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Full Length Research Article

Morphological Assessment of the Genetic Variability among 53 Accessions of West African okra [*Abelmoschus caillei* (A. Chev.) Stevels] from South Western Nigeria

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ABSTRACT: Genetic variability in fifty three accessions of West African Okra [*Abelmoschus caillei* (A. Chev.) Stevels] were evaluated using morphological traits. These accessions were collected from home gardens, seed stores and distant farms in South Western Nigeria and trials carried out in the experimental garden, University of Benin, Nigeria. The primary data on quantitative and qualitative characters collected were subjected to multivariate analyses to determine their relationship and distinctiveness. At $P < 0.05$, 14 quantitative characters were significant. Two principal component analyses were conducted. Eighteen of the total characters accounted for 90.2 % of the total variability on Principal Component (PC) axes 1 - 5 and the other, sixteen characters showed 70.1 % as the minimum descriptor for distinguishing *A. caillei*. The traits expressed by these descriptors are reflected in pigmentation of various organs; fruit characteristics and plant architecture on the crop plants. The sixteen characters suggested for core determination of this species were used for cluster analysis. All accessions clustered into seven distinct groups at Euclidean distance 8 - 10. This suggests relatively high genetic variability among the germplasm. The clustering is ecologically independent and the number of accession(s) in each cluster suggests *A. caillei* as a continuous complex of varieties. This collection requires more evidence probably molecular evaluation for taxonomic treatment of the taxon.
Keywords: Okra, Genetic Variation, Multivariate Analysis, Principal Component Analysis, Cluster Analysis

INTRODUCTION

West African Okra [*Abelmoschus caillei* (A. Chev.) Stevels], belongs to the family Malvaceae. It is indigenous to the humid West and Central Africa. The distribution extends in West Africa from Guinea to Nigeria, Cameroon to Gabon and the Democratic Republic of Congo in Central Africa and Uganda in East Africa. However, it is wide spread and its cultivation in Africa lies between 12 ^{0}N and 12 ^{0}S and most commonly found between 5^{0}N and 10^{0}N (Siemonsma and Hamon, 2002).

West African Okra is an important food component for those who include it in their diet (Omonhimwin and Osawaru, 2005). When prepared as a sauce, it facilitates the consumption of starchy foods, which are the main diet of Africans especially in rural villages and in the drier regions where a slimy vegetable is needed as a supplement for the more coarse staple food like millets (Schippers, 2000). *A. caillei* is especially liked for its ability to "draw" well and to retain its mucilaginous characteristics. However, lemon may be added to soup to reduce glutinous texture and make it more solid (Osawaru and Dania-Ogbe, 2010). It also contributes to protein, mineral, vitamins and source of roughages in human diet.

Mucilage from West African Okra has been reported as plasma replacement or blood volume expander and the leaves are used as a basis for poultice, as an emollient, sudorific, antiscorbutic and to treat dysuria (Siemonsma and Hamon, 2002). Osawaru and Dania-Ogbe (2010) reported the use of the mucilage in traditional midwifery in Southern Edo State of Nigeria. Other traditional uses of the whole and part of the plants can be found in Osawaru and Dania-Ogbe (2010).

The industrial applications are numerous. The mucilage has been added as size to gaze certain paper used in confectionary. The stem is fairly large with bark and fibres which are suitable for spinning into rope and for paper and card board manufacturing (Chevalier, 1940, Charrier 1984). Locally, the fibres are also used to make fishing lines, game traps and sponges (Osawaru and Dania-Ogbe, 2010). West African okra is used as a source of gum. The ground pulp of stems is used as a stabilizer when making "Pita" beer in northern Ghana (Schipper, 2000).

Various authors, Siemonsma (1982) and Stevels (1988) have contributed to the taxonomy of Okra (*Abelmoschus*) and suggested needs for a thorough revision (Attire *et al.*, 1991), Stevels (1988) established

West African Okra as a distinct taxon as earlier reported by Chevalier (1940). The bases of their delimitations and circumscription are morphological and cytological evidences. It is highly polymorphic and unique in fruit and indumentums characters. Smith *et al*. (1991), opined that morphological characterization is the first step in the description and classification of germplasm collections. The objective of this study is to assess the genetic diversity of West African Okra using morpho-agronomic characters, among 53 accessions from Nigeria. Information derived may be valuable for base and active collection and possibly help plant breeders to improve the crop plant.

MATERIALS AND METHODS

Study Area

The site for the trial was the Experimental garden, Plant Biology and Biotechnology Department, University of Benin, Benin City. It lies within the Tropical Rainforest (TRF) zone. The relief is characterized by lowland of less than 300 – 600 meters above sea level. The climate includes high rainfall up to 2000 mm - 3000 mm of bimodal pattern with peaks at July and September respectively, high temperatures ranging between 20 ^{0}C-40 ^{0}C and high atmospheric humidity (Omuta, 1980). Radiation is fairly high and varies according to different period of the year. Values above 1,600 hours per year have been reported in surrounding areas such as the Nigerian Institute for Oil Palm Research (Onwueme and Singha, 1991). The soils are slightly ferrallitic with pH 7.

Field Trials

Fifty three (53) accessions of West African Okra collected by Osawaru and Dania-Ogbe (2010) were subjected to trial on the experimental garden and evaluated for morpho-agronomical characters in the site. The seeds used were carefully removed from the pods without scarification and selected after floatation test.

Planting and Plant Husbandry

Accessions were planted using Randomized Complete Block Design (RCBD) with five replicates. Three seeds were planted into holes of 3cm deep and lightly covered with soil without tillage, at spacing of 75 x 100cm, without fertilizer. Crops were rain fed throughout the period of cultivation. Other agronomic practices like mulching, topping etc were not applied during the trials.

Thinning was done when plants were two weeks old. All stands were thinned to a plant per stand. Weeding was done weekly and manually until last plant was harvested. Pest control was done every two weeks using methods outlined by Usuanlele (2000).

Data Collection

Data was gathered from the description of vegetative and phenological Characters. These were determined according to IBPGR **(**Charrier, 1984,) and Hamon and Hamon (1991). A descriptor list was prepared based on field observations during the ethnobotanical survey and characterization. Forty-one characters made up of twenty-five qualitative and sixteen quantitative characters were used to analyze the diversity. For each of the accession, five measurements or observations were made for each character. Colour chart adopted was by the Royal Horticultural Society (RHS, 1986).

Statistical Analysis of Data

Data matrix table for the fifty-three accessions and forty-one traits for the vegetative, reproductive and agronomic characters listed in characterized rating scales were standardized as outlined by Brandolini and Brandolini (2001). These variables were subjected to three methods of multi variate analyses- MANOVA, Principal Component and Wards Hierarchical Cluster Analyses using various procedures of the GENSTAT program in order to identify the patterns of morphological variation.

RESULTS

The analysis of variance for the following characters evaluated is presented in Table 1. The results show that the accessions are significantly different between accessions at 5 % probability with respect to the 14 characters studied. The magnitude of the variance is significantly high too. This implies that these characters could be employed in distinguishing the accessions. Very high values are recorded for NSF, FLS, PHM, PHF and FFN. The characters are therefore potentially good for distinguishing *A. caillei* accession.

Principal Component Analysis (PCA)

Forty-one descriptors were used to evaluate the vegetative, reproductive and agronomic characters of the accession. Main stem (MAS), leaf pubescence (LFB), seed shape (SES), petal colour (PLC) and nature of pedicel (PLH) were generally uniform in their state. All other 36 characters were treated as outlined by Brandolini and Brandolini (2001).

Based on the multivariate states, a data matrix of the thirty six characters for fifty three accessions generated were subjected to PCA using the methods of Manzano (2006). From the results in Table 2, 18 characters of the descriptors accounted for and influenced 90.02% of the total variability within the 53 accessions. These eighteen characters were accumulated until the fifth component (Tables 2 and 3).

Generally, only Principal Component with eigen values larger than one (positive or negative) were considered. However, Jolliffe (1996), Brandolini and Brandolini (2001) suggested values as low as 0.50 in studies where standardization of the original character values were carried out. The eigen values in this study were standardized (data matrix) hence, the value 0.55 was used in this study. From these components, characters with eigen vectors as low as 0.550 were selected. These characters are designated as influencing the total variability on that component axis. At component axis 1, the characters are petal botch (PTB), rib colour of adaxial surface (RCB) Rib colour (adaxial) surface (RCD), fruit colour (FRC) petiole colour (PTC), stem colour (STC), and fruit pubescence (FRP).

Characters on component 2 (C_2) pod size index (PDI), fruit length at maturity (FLH), number of seeds/fruit (NSF), fruit width at maturity (FWN) and plant height at first flowering (PHF). In components (C_3) first fruit producing node (FPN), first flowering node (FFN), and days to first flowering (FFD) were the recorded characters. On component axes 4 and 5, stem diameter at base (SDB), maximum plant height (PHM), nature of fruit tip (NFT) accounted for distinguishing the variability of the accessions. However, number of flowered node (NFM) (on main stem) recorded eigen vector 0.71 but was not included among those influencing the total variability of the accessions. Number of flowered nodes on the whole plant body (NPN) was not used as any of the branch could be regarded as main stem especially in a diseased state of the major stem axis.

A second PCA was done to ascertain the most distinguishing characters among the accessions. The eighteen characters that contributed to 90.2% of the total variability were used. The total variance and eigen vectors are presented in (Tables 4 and 5). A total of 70.1% of the total variance attributed by 16 characters along the first 5 principal component axes with eigenvector of 0.55. Principal Component (PC) axis one, influenced 22.9 % of the total variation among the accessions. Characters influencing this variability are RCD, RCB, PTB, FRC and STC. Component axis 2 PC_2 explains 14.5 % of the total variation. This is weighted by NSF FLH, FWH and PDI. Component axes 3, 4 and 5 accounted for 13.4%, 12.5% and 6.9% variability respectively. The weighted characters for PC_3, PC_4 and PC_5 are FFD, FFN, FPN, SDB, PHM, PHF and PTC respectively.

Cluster analysis

The intraspecific variation among the 53 accession was derived from the morphometric hierarchical cluster analysis. The dendrogram for this analysis is shown in Figure 1. At a linkage distance between 10 - 15, four clusters are apparent. These are;

(a) OS/ED/51; (one accession)
(b) OS/DE/33; (one accession)
(c) OS/ED/48, OS/ED/53, OS/ED/52, OS/ON/03 OS/ED/40 & OS/ED/47; (six accessions)
(d) OS/DE/01, OS/DE/02, OS/DE/04 OS/DE/05 OS/ED/06, OS/ED/07, OS/DE/08, OS/DE/09, OS/DE/10, OS/DE/11, OS/ED/12, OS/ED/13, OS/DE/14, OS/ED/15, OS/DE/16, OS/DE/17, OS/DE/18, OS/DE/19, OS/ED/20, OS/DE/21, OS/ED/22, OS/ON/23, OS/ED/24, OS/DE/25, OS/ON/26, OS/DE/27, OS/ON/28, OS/ON/29, OS/ED/30, OS/ED/31, OS/ED/32, OS/ED/34, OS/ON/35, OS/ED/36, OS/ON/37, OS/ON/38, OS/DE/39, OS/ON/41, OS/DE/42, OS/ED/43, OS/ON/44, OS/DE/45, OS/DE/46, OS/ED/49 and OS/ED/50. (45 accessions)

At a lower Euclidean distance between 8-10, seven clusters separate. These are;

(a) OS/ON/03, OS/ED/40, OS/ED/48, OS/ED/52 and OS/ED/53; (five accessions)
(b) OS/ED/47; (one accession)
(c) OS/DE/33; (one accession)
(d) OS/ON/38, OS/DE/39, OS/ON/28, OS/ED/46, OS/ON/44, OS/ED/13, OS/ON/41, OS/DE/27, OS/ON/29, OS/ED/49, OS/ED/50, OS/ED/43, OS/ED/12, OS/DE/11, OS/ED/36, OS/DE/10, OS/ED/30, OS/DE/25, OS/DE/09, OS/ON/26, OS/ON/35, OS/ED/22, OS/ED/31, OS/DE/08, OS/DE/34, OS/DE/21, OS/ON/23, OS/DE/18, OS/ED/45, OS/DE/04, OS/ED/24, OS/DE/04, (32 accessions).
(e) OS/DE/02, OS/ED/15, OS/DE/01, OS/DE/14, OS/ED/06, OS/DE/17, OS/DE/05, OS/ED/20,

OS/DE/16, OS/ED/07, OS/DE/19, OS/ED/32; (12 accessions)

(f) OS/ON/37; (one accession)

(g) OS/ED/51; (one accession)

At a lower level linkage distance, the clusters of 45 accessions split into three clusters of 32; 12 and one accession respectively. While the cluster of six accessions split into two of one and five accessions.

DISCUSSION

The variations in 53 accessions of West African Okra were studied using morpho-agronomical characters for description. According to Peeters and Martinelli (1989), that multivariate analysis is useful for characterization, evaluation and classification of plant genetic resources when a number of accessions are assessed. Rezai and Frey (1990), Ariyo (1993), and Ariyo and Odulaja (1991) stated that when dissimilarity between a pair of varieties is defined on a multivariate criterion, it is useful to be able to determine the plant characters which cause the dissimilarity to arise and the relative contribution that the various characters make to the total variability. Camussi (1979), Abadie *et al.* (1998), and Brandolini and Brandolini (2001), reported that for the study of morphologically complex samples, multivariate analysis combines the capacity to provide synthetic summary of the most relevant traits and assessment of the relative importance of the different characters to the total difference. Multivariate analysis based on MANOVA, principal component and hierarchical cluster was used in this study. The use of statistical model and tests provide informative conclusion about a very large group of occurrences by observing a small representative.

Analysis of variance used in the study indicates high genetic diversity among accessions. This is amplified by the magnitude and significant values as shown in Table 1. Characters like NSF, PHM, FFN, PHF and FLS had values very high. This implies that these characters are indicative for distinguishing variability in the accessions. This statistical analysis has also been used for studying genetic variability in crops such as garlic and Bambara groundnut (*Vigna subterranean* (L) Verde), (Ntundu *et al*., 2006). Genetic variability as reflected from morpho-agronomic characters is the raw material of crop breeding on which selection acts up to evolve superior genotype thus, the higher amount of variation expressed for a character in the breeding material, greater is the scope for its improvement through selection. However these characters are mainly quantitative. Berinyuy *et al* (2002), Brandolini and Brandolini (2001), Omonhinmin and Osawaru (2005) emphasized the importance of inclusion of qualitative and quantitative characters in the evaluation, identification and description of genetic variability of genetic mixtures.

PCA measures axes along which variation between accessions is maximized. According to Camussi *et al*. (1985), Cowen and Frey, (1987), Peeters and Martinelli (1989) PCA can be used to obtain ideas about how to identify groups of accessions that have desirable traits for breeding and enlightening the pattern of variation in a germplasm collection, to identify relationships among accessions and possible gaps. The use of PCA to study variability in germplasm collections of many species have been reported (Julier *et al*., 1995; Veassy *et al*., 2001; Naghavi and Jahensouz, 2005; Bharagava *et al*., 2007; Nooryazdan *et al*., 2010). It is a method of data reduction where the original variables decreased to a limited number of uncorrelated new variables. Two PCA were carried out in the present study. From the result of the first analysis it was clear that characters describing variation of the accessions are qualitative and quantitative. The qualitative characters include PTB, RCD, RCB, FRC, STC, PTC. These characters described pigmentation among the various organs of the accessions. These qualitative characters are discrete, easily identified and rarely affected by environment. This trend has been observed by Ariyo (1993), Manzano (2006). The quantitative characters include for fruit, fruiting habit and growth habit. These quantitative characters describe the fruit characteristic, plant architecture and flowering and fruit earliness among accessions. The quantitative characters describing the fruit are pod size, fruit length at maturity, number of seeds/fruit and fruit width at maturity. Stevels (1988); Siemonsma and Hamon (2002) stated that the greatest diversity among *A. caillei* is seen in its fruits and indumentum. Fruit of *Abelmoschus* is here suggested as a diagnostic feature for interspecific determination. This view has also been supported by Ariyo (1993) and Kehinde (1999).

Pods are usually large and of various shapes. The position of the pods on the stems is usually erect with few horizontal or pendulous pods. Plant height at first flowering (PHF), first fruit producing node (FPN), first flowering node, (FFN), stem diameter at base (SDB),

and maximum plant height (PHM) describe the plant architecture. West Africa okra has a robust growth habit at maturity. Hamon and Hamon (1991), stated that the best time to identify *A. caillei* is at the peak of the vegetation growth usually at 84-125 days after sowing. These characters would be very effective as a means of distinguishing the accessions and also a determinant in evaluating the genetic variability in *A. caillei.* The significance of days to flowering in numerical taxonomy has been highlighted by Sneath and Sokal (1973) and Ariyo (1993).

From the second PCA, all characters earlier highlighted were re-affirmed except nature of fruit tip (NFT) and fruit pubescence (FRP). These sixteen characters are here suggested as minimum descriptors necessary for core collections. In addition to pigmentation, and fruit characteristics, emphasized by Ariyo (1993), Siemonsma and Hamon (2002), this study included flowering and earliness to fruit and plant architecture as significant determinant features of the genetic variability in the crop plants.

The hierarchical analysis of the large amount of variation observed among the accessions at two phenon levels were expressed in four and seven clusters. The largest cluster at each level (45, 32) members may be seen as a variation complex that may require further evidence probably molecular for clarity or the use of another statistical testing like Conomical discriminant analysis.

The grouping of the accession into six clusters show that there was no correlation between ecological habitat and the diversity expressed among accession. This has been shown not to be significant from the report of Murthy and Arunachalam (1966). They rather suggested that genetic drift and selection in different environment can cause greater diversity among genotypes. The likely reason for the genetic similarity among these accessions from the different region is that the crop plant might have originally been introduced from the same region. This is probably true as workers like Charrier (1984), Siemonsma (1982) and Stevels (1988) point West Africa subcontinent as probable centre of origin of the crop plant. This agreed with Adewale *et al*. (2008) with the use of genetic maker in the study of West African Okra and other Asiantic collections. The level of variability may be due to low selection and domestication as there is a related species – *A. esculentus* grown among local farmers. This high variability suggests that little influence has result from domestication as there is the widespread of related species of *Abelmoschus.*

Apart from the taxonomic implication the variation observed would be of great importance to germplasm collector, plant breeders and also serve as means for designing a core collection strategy. In addition it, would also serve as a source of desirable characters, for improvement in the genus *Abelmoschus*. Genetic variability is the raw material of crop breeding industry on which selection acts to evolve superior genotype.

Table 1: Analyses of variance for quantitative characters

SOURCE	D.F	MSNFP	MSNSF	MSFLS	MSNFM	MSSDB	MSPHF	MSFFN(d)
Block	9	63.667	5.501	9.432	2.307	0.043223	91.22	24.64
Treatments	52	185.672*	1521.119*	1854.874*	40.409*	4.726279*	3787.4*	5618.45*
Error	467	7.663	3.638	7.062	2.292	0.008133	51.35	17.7
Total	528							

SOURCE	D.F	MSPHM	MSPLH	MSFFD	MSFPN	MSFLH	MSPDI	MSFWH(d)
Block	9	4.433	0.02934	26.16	3484	0.2877	2.066	0.15271
Treatments	52	5095.672*	2.05450*	160.52*	158.368*	24.4919*	4.007*	1.17641*
Error	467	3.67	0.04023	23.58	2.989	0.3518	1.553	0.05231
Total	528							

* = Significant at 5% MS = Mean Square

Table 2: Rotated component matrix for eighteen characters

	Component								
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
SDB	*0.936	0.136	-0.02650	-0.01566	0.0003725	0.03446	0.05951	0.08070	-0.01201
PHM	*0.909	0.04407	-0.121	-0.00448	0.06596	0.02067	0.09119	-0.06417	-0.01481
PHF	*0.858	0.208	-0.143	-0.03113	0.01826	0.04293	0.02763	0.122	0.03976
FFD	*0.852	0.002317	0.09216	-0.02595	0.137	-0.00172	-0.117	0.01437	0.188
FFN	*0.694	0.003486	-0.02735	0.156	-0.04782	0.004570	0.06368	-0.101	-0.166
FPN	*0.564	-0.106	-0.226	0.155	-0.09072	0.08905	0.03911	-0.157	0.264
NSI	0.550	-0.137	-0.05841	0.182	-0.294	-0.07405	-0.245	0.03337	0.04461
FDH	0.180	**0.845	0.02412	0.201	0.06171	-0.06646	-0.05416	0.05025	0.102
FWH	0.0546	**0.794	0.09920	0.05756	0.07555	0.06239	-0.09213	0.130	0.264
PDI	0.0371	**0.784	-0.130	0.09275	0.102	0.01670	0.228	0.154	-0.08942
NFT	0.278	**0.578	0.216	0.101	0.08855	-0.00697	0.119	-0.09674	0.02880
FRP	0.0289	**0.545	-0.06857	0.535	0.02073	0.135	-0.01408	0.408	0.08496
STC	0.0976	0.115	***0.927	0.0820	0.03724	0.008456	0.113	0.006352	-0.08188
PTC	0.0584	0.05242	***0.916	-0.09.083	-0.05374	0.008548	0.103	0.009048	0.01312
RCD	-0.259	-0.146	***0.579	-0.185	-0.169	-0.373	-0.296	-0.07785	-0.234
RCR	0.0098	0.230	0.07765	****0.862	0.166	-0.09765	-0.03.666	-0.02376	0.04695
PTB	0.0918	0.429	-0.143	****0.548	-0.001391	0.04685	-0.02.551	0.458	0.03451
FRC	0.0827	0.01015	-0.02388	0.139	*****0.897	-0.02500	-0.04184	-0.125	0.07387
SUB	0.0665	0.365	-0.03995	0.03487	*****0.713	-0.02870	0.01629	0.333	0.126
PHM	0.111	0.151	-0.134	-0.08839	0.001558	0.865	0.02322	0.002244	-0.159
PHF	0.112	-0.332	-0.193	0.007423	0.134	-.662	0.009678	-0.07491	0.09818
FFD	0.0235	0.109	0.102	-0.02725	0.02916	-0.04418	******0.908	0.116	-0.03816
FFN	0.145	-0.227	0.204	-0.04168	-0.306	0.206	0.516	0.238	-0.309
FPN	0.0080	0.217	0.02637	0.05489	0.01238	0.04623	0.219	0.850	-0.02942
NSI	0.0874	0.215	0.162	0.04145	0.07747	-0.165	-0.147	-0.03420	0.847
FDH	0.124	-0.07002	.269	0.359	0.004014	-0.164	0.226	0.234	0.468
FWH	0.0457	-0.04390	0.08353	-0.08438	0.160	-0.09705	-5.536.02	0.02778	0.04796
PDI	0.300	0.192	-0.114	0.166	0.08417	0.417	-.157	.258	.109
NFT	0.178	-0.03842	-0.08415	-0.01761	-0.003702	0.02692	5.936.02	-0.00384	0.09310
FRP	0.0261	-0.08052	-0.114	-0.08309	0.08537	0.04446	0.118	0.04816	0.05676
STC	0.0917	-0.197	0.07670	-0.07408	-0.01649	-0.09930	4.419.02	-0.00224	0.06573
PTC	0.215	-0.194	0.03675	0.07634	-0.105	0.01406	4.067.02	-0.02989	0.02022
RCD	0.0121	-0.105	0.152	0.07924	-0.03826	0.129	2.994.02	-.132	0.000491
RCR	0.161	-0.01752	-0.287	0.07762	-0.02598	0.02221	-0.03174	0.06170	-0.120
PTB	0.0994	-0.01986	-0.181	0.122	-0.02930	0.07168	0.243	0.126	0.04599
FRC	0.0395	-0.296	-0.196	-1.95	0.178	-1.14	0.03761	-0.127	0.136

*, **, ***, ****, ***** and ****** = Values selected for first, second, third, fourth, fifth and seventh principal component analyses

Table 2: Rotated component matrix for eighteen characters (Contd.)

	Component								
	10	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**
SDB	-0.07424	0.05256	-0.01942	0.02000	0.03689	-0.02683	0.007334	0.06414	-0.0112
PHM	0.05396	-0.00505	0.09516	0.109	0.01431	-0.08809	0.08726	0.08410	-0.0895
PHF	-0.07130	0.113	-0.114	0.165	-0.02020	-0.01679	-0.144	-0.00853	0.0570
FFD	-0.03830	-0.02773	-0.06477	-0.202	0.08419	0.178	0.05152	-0.01269	-0.108
FFN	-0.00025	-0.00588	0.188	-0.02547	0.270	0.07892	0.128	-0.159	0.336
FPN	0.08548	0.352	-0.182	0.101	-0.131	-0.152	0.186	0.09683	-0.347
NSI	0.113	0.212	0.407	-0.02547	0.123	-0.09513	0.240	0.202	0.307
FDH	0.159	0.05577	-0.104	-0.134	0.04917	-0.09937	0.01365	0.102	-0.106
FWH	-0.143	-0.209	-0.05088	0.07227	-0.09994	-0.118	0.07381	0.01562	0.01227
PDI	-0.197	0.04356	-0.01429	-0.06586	-0.221	0.07349	-0.07160	-0.06412	0.03917
NFT	0.337	0.004478	0.236	-0.208	0.07180	-0.107	-0.139	-0.111	-0.283
FRP	-0.02119	-0.04428	-0.116	-0.214	-0.07064	0.05415	0.09373	-0.193	-0.177
STC	0.06322	-0.04673	0.01799	0.02805	0.04889	-0.02872	-0.06363	-0.115	0.01644
PTC	0.07795	-0.08089	-0.157	-0.134	0.01782	0.133	-0.09428	-0.04583	-0.07798
RCD	-0.121	0.06472	-0.00245	0.05254	-0.225	0.203	-0.07938	0.07761	-0.107
RCR	-0.07425	-0.02253	-0.03288	0.09032	0.111	0.03945	0.02356	0.209	-0.05024
PTB	-0.07952	0.02328	-0.136	-0.243	-0.115	0.153	0.06702	-0.235	-0.03117
FRC	0.149	0.02188	0.02794	0.09543	-0.212	-0.01558	0.01244	-0.04779	0.09872
SUB	0.01331	-0.04300	0.102	-0.219	0.214	-0.03786	-0.03458	0.05510	-0.04048
PHM	-0.172	0.115	0.120	-0.04768	0.009802	0.117	-0.141	0.05742	-0.03017
PHF	-0.07934	0.125	0.130	0.148	0.02495	-0.06004	-0.372	-0.02930	0.05299
FFD	-0.04039	0.111	0.126	0.03798	-0.03660	-0.01785	-0.01847	0.159	-0.04369
FFN	-0.09099	-0.166	-0.04312	0.01200	-0.02329	0.165	0.04019	0.113	0.213
FPN	0.01645	-0.01914	0.08575	0.05062	-0.03.020	-0.164	0.03630	0.156	-0.03124
NSI	0.06119	0.148	0.05225	0.08078	0.04941	0.04094	-0.141	0.03515	0.04217
FDH	-0.147	-0.226	0.239	-0.03767	-0.347	-0.257	0.180	0.08252	0.05073
FWH	0.862	-0.04271	0.06487	0.08396	-0.177	0.171	-0.105	0.01542	0.03898
PDI	-0.433	-0.251	-0.03788	0.321	0.247	0.01862	0.149	-0.03313	-0.182
NFT	-0.04179	0.860	0.118	0.160	-0.09729	0.106	0.104	-0.141	0.127
FRP	0.06122	0.07879	0.912	-0.01156	-0.05490	0.02978	-0.02156	0.05773	0.004069
STC	0.05691	0.156	-0.01775	0.865	0.005678	0.05705	-0.07676	-0.159	0.001793
PTC	-0.236	-0.127	-0.05104	0.01165	0.810	-0.102	0.102	0.03401	-0.03809
RCD	0.169	0.08306	0.02711	0.06102	-0.08817	0.873	0.185	0.05231	-0.03930
RCR	-0.190	0.141	0.02072	-0.08621	0.126	0.241	0.807	0.09066	-0.07689
PTB	0.01200	-0.152	0.08.747	-0.186	0.02167	0.06365	0.08543	0.836	-0.01748
FRC	0.122	0.368	0.01715	0.008791	-0.126	-0.128	-0.161	-0.02.482	0.659

NFP: No. of fruits produced
NSF: No.of seeds per fruits
NFN: No.of flowered node
SDB: Stem diameter at base
PHM: Maximum plant height
FFN: First flowering node
PHF: Plant height at first flowering
FLH: Fruit length at maturity
FWH: Fruit width at maturity
FLS: Flowering span
PLH: Pedicel length at fruit maturity
FPN: First fruit producing node
PDI: Pod size index
FFD: Days to first flowering
MAS: Main stem
LFB: Leaf pubescence
SES: Seed shape
PLC: Petal colour
PLH: Nature of pedicel
PTB: Petal botch
RCB: Rib colour of adaxial surface
RCD: Rib colour (adaxial) surface
FRC: Fruit colour
PTC: Petiole colour
STC: Stem colour
FRP: Fruit pubescence
SDB: Stem diameter at base

Table 3: Total variance explained for eighteen characters

		Initial Eigenvalues			Extraction Sums of Spared Loadings			Rotation Sums of Squared Loadings		
		Total	% of Variance	Cumula-tive %	Total	% of Variance	Cumul-ative %	Total	% of Variance	Cumul-ative %
Component	1	5.252	29.180	29.180	5.252	29.180	29.180	4.135	22.972	22.972
	2	3.616	20.089	49.269	3.616	20.089	49.269	2.606	14.476	37.448
	3	2.222	12.344	61.613	2.222	12.344	61.613	2.408	13.381	50.828
	4	1.184	6.579	68.192	1.184	6.579	68.192	2.244	12.468	63.297
	5	1.080	6.003	74.194	1.080	6.003	74.194	1.242	6.898	70.195
	6	0.837	4.649	78.843	.837	4.649	78.843	1.152	6.403	76.597
	7	0.793	4.408	83.251	.793	4.408	83.251	.919	5.106	81.703
	8	0.621	3.450	86.701	0.621	3.450	86.701	.900	4.997	86.701
	9	0.476	2.643	89.343						
	10	0.458	2.545	91.889						
	11	0.353	1.963	93.851						
	12	0.293	1.627	95.478						
	13	0.244	1.356	96.834						
	14	0.208	1.156	97.990						
	15	0.168	0.932	98.922						
	16	0.09327	0.518	99.440						
	17	0.05758	0.320	99.760						
	18	0.04319	0.240	100.000						

Table 4: Rotated component matrix for eighteen characters

	Component							
	1	2	3	4	5	6	7	8
SDB	-0.09083	0.206	0.101	0.629	0.387	0.399	-0.144	0.298
PHM	0.106	0.297	-0.06744	0.875	-0.05575	-0.05383	0.03974	-0.109
PHF	0.02965	0.426	-0.002731	0.843	-0.05912	-0.05787	0.157	0.03546
FFD	-0.244	-0.01416	0.582	-0.301	0.009926	-0.113	-0.565	0.01876
FFN	-0.02206	-0.05595	0.962	0.02071	-0.145	-0.08672	0.0008171	0.006780
FPN	-0.09382	0.09561	0.926	0.01251	0.02633	0.06750	0.08550	-0.124
NSI	0.09187	0.698	-0.135	0.321	-0.194	0.06014	0.06052	-0.338
FDH	0.05697	0.847	0.03841	0.233	-0.06151	0.01142	-0.04280	0.01065
FWH	0.177	0.550	0.293	0.03109	0.123	0.08473	0.661	0.08984
PDI	0.149	0.822	0.04280	0.305	0.06195	0.04673	0.196	0.151
NFT	0.09114	0.04749	-0.05287	-0.01870	-0.119	0.948	0.07474	-0.03579
FRP	0.539	-0.03159	-0.266	0.03176	0.03460	-0.04462	0.09502	0.679
STC	0.633	-0.136	-0.02018	0.08183	0.539	0.04237	0.145	-0.338
PTC	0.373	-0.09267	-0.145	-0.05545	0.804	-0.185	0.03668	0.09006
RCD	0.874	0.222	-0.185	0.03123	0.03764	0.01498	-0.02088	-0.03855
RCR	0.873	0.06749	-0.134	-0.06897	0.184	0.09095	0.144	0.131
PTB	0.941	.125	-0.04185	0.05888	0.123	-0.03447	0.03504	0.01618
FRC	0.854	6.787.03	0.129	0.09691	0.03874	5.740.02	0.06844	0.180

Table 5: Total variance explained for thirty-six characters

Component	Initial Eigenvalues			Extraction Sums of Spared Loadings			Rotation Sums of Squared Loadings		
	Total	% of Variance	Cumula-tive %	Total	% of Variance	Cumula-tive %	Total	% of Variance	Cumul-ative %
1	6.219	17.274	17.274	6.219	17.274	17.274	4.731	13.143	13.143
2	4.690	13.029	30.303	4.690	13.029	30.303	3.608	10.023	23.166
3	3.104	8.621	38.924	3.104	8.621	38.924	2.671	7.421	30.587
4	2.615	7.348	46.272	2.645	7.348	46.272	1.796	4.989	35.576
5	2.248	6.316	52.518	2.248	6.246	52.518	1.727	4.796	40.373
6	1.769	4.913	57.431	1.769	4.913	57.431	1.714	4.760	45.132
7	1.634	4.538	61.968	1.634	4.538	61.968	1.661	4.614	48.747
8	1.538	4.272	66.240	1.538	4.272	66.240	1.601	4.446	54.193
9	1.291	3.585	69.825	1.291	3.585	69.825	1.449	4.026	58.219
10	1.137	3.157	72.982	1.137	3.157	72.982	1.436	3.988	62.207
11	1.075	2.985	75.968	1.075	2.985	75.968	1.430	3.974	66.180
12	0.876	2.409	78.377	0.867	2.409	78.377	1.377	3.825	70.085
13	0.856	2.379	80.736	0.856	2.379	80.756	1.320	3.667	73.672
14	0.794	2.206	82.962	0.794	2.206	82.962	1.277	3.547	77.219
15	0.708	1.967	84.929	0.708	1.967	84.929	1.244	3.456	80.675
16	0.676	1.876	86.805	0.676	1.876	86.805	1.197	3.324	83.999
17	0.601	1.669	88.474	0.681	1.669	88.474	1.110	3.085	87.084
18	0.558	1.550	90.024	0.558	1.550	90.024	1.058	2.940	90.024
19	0.468	1.299	91.323						
20	0.450	1.249	92.572						
21	0.392	1.089	93.661						
22	0.369	1.026	94.688						
23	0.306	0.849	95.537						
24	0.284	0.790	96.327						
25	0.261	0.726	97.054						
26	0.188	0.522	97.575						
27	0.174	0.482	98.058						
28	0.142	0.396	98.453						
29	0.129	0.358	98.811						
30	0.114	0.317	99.128						
31	0.09103	0.253	99.381						
32	0.07702	0.214	99.595						
33	0.06268	0.174	99.769						
34	0.04218	0.117	99.886						
35	0.03133	0.08703	99.973						
36	0.009624	0.02673	100.000						

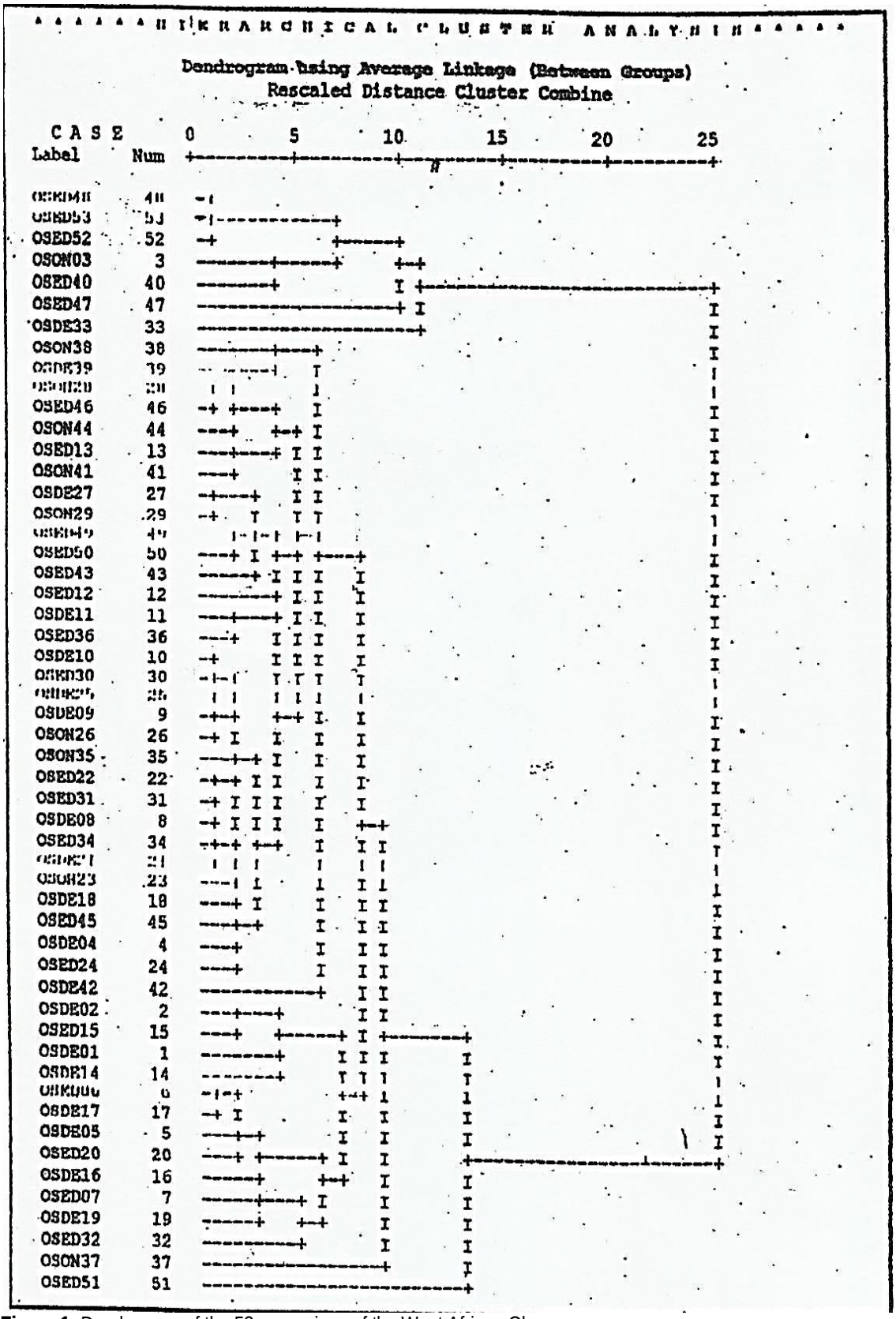

Figure 1: Dendrogram of the 53 accessions of the West African Okra.

CONCLUSION

The evaluation of qualitative and quantitative characters have confirmed the wide and continuous variation of *A. caillei* exhibited by cultivated plants, for which more and different techniques will be needed to classify. The presence of genetic diversity is important in this crop plant-*A. caillei* for improvement of the genus *Abelmoschus*. An understanding of the magnitude and patterns of genetic diversity has an important implication in breeding programmes and for conservation by the genetic resources.

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