242	-0.0213	-0.0276	-0.0183	-0.0166
Cuba Ovate 5^{1}	13	0.2285	0.0022	0.0119	-0.0213	0.0047	-0.0086
AU-2452^{6}	14	-0.1520	0.0240	-0.0283	0.0625	0.0010	-0.0128
AC-31324^{4}	15	0.0618	-0.0520	0.0269	-0.0004	-0.0128	0.0105
Cuba 19^{1}	16	-0.0421	-0.0073	-0.0157	0.0455	-0.0280	0.0017
A-60-282-1^{5}	17	-0.0374	-0.0213	-0.0035	-0.0178	0.0223	0.0036
Ex-Giwa 34^{1}	18	-0.0968	-0.0365	0.0007	-0.0140	0.0149	-0.0031
AC-313-29^{3}	19	-0.1254	-0.0511	0.0011	-0.0460	0.0080	-0.0200
Pankeshin_JG	20	-0.1243	-0.0276	-0.0018	-0.0107	0.0113	-0.0060
2QQ 17^{1}	21	-0.1064	-0.0071	0.0330	0.0102	-0.0587	-0.0138
Cuba 19^{3}	22	-0.0825	-0.0315	0.0050	0.0195	0.0393	-0.0077
AU-2452-5^{A}	23	-0.1248	-0.0120	-0.0166	-0.0035	-0.0010	-0.0029
AU-719^{2}	24	-0.0195	-0.0285	0.0019	0.0002	0.0145	0.0024
Ifeken 400	25	0.0638	-0.0086	0.0087	0.0160	0.0340	0.0094
V-100-10^{1}	26	-0.0493	-0.0486	0.0033	-0.0287	0.0142	0.0012
V1-400	27	-0.0072	0.1452	-0.1273	-0.0312	0.0106	0.0068
Cuba 108	28	0.0128	-0.0163	0.0091	0.0289	0.0122	0.0121
Tianung 1	29	0.0523	-0.0129	-0.0151	-0.0277	0.0002	0.0149
Tianung 2	30	-0.0323	-0.0538	0.0208	-0.0143	0.0098	0.0012
Ex Shika	31	-0.0323	-0.0531	0.0208	-0.0143	0.0098	0.0012
108/4 /47B	32	0.1112	0.0050	-0.0034	0.0100	0.0069	0.0157
Local var.	33	-0.0929	-0.0525	0.0143	0.0018	-0.0281	-0.0120

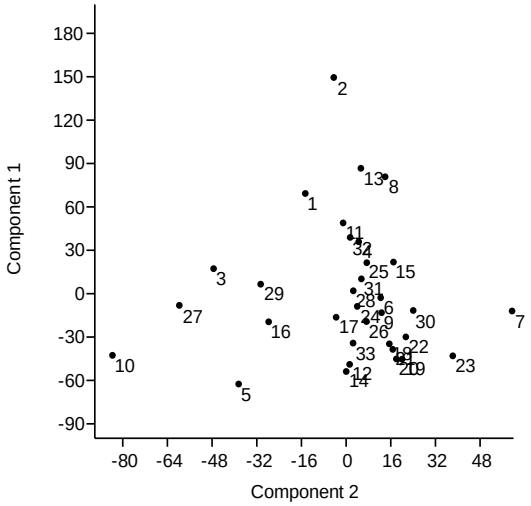

Figure 1. Configuration of the 33 genotypes of kenaf under principal component axes 1 and 2.

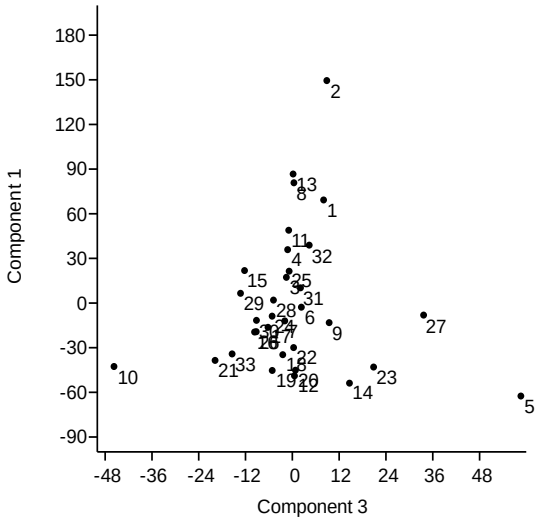

Figure 2. Configuration of the 33 genotypes of kenaf under principal component axes 1 and 3.

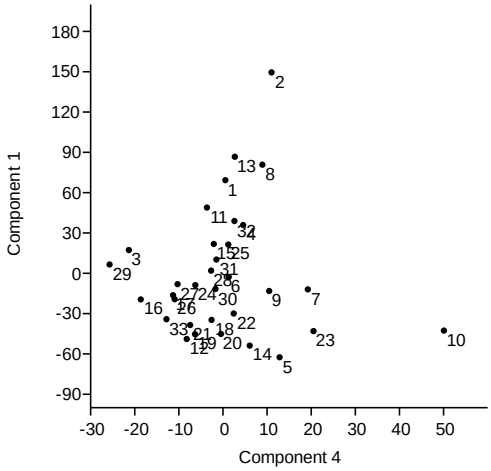

Figure 3. Configuration of the 33 genotypes of kenaf under principal component axes 1 and 4.

Table 5. Mean value, standard error, range and coefficient of variation of parameters of the 33 genotypes of kenaf in four cluster.

Cluster		Plant character													
		PH	BSD	MSD	TSD	DTFF	D50%F	SWT	LINT	NND	BCD	BDWT	CDWT	LLGT	PLGT
I	Mean	237.39	2.44	1.43	0.87	54.80	71.67	172.01	15.56	59.37	2.36	10.57	24.5	14.74	19.59
	SE	4.66	0.10	0.06	0.04	1.90	1.68	17.05	1.32	4.63	0.17	0.74	2.14	0.32	1.63
	Max	252.77	2.75	1.57	0.99	62.33	78.33	234.83	19.83	74.87	2.61	12.70	30.27	15.93	25.47
	Min	225.17	2.23	1.27	0.74	52.0	70.33	133.15	13.27	49.33	1.71	8.35	19.91	14.15	16.29
	CV (%)	4.39	9.45	9.60	11.07	7.76	5.03	22.17	18.95	17.43	15.53	15.64	19.52	4.87	18.63
II	Mean	201.50	2.27	1.46	0.83	71.83	86.89	65.52	15.85	49.94	2.10	10.31	26.57	14.12	16.84
	SE	5.98	0.22	0.09	0.05	10.40	9.16	10.87	1.69	3.18	0.21	1.14	2.98	0.47	0.74
	Max	224.03	2.74	1.78	1.05	115.10	122.33	97.50	22.47	56.43	2.74	14.26	35.13	16.23	19.06
	Min	188.30	1.27	1.21	0.72	51.67	62.33	27.70	12.03	39.13	1.57	5.84	16.85	13.22	15.20
	CV (%)	7.27	23.37	14.39	15.50	35.46	25.83	40.65	26.08	15.61	24.35	26.98	27.46	8.13	10.74
III	Mean	264.83	2.58	1.50	0.78	58.23	75.10	47.83	17.10	57.76	2.57	9.11	22.78	14.38	17.93
	SE	6.25	0.13	0.06	0.02	3.74	2.45	3.99	1.75	3.29	0.10	0.76	2.54	0.44	0.82
	Max	306.10	3.11	1.79	0.94	76.67	89.33	77.66	22.24	72.17	3.05	13.80	38.86	16.38	20.92
	Min	242.67	1.70	1.28	0.66	37.33	69.67	33.57	11.35	35.33	1.91	6.12	11.06	11.80	12.55
	CV (%)	7.47	15.53	12.12	10.20	20.32	10.33	26.37	21.23	18.01	12.48	26.40	35.20	9.70	14.50
IV	Mean	249.71	2.35	1.50	0.85	56.50	70.44	89.90	14.31	52.94	2.42	8.30	20.75	14.07	17.84
	SE	2.35	0.08	0.03	0.04	1.44	1.92	5.93	0.54	2.19	0.12	0.75	2.02	0.27	0.79
	Max	264.70	2.76	1.71	1.12	63.33	87.00	124.30	17.19	63.83	3.29	12.59	35.88	16.20	24.50
	Min	236.53	1.84	1.35	0.68	47.67	61.67	64.64	11.40	38.33	1.83	4.75	11.54	12.69	14.20
	CV (%)	3.26	11.35	7.35	14.68	8.85	9.42	22.56	13.08	14.34	17.47	29.66	33.72	6.62	15.33
Total	Mean	242.65	2.41	1.45	0.82	59.56	75.48	255.48	15.44	54.83	2.40	9.44	22.99	14.27	17.95
	SE	3.21	0.04	0.02	0.01	1.36	1.21	4.77	0.35	0.95	0.05	0.27	0.84	0.14	0.29
	Max	306.30	3.41	1.95	1.13	116.00	123.00	264.83	25.50	78.50	3.90	15.47	45.29	19.70	27.00
	Min	59.50	1.09	0.75	0.51	36.00	61.00	54.27	10.70	33.50	1.24	4.05	9.00	10.80	11.85
	CV (%)	13.17	17.38	14.69	16.08	22.80	16.01	55.78	22.33	17.28	18.92	28.80	36.19	9.93	16.03

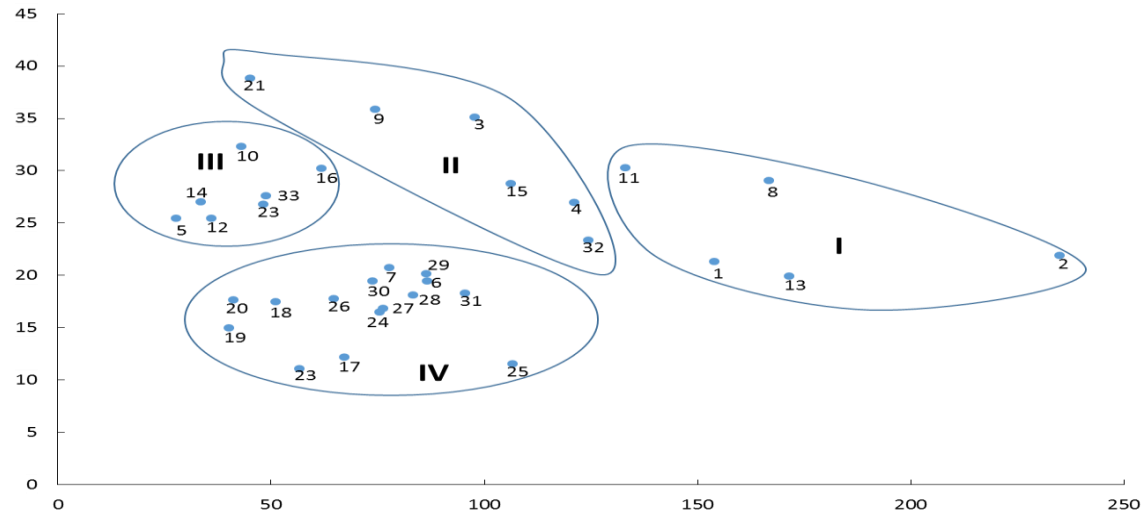

Figure 4. Genetic relatedness among the 33 kenaf genotypes in four clusters.

DISCUSSION

The stems and leaves of the plants were predominantly green indicating presence of chlorophyll pigments and the crops affinity for nitrogen, magnesium and sulphur. Attention needs to be paid to these nutrient elements when cultivating or improving the crop. The wide variation in the botanical, as well as agro-morphological characteristics of the crop proves there is a wide genetic diversity among the genotypes. Plant breeders can, therefore, easily make choices among the germplasms for breeding programmes. Ogunniyan and Olakojo (2014) found genetic variation among maize varieties using variation in their botanical characteristics. Ogunbodede and Ajibade (2001) also reported variation in kenaf genotypes. Major distinctions in the characters is capable of facilitating rapid identification and classification of distinct lines during breeding programmes.

The first 6 principal axes of the 13 axes that explained about 99.9% variance accounted for about 81.5% of the total variance. These 6 principal axes shows very strong discriminating ability among the characters that contributed to the variation among the genotypes. Thus, the characters that associate with these axes can be used to distinguish genotypes of the crop. Contributions of characters of accessions to each of the components based on the eigen vectors have been used to estimate genetic variability among the accessions (Ariyo, 1987, 1993; Granati *et al*., 2003; Kamara *et al*., 2003; Nwangburuka *et al*., 2011; Denton and Nwangburuka, 2012). The discriminating ability of PC I was strongest, but it did not adequately distinguish the genotypes. It accounted for only 26.7%, and basically accounted for variation in the girth of the plant, specifically the BSD, MSD and TSD. It may, therefore, be assumed that the thickness of the plant at various height of the plant contributed to the variation among the genotypes. Principal component II which accounted for 16.5% described variation in the flowering pattern whereas PC III described variation due to yield components by accounting for only 13.0%. The BCD and LLGT explain variations across the six PCs indicates that variations existed at each point of consideration. It is also noteworthy that BSD, MSD, TSD, DTFF, D50%F, BDWT and CDWT contributed large variability by respectively having eigen vectors 0.8832, 0.8866, 0.8963, 0.8413, 0.6761, 0.8063 and 0.8138, each of which was above 0.6000 on the first three PCs. This implies that any of these characters can be used more efficiently in discriminating among kenaf genotypes than other. Based on the totality of the contribution of each attribute and configuration on the first three principal axes, Genotypes 2, 5 and 10 were most distinct and were expected to possess useful attributes if further examined. Principal component analysis showed that days

to flowering, plant diameter and leaf shape were traits responsible for major variation among the genotypes (Faruq *et al.*, 2013).

PC I distinguished 30 genotypes whereas PC II suggested variation between another two. The PC I and PC II adequately distinguished 32 of the 33 genotypes suggests a high level variability among the genotypes. Only Cuba 108 was not distinguished until the fourth PC. It may be that Cuba 108 has many attributes in common with other genotypes. Genotypes AU-24524[3] (5), A-60-282-5[1] (7), AC-31324[4] (15), Tianung 2 (30) and Ex-Shika (31) are related, but it is evident that AU-24524[3] (Genotype 5) is more distant among these five genotypes. Hence, it may be a source of useful genes to emphasize in breeding program.

Though the highest number of genotypes were clustered into group IV (about 46% of the total number of genotypes), there was an almost equal number of genotypes distributed in the other three groups. About 15, 18 and 20% of the total genotypes respectively clustered in group I, II and III. Range of days to 50% flowering among the clusters (70.44 to 86.89) confirms that kenaf are either ultra-early-, or early to medium- or late-maturity. Webber *et al*. (2002) described kenaf as early maturing varieties when they flower between 75 and 105 days, or semi-early maturing varieties when they flower between 105 and 120 days, after planting. According to the authors, flowering in late maturity kenaf varieties is between 120 and 140 days after planting. Genotypes in groups I and IV flowered earlier than 75 days after planting whereas those in groups II and III flowered at 75 days after planting or above. Based on this classification, genotypes in groups I and IV can be regarded as ultra-early maturing. Alexopoulou *et al*. (2000) reported that flowering of early maturity kenaf varieties is irrelevant to the day length. These ultra-early maturing genotypes may need to be evaluated to effects of day length on flowers production. Findings of Balogun *et al*. (2009) corroborated that flower initiation is associated with reduced vegetative growth, and in turn, low fibre yield as found in this study. Variation existed among the clusters in all the parameters studied indicating that any of these parameters can be reliably used to distinguish the genotypes. The higher standard error and coefficient of variation in plant height in clusters III, as well as the higher standard errors and coefficients of variation in SWT and BDWT suggests greater divergence among the genotypes. Faruq *et al*. (2013) also reported significant differences among the genotypes in fibre weight and days to 50% flowering. Genotypes that clustered into groups I and II may be good candidates for fibre production in breeding programmes because of their higher bast and core fibres.

CONCLUSIONS

Wide variation exists in the botanical traits, thus genetic diversity, of the genotypes. The stems and leaves of the plants were predominantly green. Leaves of most genotypes were palmate, deeply lobed and had serrate margin. The first six principal component had eigen values greater than one, and accounted for about 81.5% of the total variance. The BSD, MSD, TSD, DTFF, D50%F, BDWT and CDWT can be used more efficiently in discriminating among kenaf genotypes than other characters. The kenaf genotypes investigated were ultra-early and early maturing. Genotypes that clustered into groups I and II may be good candidates for fibre production. Genotypes 2QQ 1[3] and AU-60-282[6] were most distinct in all the three configurations.

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