Multivariate Analysis of Cashew (*Anacardium occidentale* L.) Germplasm in Nigeria

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Abstract

Multivariate analyses were carried out on fifty-nine germplasm accessions of cashew derived from both local and exotic populations established at the research plots of Cocoa Research Institute of Nigeria (CRIN), Ibadan, southwestern Nigeria, to assess the extent of variability and pattern of genetic diversity among these cashew populations. Data collected on 36 quantitative and 33 qualitative plant characters were subjected to taximetric tools of Euclidean distance of complete linkage (furthest neighbour) and principal component analysis (PCA).

The multivariate analyses tentatively grouped the selections into four distinct morphogenetically diverse clusters. The groupings appear to be a function of origin, eco-geographical distribution, genetic and/or agronomic affinity of the selections. Brazilian populations distinctly clustered together in two major groups while local clones and Indian selections dominated the other two major clusters with each group having its unique fruiting and tree growth habits. The clustering pattern at sub-cluster levels clearly reflects affinity of each genetic population. The principal component analysis and the potency indices showed that fruit characters are the most discriminating parameters for delineating cashew at the varietal level.

Key words: Accessions, *Anacardium occidentale*, genetic variability.

Introduction

Cashew is an important tropical fruit crop that originated from South American countries like Bolivia, Brazil, Ecuador and Peru (Valvilov, 1951; Behrens 1998) and is widely cultivated in tropical regions of the world. Cashew production is centralized in Third World countries and major producers of cashew nuts are India, Tanzania, Mozambique, Nigeria, Guinea-Bissau and Kenya. In 2002, major producers of cashew nuts are India (460,000 tonnes), Nigeria (186,000 tonnes), Brazil (178,000 tonnes) and Tanzania (123,000 tonnes) (FAO, 2004). The crop was introduced from Brazil into Nigeria by Portuguese adventurers during the 16th century (Venkataramah, 1976; Mitchell and Mori, 1987). Initially, the trees were mainly planted for afforestation and erosion control especially in the former eastern region of Nigeria with sloppy topography. The crop however became an important plantation crop in the 1950s with the establishment commercial plantations at Oghe, Oji, Udi and Mbala in the old eastern Nigeria by the Eastern Nigerian Development Corporation (ENDC) and at Iwo, Eruwa and upper Ogun in the old western Nigeria by the Western Nigerian Development Corporation (WNDC). Records showed that these plantations were planted to nuts introduced from India in the early 1950s (Sanwo, 1974).

Little or no attention was given to cashew in Nigeria until 1971 when the Cocoa Research Institute of Nigeria (CRIN) was mandated to carry out genetic improvement in the crop species. Realizing the importance of genetic diversity as the raw materials for crop improvement as opined by Allard (1970) and Brown (1989), the Institute embarked upon germplasm acquisition programme for local land race (clones) from farmer's fields and exotic Indian accessions from existing ENDC and WNDC's plantations (Togun, 1977; Akinwale and Esan, 1989). Between the period 1974 and 1978, CRIN introduced more genetic materials directly from India (Sanwo, 1979). In spite of all these efforts, very little progress was achieved by CRIN in increasing cashew production in the 1980s and this was attributed to narrow genetic base of the introductions. This low production was clearly evident as annual cashew nut production in Nigeria ranged between 22,000 tonnes and 30,000 tonnes for the period 1965 to 1990 (FAO, 2004).

Broadening the genetic base by introducing new alleles present in exotic germplasm (Faenza *et al.,* 1982) and a systematic exploitation of heterosis (Masawe, 1994) have been suggested as means to overcome some of the problem. As part of efforts to increase the genetic base of the cashew germplasm in Nigeria and consequently improving the crop, CRIN embarked upon an expedition in the mid-1980s and this led to acquisition of exotic Brazilian materials from a private commercial farm. These genetic materials were originally introduced from Brazil in 1982 by the farmer. It is expected that several introductions of genetic materials of different geographical origin and possible genetic introgression among materials that coexist for long time would have resulted into considerable variation in the cashew genetic resource in the country. Cashew improvement is however limited by the lack of adequate knowledge of genetic diversity of the existing germplasm of both local and exotic origin. Mneney *et al.* (2001) opined that adequate knowledge and information about the genetic similarity of gene pool around the world is essential for the identification of parental lines in order to exploit heterosis and introduce valuable characters into the cashew

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breeding programme. The use of polymorphic markers has been recently promoted for identification of varieties and estimation of genetic similarity among populations (WILLIAMS *et al.,* 1990, ZIEGENHAGEN *et al.,* 1993; KRABEL *et al.,* 1998; CASAS *et al.,* 1999). RAPD analysis has been used to study the genetic relationship in Indian cashew germplasm and has been found to corroborate the results obtained from morphogenetic marker study (DHANARAJ *et al.,* 2002 SAMAL *et al.,* 2003). SAMAL *et al.* (2003) however remarked that classical phenotype features are still extremely useful; although the efficiency of selection may be influence by developmental stages or by environmental effects on measured traits. Environmental influence can be minimized by appropriate experimental breeding design. Moreover, breeding of cashew is mostly based on traditional methods of selection of useful traits which are basically phenotypic like nut size, nut weight, sex ratio, length of panicle and yield performance (MNENEY *et al.,* 2001). The choice of phenotypic markers in this study was informed by its

possible practical implication on cashew breeding programme and immediate impacts on the poor resource farmers in a third world country like Nigeria. However, BROWN (1989) opined that an important way to increase productivity in any crop plant is to assess the genetic diversity in order to select desirable genotypes from the existing variants and to use the superior types in breeding programme. Therefore, it becomes imperative to quantify the extent of variation among the cashew germplasm collections in Nigeria by using phenotypic markers. Edgar Anderson pioneered the use of quantitative analysis in evaluating genetic affinity in crop species (AWOPETU, 1982). However, SNEATH and SOKAL (1973) reported that attempts at a numerical consideration of taxonomic relationships dated back to more than 200 years, but that integrated approaches to this technique has been intensified in the last few decades. Details on such developments are available in SOKAL and SNEATH (1963), SNEATH and SOKAL (1973), CLIFFORD and STEPHENSON (1975).

Table 1. – List of the 59 Cashew accessions and their pedigree.

S/No.	Accession No.	Original site of collection	New Site planted	S/No	Accession No.	Original site of collection	New Site planted
1	CC01	Ochaja	CRIN Ibadan	31	CSI62	India/WNDC Iwo	CRIN Ibadan
2	CC02	”	”	32	CSI63	”	”
3	CC03	”	”	33	CSI66	”	”
4	CC04	”	”	34	CSI67	”	”
5	CC05	”	”	35	CSO01	Brazil	”
6	CC06	”	”	36	CSO02	”	”
7	CC07	”	”	37	CSO03	”	”
8	CC08	”	”	38	CSO04	”	”
9	CC09	”	”	39	CSO05	”	”
10	CC10	”	”	40	CSO06	”	”
11	CC11	”	”	41	CSO07	”	”
12	CSI00	India/WNDC Iwo	”	42	CSO08	”	”
13	CSI01	”	”	43	CSO09	”	”
14	CSI05	”	”	44	CSO10	”	”
15	CSI06	”	”	45	CSO11	”	”
16	CSI07	”	”	46	CSO12	”	”
17	CSI09	”	”	47	CSO13	”	”
18	CSI10	”	”	48	CSO14	”	”
19	CSI11	”	”	49	CSO15	”	”
20	CSI13	”	”	50	CSO16	”	”
21	CSI14	”	”	51	CSO17	”	”
22	CSI18	”	”	52	CSO18	”	”
23	CSI23	”	”	53	CSO19	”	”
24	CSI27	”	”	54	CSO20	”	”
25	CSI30	”	”	55	CSO21	”	”
26	CSI31	”	”	56	CSO22	”	”
27	CSI36	”	”	57	CSO23	”	”
28	CSI51	”	”	58	CSO24	”	”
29	CSI58	”	”	59	CSO25	”	”
30	CSI61	”	”				

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Table 2. – List of 36 quantitative characters and their acronyms.

Characters	Acronyms	Characters	Acronyms
Weight of whole fruit (g)	WWF	Kernel weight (g)	KWH
Apple weight (g)	AWT	Kernel to nut ratio	KNR
Apple length (cm)	ALT	Volume of CNSL/nut	VCN
Apple upper circumference (cm)	AUC	Number of flowers per panicle	FPP
Apple lower circumference (cm)	ALC	Number of male flowers per panicle	MPP
Apple fluid weight (g)	AFW	Number of hermaphrodite per panicle	HPP
Apple dry weight (g)	ADW	Number of abnormal flowers	APP
Nut weight (g)	NWT	Flower sex ratio	FSR
Number of nut per panicle	NNP	Percentage pollen stainability	PPS
Total nut yield per tree	NYT	Percentage pollen germination	PPG
Number of nut per tree	NNT	Pollen grain size (um)	PGS
Nut length (cm)	NLT	Tree crown spread (m)	TCS
Nut lower width (cm)	NLW	Tree trunk circumference	TCM
Nut upper width (cm)	NUW	Number of leaves per twig	LTW
Nut lower length (cm)	NLL	Tree height (m)	THT
Nut upper length (cm)	NUL	Days to 50% flower Anthesis	DFA
Nut thickness (cm)	NTK	Days to 50% fruit maturity	DFM
Shell weight (g)	SWH	Harvesting Period	HPD

Table 3. – List of 33 qualitative characters and their acronyms.

Character	Acronyms	Character	Acronyms
Apple colour	ACL	Colour of CNSL	CNL
Apple ridges	ARG	Leaf shape	LSH
Apple skin texture	AST	Leaf size	LSZ
Apple shape	ASH	Shape of leaf apex	LAS
Apple cavity atapex	ACA	Angle of leaf petiole to stem	ALP
Apple apex	APA	Branching pattern	BPT
Apple base	ABS	Colour of young leaves	CYL
Apple juice astringency	AJA	Colour of mature leaves	CML
Nut shape	NSH	Crack on trunk bark	CTB
Nut base shape	NBS	Crotch angle of main branch	CAM
Nut apex shape	NAS	Tree habit	THB
Suture relative position	SRP	Secondary flowering habit	SFH
Nut flank	NFK	Leaf margin	LMG
Nut stylar scar	NSS	Colour of boot leaves	CBL
Nut attachment to apple	NAA	Susceptibility to Inflorescence blight	SIB
Nut suture	NSU	Susceptibility to stem girdling	SSG
Colour of mature nut	CMN		

In the present study, multivariate analyses of Euclidean distance of complete linkage and principal component analysis (PCA) were employed in the analysis of phenotypic data of 59 cashew germplasm accessions of both local and exotic origins with the view to estimate genetic variability extant in this crop species in Nigeria.

Materials and Methods

Table 1 is a list of the experimental materials consisting of both local and exotic biotypes of cashew established at the research plots of the Cocoa Research Institute of Nigeria (CRIN), Ibadan (Lat. 07° 10'N, Long. 03° 52'E) southwestern Nigeria. The local accessions were eleven clones selected from farmer's farms in Ochaja, Kogi State (guinea savannah ecology), while the exotic accessions comprise twenty-three and twenty-five Indian and Brazilian introductions respectively. The farmer's clones are the materials selected from the early introductions of which the origin cannot be ascertained (SANWO, 1980). Meanwhile, the Indian selections are the open pollinated progenies of the materials originally introduced by the Eastern and Western Nigerian governments in the 1950s for its plantations, while the Brazilian materials was introduced from Brazil by Kosoni-Ola Farms Limited, Oro, Kwara State in 1982. All the materials were planted at present location (CRIN, Ibadan) in 1987. The age of the trees was about 12 years at the inception of this study. The trees were planted at spacing of 10 m x 10 m in randomized complete block design (RCBD) layout with three replications. Each accession was represented by three entries per block. Routine maintenances were carried out on the experimental plots. *Table 2* and *3* show the list of selected characters used for data collection based on the Cashew Descriptor of the International Board for Plant Genetic Resources (IBPGR 1986). The data collected for 3 years (1999, 2000 and 2001) were subjected to cluster analyses, using taximetric principle of Euclidean distance complete linkage (furthest neighbour) and the principal component analysis. Analyses were performed using the N.T.S.Y.S. PC package version 1.8 (RHOLF, 1989).

Results

Figure 1 shows the dendogram from Euclidean distance of complete linkage clustering method as a measure of the extent of genetic relationships among the cashew accessions. *Table 4* is the corresponding cluster and sub-cluster derivatives from *figure 1*. The dendogram shows similarity indices ranging between 22.00% and 100.00%. At 62.00% similarity level, the dendogram group the 59 accessions to four main clusters similar to the result of principal component analysis (PCA) as shown in *Figure 2*. The summary characteristics of the groups and their respective means are presented in *Table 5*.

Group I

Thirteen accessions of Brazilian origin clustered in this group, but further divided into two sub-clusters (A
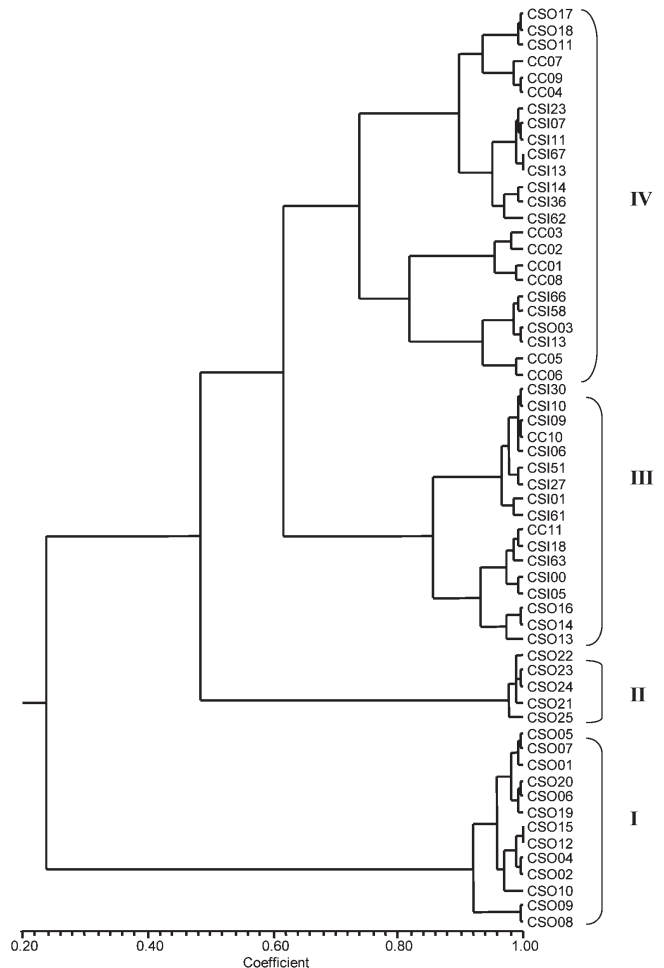

Figure 1. – Complete linkage dendogram showing the relationships among the fifty-nine cashew accessions.

and B) of 2 and 11 accessions respectively. These are mostly Brazilian accessions exemplified by large apple and medium-large sized nuts. They are characteristically early and high yielding with determinately intensive branching resulting into large open canopies. The apple produces high contents of juice and dry matter. Higher nut yield both in terms of number of nuts per tree and kilograme/tree was recorded in these trees despite few clustering of about 3 fruits per panicle and this can be linked to the prolific flowering and highly fertile pollens among these selections. They produce nuts with high content of kernel to nut ratios and moderate quantity of cashew nut shell liquid (CNSL). Period of fruit harvest among these accessions is short and no incidence of inflorescence blight and stem girdling was recorded in this group. The potentials abound in this set of trees suggest possible selection of high yielding varieties of cashew that produce high quality grade nuts in the short term for the poor resource cashew farmers. These materials will also be useful in any cashew improvement work among major producing countries in the West and East Africa sub-regions.

Group II

Five Brazilian accessions clustered together in this group. They are made up of jumbo-sized apple and nut

Table 4. – Summary of the major clusters and sub-clusters of 59 cashew accessions derived from multivariate analyses.

Cluster No.	Sub-clusters	List of accessions.
I	A	CSO08, CSO09.
	B	CSO10, CSO02, CSO04, CSO12, CSO15, CSO19, CSO06, CSO20, CSO01, CSO07, CSO05.
II	C	CSO25, CSO21, CSO24, CSO23, CSO22.
III	D	CSO13, CSO16, CSO14, CSI05, CSI00, CSI63, CSI18, CC11.
	E	CSI61, CSI01, CSI27, CSI51, CSI06, CC10, CSI09, CSI10, CSI30.
IV	F	CC06, CC05, CSI31, CSO03, CSI58, CSI66
	G	CC08, CC01, CC02, CC03.
	H	CSI62, CSI36, CSI14, CSI13, CSI67, CSI11, CSI07, CSI23.
	I	CC04, CC09, CC07, CSO11, CSO18, CSO17.

accessions with a great deal of dry matter content but low juice astringency. They produce few fruits per panicle but large shell and kernel ratios. They contain high level of cashew nut shell liquid (CNSL) and long-spanned fruiting habits. The trees of these accessions produce very large leaves and exhibited spreading growth habit with extensive branching characteristic. The selections produce inflorescences with few staminate and hermaphrodite flowers and their pollen grains are large with moderate fertility. A nut yield in terms of nuts per tree was very low and this is probably due to large fruit size. These materials would be good source of genes that could be exploited in any improvement work to improve on fruit size and quality. The trees also offer potential for the future growing of cashew for the purpose of juice and other derivatives productions. These trees would be useful source of materials for genetic study to understand the nature of genes responsible for fruit and agronomic traits in cashew. The potentials within these germplasm stocks would only be useful for the long term breeding programme in cashew.

Group III

Two sub-clusters (D and E) were generated by this group and it contains a total of seventeen accessions of different geographical origins, however, it was predominated by the Indian selections with twelve entries. Only two local clones were recorded in this cluster. Three Brazilian accessions that exist within this group fused together at the same linkage level as a sub-cluster suggesting the extent of genetic similarity. Cashew accessions in this group and sub-groups generally produce small but many fruits per panicle. Suffice that the trees produce high number of nuts per tree but the average nut weight was very small, and this resulted into low total output in kilogramme. Red apple with round shape is predominant among these trees. Other traits of this group are profuse flowering, very low CNSL and low apple dry matter contents. The apple juice content is also low but highly astringent. They produce small pollen grains that are highly fertile. The trees produce small leaves but with characteristic compact canopies

and mostly mid-season producers that had moderate-spanned fruiting habits. Pockets of trees with secondary flowering habit were noticed in this group. Moderate incidence of inflorescence blight and stem girdling were recorded among these accessions. The prolific flowering and fruiting habit and compact nature of the canopy could be exploited in future breeding work.

Group IV

It is heterogeneous group of the three selected populations. 9 of the eleven local clones were found within this group and this probably suggests high level of genetic introgression among these materials over the period of time. Only four Brazilian accessions fused in the group while the eleven others were Indian introductions. The clustering pattern of accessions within the group depicts origin and breeding history as the farmers' clones and Brazilian accessions fused together respectively. These trees produce the highest over all nut yield (kg) per tree

resulting from prolific fruiting and nut yield per tree. They are characteristically tall and upright trees with regular flowering and fruiting habits. High pollen grain fertility and very high flower sex ratios corroborate the prolific fruiting of these selections. The level of adaptation of these long introduced genetic materials was reflected in their yield performance.

Principal Component Analysis (PCA)

Figure 2 shows the principal component analysis (PCA) of the cashew accessions with the aid of the first two principal component axes which accounted for about 33.20% of the total variation. The divergent spread of the accessions across the PCA axes was similar to the four groups derived in the dendogram. The principal component analysis indicated the extent of genetic diversity of the selected cashew accessions based on the evaluated characters. The linear transformation performed by the principal component methods generated

Table 5. – Cluster means and description of some selected phenotypic traits showing variations among the 4 major groups derived from the multivariate analysis.

Chara	Group I	Group II	Group III	Group IV
Apple				Min
WWF (g)	96.23 (large)	178.89 (jumbo)	39.35 (small)	75.22 (medium)
AWT (g)	85.32 (large)	162.27 (jumbo)	32.75 (small)	67.47 (medium)
AFW (g)	80.12 (high)	155.17 (very high)	47.81 (low)	61.33 (intermediate)
ADW (g)	5.05 (high)	7.12 (high)	1.92 (low)	3.78 (intermediate)
ACL	1.15 (predominantly yellow)	1.2 (predominantly yellow)	1.96 (predominantly red)	1.5 (mixture)
ASH	2.08 (conical-obovate)	1.20 (predominantly cylindrical)	3.11 (predominantly round)	1.98 (predominantly cylindrical)
AJA	3.92 (low-slight)	3.00 (low)	6.94 (high)	5.91 (high)
ABS	2.07 (round)	1.80 (round)	323 (flat)	3.45 (flat)
Nut				
NWT (g)	9.91 (medium-large)	16.81 (jumbo)	4.04 (small)	6.64 (small-medium)
NNP	2.93 (moderate)	1.24 (low)	8.15 (high)	5.28 (high)
NNT	1446.14 (high)	406.52 (low)	1955.95 (high)	1944.07 (high)
NYT (kg)	14.04 (high)	7.82 (low)	8.74 (low)	13.30 (high)
NTK (cm)	1.83 (large)	1.95 (large)	1.21 (small)	1.62 (intermediate)
SWH (g)	5.52 (large)	10.59 (very large)	3.06 (small)	4.21 (small-intermediate)
KWH (g)	4.27 (large)	6.27 (very large)	1.86 (small)	2.28 (small-intermediate)
KNR	0.43 (high)	0.31 (intermediate)	0.36 (high)	0.37 (high)
VCN (ml)	1.43 (high)	1.98 (high)	0.48 (low)	0.85 (intermediate)
NAA	5.46 (intermediate)	7.00 (tight)	3.00 (loose)	3.16 (loose)
CMN	3.15 (ash-grey)	3.20 (ash-grey)	2.17 (dark-grey)	2.16 (dark-grey)
Flora				
FPP	286.88 (high)	54.69 (low)	439.01 (high)	398.86 (high)
MPP	239.67 (high)	45.22 (low)	244.11 (high)	256.71 (high
HPP	52.04 (high)	9.14 (low)	59.57 (high)	77.21 (high)
APP	0.15 (low)	0.11 (low)	0.28 (moderate)	2.11 (high)
FSR	0.23 (moderate)	0.21 (moderate)	0.26 (moderate)	0.43 (high)
PPS	80.73 (high)	69.41 (moderate)	87.63 (high)	86.51 (high)
PPG (um)	37.26	29.92	37.18	36.40
PGS	54.09 (large)	61.02 (large)	46.14 (small)	50.20 (intermediate)
Tree				
TCS (m)	9.92 (intermediate)	13.79 (large)	7.01 (small)	10.74 (intermediate)
TCM (m)	1.11 (intermediate)	1.38 (large)	1.02 (intermediate)	1.22 (intermediate large)
LTW	13.53 (High)	10.60 (intermediate)	15.20 (high)	14.95 (High)
THT (m)	9.55 (Intermediate)	8.58 (intermediate)	9.15 (intermediate)	12.09 (Tall)
LSZ	5.76 (Intermediate)	7.00 (Large)	3.00 (small)	4.91 (small-intermediate)
CTB	1.00 (low)	1.2 (low)	2.82 (intermediate)	3.33 (intermediate)
CAM	3.24 (acute)	7.00 (obtuse)	3.07 (very acute)	3.50 (acute)
SFH	0.03 (very low)	0.00 (absent)	0.47 (present)	0.12 (very low)
BPT	2.00 (intensive branching)	1.00 (Extensive branching)	2.00 (intensive branching)	1.83 (intensive branching)
THB	5.00 (upright open canopy)	7.00 (Spreading canopy)	3.05 (Upright compact canopy)	5.33 (upright open canopy)
SIB	0.00 (no incidence)	0.00 (no incidence)	2.47 (low incidence)	3.41 (moderate incidence)
SSG	0.00 (no incidence)	0.00 (no incidence)	2.58 (low incidence)	3.66 (moderate incidence)
Maturity				
DFA	71.92 (Early)	211.20 (late)	158.29 (mid-season)	112.04 (Early/mid-season)
DFM	145.84 (Early and regular)	283.40 (late and irregular)	206.65 mid-season/long)	194.71 (mid-season and regular)
HPD	24.62 (short)	57.60 (long)	40.00 (moderate)	43.79 (moderate)

another 69 independent variables, known as principal components, which are described by their latent roots (Eigenvalues) and vectors (*Tables 6*). The latent roots associated with each principal component measures the contribution of each principal component to the total variance, while the coefficients of the latent vector associated with a given principal component indicate the degree of contribution (or loading) of each original variable to the principal component in question. ROJAS *et al.* (2000) stated that there has not been an established test for evaluating the significance of latent roots and therefore suggested the criterion established by KAISER (1960), as adapted in this investigation. According to this criterion, the first nineteen principal components qualify, accounting for about 96.17% of the total variation (*Table 6*) and this showed the trend of variation across the variables analyzed. The first four principal axes accounted for 50.14% of the variance.

Table 7 is the summary of the characters associated with the first four principal components and their degree of importance (potency index) of each variable. The nut characters (weight, number per panicle, number per tree, yield per tree, thickness, lengths of the lower and upper parts, shell weight, kernel weight and shelling percentage) dominated the first principal axis. However, apple characters (weight, length, circumfer-

ences of the upper and lower parts, fluid/juice content and dry weight) mainly dominated the second principal axis. In addition to the quantitative characters with high positive component loads in the second principal component were colour and shape of the apple. However, third principal component (8.82%) was associated with number of nuts per tree, total nut yield, number of nut per panicle, pollen grain fertility, and medium-sized nut. The component distinguished cashew accessions with very high clustering per panicle, high nut yield with high pollen grains fertility but the nuts are of medium-sized type. Other characters with high component loads were spread along principal components 5–15 with about 90.00% of the total variation. The spread of the variation across many principal component axis suggests that in genetic variability study involving identification of parental lines or varieties, phenotypic characters from fruit (nut and apple), floral, pollen and vegetative especially leaf, canopy type, tree habit and branching pattern should be selected.

Discussion

Generally, the similarity in the clustering patterns obtained among the two numerical techniques probably attest to the reliability of the methodology with respect
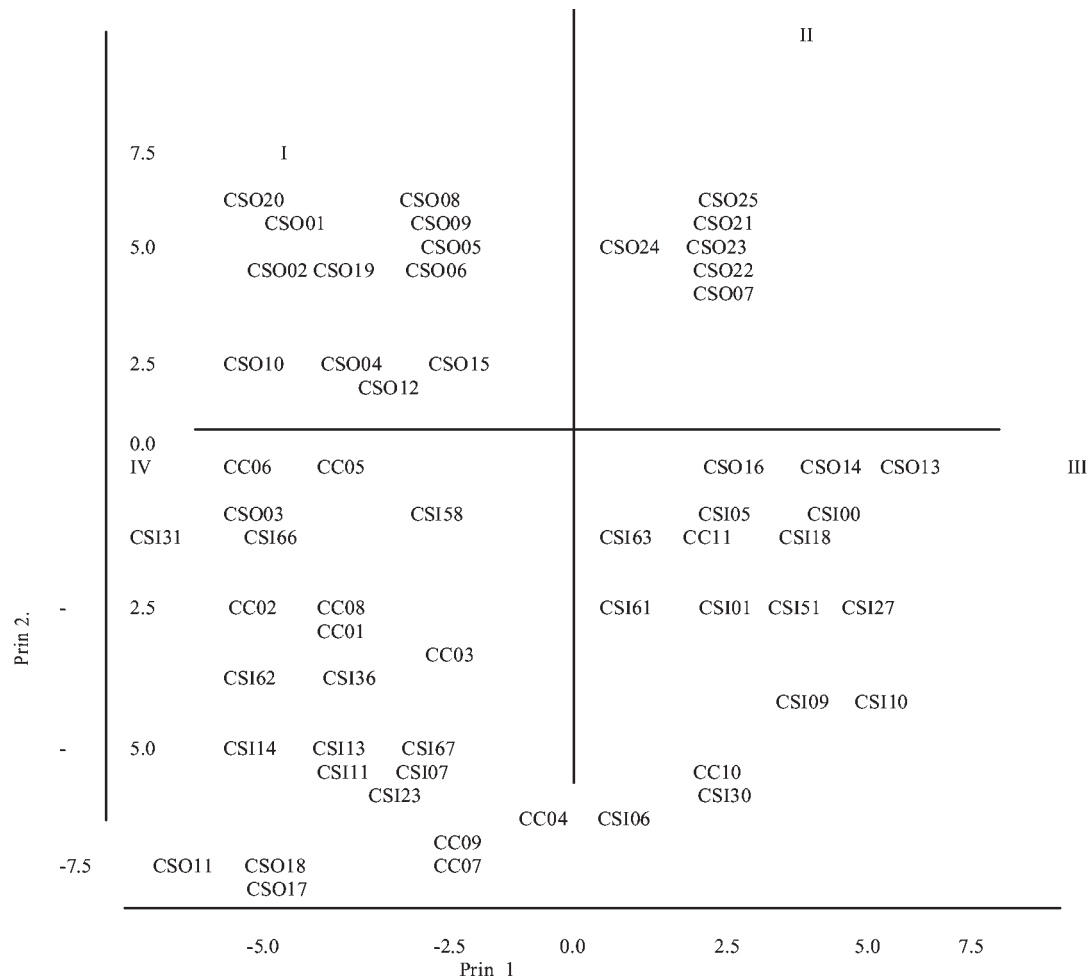

Figure 2. – The Principal Component Analysis (PCA) of the fifty-nine selected cashew accessions using the first two principal component axes.

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Table 6. – Eigenvalues of correlation matrix, the proportion and total variance for the first 20 principal component axes of the cashew accessions.

Prin.	Eigenvalue	Difference	Proportion	Cumulative
1	14.68	3.72	0.18	0.18
2	10.97	4.79	0.15	0.33
3	6.18	0.75	0.09	0.42
4	5.43	1.48	0.08	0.50
5	3.94	1.03	0.05	0.56
6	2.91	0.28	0.05	0.60
7	2.63	0.21	0.04	0.64
8	2.42	012	0.04	0.68
9	2.31	0.23	0.03	0.71
10	2.08	0.19	0.03	0.76
11	1.89	0.22	0.03	0.78
12	1.67	0.04	0.03	0.81
13	1.63	0.18	0.03	0.83
14	1.45	0.07	0.02	0.86
15	1.37	0.11	0.02	0.88
16	1.26	0.03	0.02	0.90
17	1.23	0.06	0.02	0.92
18	1.17	0.11	0.02	0.94
19	1.06	0.09	0.02	0.96
20	0.10	0.00	0.02	0.98

to the collected data. The clustering pattern of the accessions probably reflects the genetic history, eco-geographical origins or collections, and/or agronomic affinity of the selections. The clustering of accessions on the basis of previous breeding history, geographical distribution and agronomic parameters was similar to the report of SWAMY *et al.* (2002). AWOPETU (1982) and AWOPETU and ALIYU (2000), pointed out that entries from the same location might have evolved similar growth forms which often influence the pattern of fusion. Similar results have also been reported in Yam (CRUZ *et al.,* 1999), Cocoa (LACHENAUD and OLIVER, 2001), Gerbera (ANURADHA and NARAYANA-GOWDA, 2001), Lapsi (*Choerospondias axillaries* (Roxb.) B. L. BURTT and A. W. HILL) (PAUDEL *et al.,* 2002).These submissions possibly lend credence to the fusion together of the accessions of Brazilian origin in groups 1 and 2, and local selections in groups 3 and 4

of the dendograms. Nine sub-groups obtained from the dendograms represent morphogenetic variants of the four major groups on the basis of fruit (apple and nut), floral, fruiting, tree habit and leaf characteristics. Variation recorded among the selected accessions lends credence of the suggestion that population of a crop species from different ecological environment usually exhibit adaptive characteristics in morphological and agronomic traits (ALLARD, 1970; EDEMA and FAKOREDE, 1978). Such variants might have arisen from deliberate selection of preferred biotypes by farmers and consumers, changes connected with genetic aberrations (mutation) or gene transfer (introgression and hybridization), in addition to adaptation to local environment. The incidence of inflorescence blight disease and stem girdling insect recorded on cluster III and IV accessions that were dominated by local clones and Indian selections reflects the long

Table 7. – Character associated with the first four principal components and their degree of importance (potency index) of each variable.

Character	Prin. 1	Prin. 2	Prin. 3	Prin. 4	Potency Index
Apple					
WWF	0.196	0.225*	0.106	0.064	0.521
AWT	0.156	0.301*	0.108	0.028	0.482
ALT	0.131	0.262*	0.136	0.042	0.391
AUW	0.234*	0.281*	0.042	0.101	0.223
ALW	0.228*	0.301*	0.112	0.046	0.212
ADW	0.125	0.241*	0.136	0.020	0.394
AFW	0.182	0.298*	0.105	0.112	0.401
ACL	-0.204*	0.228*	0.045	0.105	0.361
ASH	0.121	0.205*	0.124	0.084	0.296
Nut					
NWT	0.362*	0.080	0.056	-0.050	0.791
NNP	0.342*	0.010	0.107	0.041	0.464
NNT	0.289*	-0.021	-0.097	0.234*	0.303
TYT	0.239*	0.081	-0.024	-0.008	0.342
NTK	0.250*	0108	0.053	0.038	0.240
NLL	0.281*	0.056	0.321*	0.020	0.294
NLT	0.062	0.205*	0.048	-0.040	0.272
NUL	0.293*	-0.138	0.063	-0.081	0.342
SWH	0.299*	-0.180	-0.338*	0.029	0.421
KWH	0.323*	0.059	--0.224*	0.023	0.222
KSR	-0.286*	0.031	0.198	0.054	0.262
VCN	0.060	0.124	0.262*	0.041	0.223
Floral					
FPP	0.013	-0.121	0.234*	-0.101	0.351
MPP	0.024	-0.060	0.267*	0.024	0.323
HPP	0.014	-0.080	0.282*	0.373*	0.308
PPS	0.063	-0.138	0.269*	0.024	0.233
PPG	-0.070	-0.077	0.339*	0.044	0.322
PGS	-0.162	-0.035	0.232*	-0.302*	0.201
Vegetative					
LTW	-0.116	0.188	-0.226*	-0.041	0.142
TCS	-0.124	0.036	0.057	0.331*	0.139
THT	-0.052	0.061	-0.020	-0.324*	0.182
TCM	-0.014	0.043	-0.048	-0.197	0.154
LSZ	0.301*	0.200*	0.121	0.056	0.106

* Characters with ≥ 0.200 deviation.

history of introduction, adaptation and coexistence of the pests and the crop. It is important to note that the accessions from same regions tend to show similarity in some agronomic traits and this probably reflects the previous breeding history and adaptive genes that are resipotory in the selections. Yield quality characteristics such as, fruit size, nut yield, juice content and astringency, tree growth and branching pattern as well as flowering and fruiting habit, greatly influenced the clustering patterns of the accessions.

Major groups and sub-groups identified in this investigation are expected to enhance the selection of parents for use in breeding programme aimed at improving cashew production in Nigeria. EZEAKU and AWOPETU (1992) and AWOPETU and ALIYU (2000) observed that crosses between groups and sub-groups are apt to generate more genetic variability than crosses within groups and sub-groups. It is also expected that knowledge of the groups and sub-groups identified may be used to develop cashew genotypes for specific purpose. The

grouping of the accessions provides preliminary answer to the identification of parental lines for future breeding works on cashew in Nigeria and the proposed West Africa cashew improvement network programme. Similarly, the study also provide a short term solution to the identification of potential improved cashew varieties that combine high yielding with quality nut grade for the Nigerian cashew industry. The long term application of results of this study will greatly improve the quality of cashew nuts that will be produce for Nigerian cashew industry and global trade at large. The results also showed that the genetic base of Nigerian cashew has been enhanced and this effort will result in rapid improvement in the production of cashew in the country.

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