

Genetic Diversity of Shea Butter Tree (*Vitellaria paradoxa* C.F. Gaernt) in the Guinea Savanna of Nigeria Based on Morphological Markers

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Abstract: The knowledge and understanding of the extent of genetic variation of shea genotypes is important for conservation and improvement of the crop. The study was conducted to assess genetic diversity among shea genotypes in different agro ecological zones with the aim of establishing the extent of variation in the crop. In this study, 60 shea genotypes from different locations were evaluated for genetic variability and assessed based on 24 agro morphological characters. The study was conducted in three agro ecologies in the Guinea savanna of Nigeria. The shea genotypes were naturally established, but selected and preserved by farmers on their cropping areas. Data on morphological traits were analyzed using analysis of variance, descriptive analysis, cluster and principal component analyses. Results of the analysis of variance showed that the mean squares for agro ecology were highly significant ($p \leq 0.05$) for traits related to trees, fruits and leaves. The first three principal components axes accounted for 66.57% of the variation among genotypes. Fruits and nuts diameter, nut length, leaf length, leaf width and petiole length contributed most of the variation. There was wide genetic diversity among shea trees within and among agro ecological zones, as was clearly distinct with traits related to fruits and nuts. This implies that a breeding programme can be initiated to improve on the fruit yield of the crop.

Key words: Genetic diversity • Agro ecology • Guinea savanna • *Vitellaria paradoxa*

INTRODUCTION

Vitellaria paradoxa is an important tree species in Sub-Sahara parkland and it provides a range of forest products and play vital roles in the rural economy [1]. It is typically a savanna woodland tree species. Its natural habitat stretches over Africa. The economic importance of shea has led research scientists to undertake investigation into its silver-culture and ecology [2], but little is known of the pattern of genetic variation within its natural range. Variability in shea trees is enormous and not yet fully understood.

Genetic diversity assessment has potential uses in evolution, breeding and conservation of genetic resources [3]. The extent of diversity in the accessions is paramount for improvement and utilization of genetic

resources. Genetic diversity is therefore the backbone of conservation of plant genetic resources for both present and future use. Genetic diversity of species also helps formulate appropriate sampling strategies for both *in situ* and *ex situ* conservations, with the aim to protect the variability of taxa so as to preserve ecological processes, rate of establishment, survival and fecundity [4].

Genetic diversity provides plant breeders with options to develop productive crops that are resistant to virulent pests and diseases and adapted to changing environments. The ability to identify genetic variation is indispensable to effective management and use of genetic resources. It was therefore prudent to subject the shea genotypes to genetic characterization using morphological markers to understand the extent of available genetic variation. The characterization of shea

tree is mainly based on phenotypic data. A continued phenotypic evaluation of diversity will facilitate the formulation of conservation strategies to identify populations that represent germplasm collections for *ex situ* and *in situ* conservation. This is particularly important for tree crops like shea tree because very large number of samples obtained by random sampling require large area for the conservation as living specimens.

In Nigeria the shea tree occurs mainly in the wild. It thrives well within the Guinea and Sudan savanna areas as well as the lower Sahel region of the country. The interest in shea is linked to its multiple physical and chemical properties. Some studies have been carried out in Nigeria on the processing of shea butter. Very few studies have been carried out on the morphological characteristics of shea trees in Nigeria, in order to identifying the different shea varieties that exist in the country. Studies carried out in some West African countries have shown the existence of a high intra-specific variation [5, 6] among shea trees. A phenotypic variation among variation of shea trees and a correlation between its different physical properties have been reported in Ghana [7], Mali [8], Cote d'Ivoire [9] and in Nigeria [10]. A preliminary step in the identification of the various genotypes of the shea trees that may exist in Nigeria is to identify the phenotypes. Little of such studies have been carried out in the country. There is thus need to assess the levels and distribution of genetic diversity within and between populations of shea trees in the Guinea savanna of Nigeria.

MATERIALS AND METHODS

The shea genotypes in this study were naturally established, but selected and preserved by farmers on their cropping areas. Sixty shea genotypes from six locations within three agro ecological zones in the Guinea savanna of Nigeria were used in this study. According to Palmberg [11], when the variation of the properties of a particular species over a given surface area is to be undertaken for the first time, the sampling sites should be chosen over a large grid as a function of the ecological gradient of the area in order to take into account differences that may be due to climate or ecology. Shea trees from each zone were sampled. In each state, two locations separated by at least 50 km apart were chosen and in each location, a single site containing shea trees was randomly selected for sampling. In each location 10 shea trees separated by a distance of at least 25m to avoid possible effects of inbreeding were sampled. A minimum of 10 trees are required to describe the

variation that may exist in a particular species growing within the same parkland [11]. The geographical coordinates and area of each location were taken using a Geographical Positioning System (GPS) apparatus (Table 1, Fig. 1). The study was conducted in Magali and Agwongo (northern Guinea savanna) in Kebbi State, Emishurun and Gbako Kasarawa (southern Guinea savanna) in Niger State and Saki and Ogbomoso (Forest-Savanna transition zones) in Oyo State, to have a total of six locations (Table 2).

Data on quantitative traits were collected from randomly selected shea trees for two years. Quantitative characters were determined by measurement with a tape rule, counting and weighing. These traits were measured with reference to the IPGRI shea Descriptor [12]. The traits were measured on traits related to the tree, leaves and fruits and nuts. Tree height, trunk height and crown height were measured using a calibrated long stick. Trunk height (m), was measured from the base of the tree to the point of emergence of first branch, the tree height (m) was measured from ground level to the top of the tree. Crown height (m) was measured from the first leaf branch to the top of the tree. The circumference of the trunk of each tree sampled was measured at breast height from the ground using a flexible meter rule. The number of main branches were counted, while the bark thickness (mm) was measured using a Vernier calliper. Crown diameter (m) was measured as the mean diameter using two directions (North-South and East-West). From each tree, 50 mature fruits were sampled. The fruit linear dimensions namely upper diameter (x), intermediate diameter (y) and the lower diameter (z) were measured with a Vernier calliper. The fruits were then depulped and the same measurements carried out on the nuts. The weight of fruits and nuts were measured taking 100 of each fruits and nuts as sample representative. While, the fruit length (cm) and nut length (cm) were measured using a ruler. Exactly fifty leaves per tree were randomly harvested from the periphery of the tree branch while exercising caution to avoid border effect. Three traits were measured on the leaves: leaf length (LLT), leaf width (LWT) and petiole length (PLT). The geometric mean diameter (D_g) of the fruits and nuts were calculated according to Diarrassouba *et al.*, 2007, using the relationship;

$$D_g = (xyz)^{1/3}$$

where;

x is upper diameter of fruit or nut

y is intermediate diameter of fruit or nut

z is lower diameter of fruit or nut

Table 1: Location and geographical coordinates of *Vitellaria paradoxa* in the Guinea savanna of Nigeria

Agro ecologies	Location	Latitude	Longitude	Altitude	Area
Northern Guinea Savanna	Magali	10.238	4.652	154	9.45
	Agwongo	10.169	4.652	182	5.29
Southern Guinea Savanna	Emishurun	9.049	6.186	127	12.20
	Gbako kasarawa	9.142	6.009	157	26.00
Forest-savanna transition zone	Saki	8.618	3.402	500	16.30
	Ogbomoso	8.178	4.217	358	6.60

Table 2: Code names and sources of the shea genotypes

Agro ecology	States	Locations	Genotypes
Northern Guinea Savanna	Kebbi	Magali	1-10
		Agwongo	11-20
Southern Guinea Savanna	Niger	Emishurun	21-30
		Gbako kasarawa	31-40
Forest-savanna transition zone	Oyo	Saki	41-50
		Ogbomoso	51-60

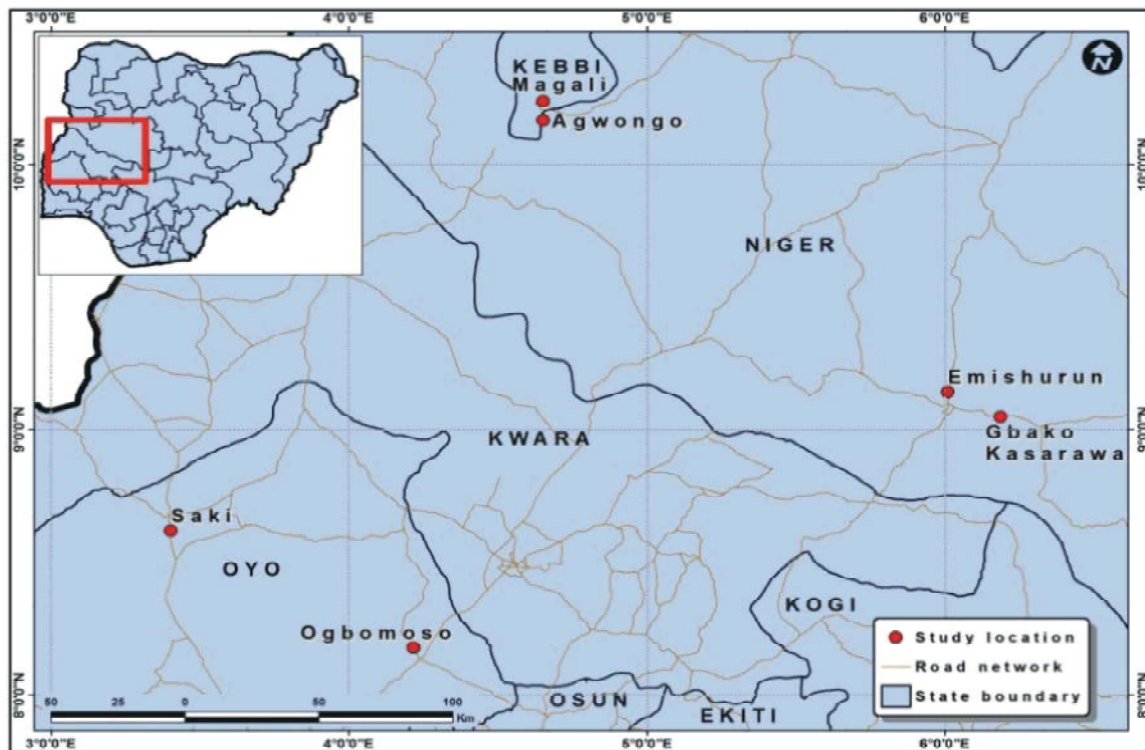


Fig. 1: Map showing the six location sites randomly selected

Data collected were subjected to analysis of variance for within and among agro ecology. Descriptive statistics (means, ranges and standard deviation) was carried out to summarise the data. Statistical models were used in the analysis of variance. Analysis of variance was carried out separately on fruits, nut and leaves traits for each agro ecology, where location, years and genotype nested within location were considered as a random effect. The statistical model for the analysis is presented as follows:

$$Y_{ijk} = \mu + R_i + L_j + G/L_{k(j)} + \epsilon_{ijk} \quad \text{Model [1]}$$

where Y_{ijk} is the measurement on the k^{th} genotype in the j^{th} location in i^{th} years, μ is the overall mean, R_i is the effect of years, L_j is the effect of location, $G/L_{k(j)}$ is the effect of genotype nested within location and ϵ_{ijk} is the error term (ref....??).

Combined analysis of variance was carried out using three different models. The first model [Model 2] was used for traits with only one sample per individual tree

(traits such as height, circumference and canopy diameter). The statistical model for the analysis is presented as:

$$Y_{ijk} = \mu + E_i + L/E_{j(i)} + G/L_{k(j)} + E_{ijk \text{ Model}} \quad [2]$$

where Y_{ijk} is the measurement on the k^{th} genotype in the j^{th} location within the i^{th} agro ecology, μ is the overall mean, E_i is the effect of agro ecology, $L/E_{j(i)}$ is the effect of location nested within agro ecology, $G/L_{k(j)}$ is the effect of genotype nested within location and ϵ_{ijk} is the error term (ref....???). The second model [Model 3] for the combined analysis of variance was used for traits related to fruits and nuts with repeated samples (traits such as fruit weight, nut weight, pulp weight, fruit length and nut length). The analysis was carried out across years and agro ecology, where agro ecology was considered as a fixed effect and year, genotype nested within location and location nested within agro ecology were treated as random effects. The statistical model is represented by the equation as follows:

$$Y_{ijk} = \mu + R_i + E_i + L/E_{j(i)} + G/L_{k(j)} + RE_{il} + \epsilon_{ijk} \quad [3]$$

where, Y_{ijk} is the measurement on the k^{th} genotype in the j^{th} location within the i^{th} agro ecology in i^{th} years, μ is the overall mean, R_i is the effect of years, E_i is the effect of agro ecology, $L/E_{j(i)}$ is the effect of location nested within agro ecology, $G/L_{k(j)}$ is the effect of genotype nested within location, RE_{il} is the interaction effect between years and agro ecology and ϵ_{ijk} is the error term. The third model [Model 4] for the combined analysis of variance was used for traits with repeated samples (traits such as fruit weight, nut weight, fruit length, nut length, leaf length, petiole length, leaf width). The analysis was carried out across years and agro ecology, where agro ecology was considered as a fixed effect and year, location, genotype nested within location and location nested within agro ecology were treated as random effects. The statistical model is represented by the equation as follows:

$$Y_{ilgjk} = \mu + R_i + E_i + B_g + L/E_{j(i)} + G/L_{k(j)} + RE_{il} + \epsilon_{ilgjk} \quad \text{Model [4]}$$

where, Y_{ilgjk} is the measurement on the k^{th} genotype in the j^{th} location in g^{th} replication within the i^{th} agro ecology in i^{th} years, μ is the overall mean, R_i is the effect of years, E_i is the effect of agro ecology, B_g is the block effect, $L/E_{j(i)}$

is the effect of location nested within agro ecology, $G/L_{k(j)}$ is the effect of genotype nested within location, RE_{il} is the interaction effect between years and agro ecology and ϵ_{ilgjk} is the error term. Pearson correlation analysis was performed on the means to study the relationships among traits.

The Principal Component Analysis (PCA) was performed to determine the pattern of variation among the genotypes and the relative importance of the various characters. Groups of populations with similar characteristics were built using Single Linkage Cluster Analysis (SLCA). The number of groups to build was chosen based on the R-square values of the cluster dendrogram to classify the genotypes into groups based on their relationships. These analyses were performed only on data related to leaf characteristics (leaf length, leaf width and petiole length) and fruit characteristics (fruit length, nut length, fruit upper diameter, fruit lower diameter, fruit intermediate diameter, geometric fruit diameter, nut upper diameter, nut intermediate diameter, nut lower diameter, geometric nut diameter, fruit weight, nut weight and pulp weight). All analyses were performed using the statistical analysis system (SAS) package version 9.2 [13] and GENSTAT Discovery Edition 4 [14].

RESULTS

Results of the analysis of variance within agro ecology showed that the mean squares for years, locations and genotypes nested within location were highly significant ($p \leq 0.05$) in all traits measured on fruits and leaves. Results of the combined analysis of variance across agro ecology showed that the mean squares for agro ecology were highly significant for all traits related to trees, fruits and leaves, with the exception to trunk height and number of main branches.

Comparison of means between the three agro ecological zones showed that populations of the transition zone had bigger circumferences of the trunk, tree height, bark thickness and crown diameter and were significantly different ($p \leq 0.05$) compared to those of the northern and southern guinea savanna zones (Table 3), which had trees with smaller circumferences producing larger fruits with larger nuts. Generally for all the trees sampled, the circumference of the trunk ranged from 1.26m in the southern Guinea savanna (low altitude) to 1.92m in the transition zone (high altitude) with an average value of (1.55m). The highest values for the circumferences of the trunk were recorded in the transition zone (Ogbomoso and Saki) with respective values of 2.7 m and 2.5 m.

Table 3: Mean values of the different agromorphological traits in each agroecology of the Guinea savanna of Nigeria

Traits (unit)	Trait mean in the agro ecological zones			
	Northern Guinea savanna	Southern Guinea Savanna	Transition zone	LSD _{0.05}
<i>Tree</i>				
Circumference of trunk (m)	1.47b	1.26b	1.92a	0.214
Trunk height (m)	1.93a	1.99a	2.22a	0.305
Tree height (m)	6.89b	7.36b	11.22a	1.813
Crown height (m)	4.79b	5.52b	8.73a	1.43
Crown diameter (3)	10.74b	9.83b	12.81a	1.307
No. of main branches	2.35a	2.20a	2.40a	0.328
Bark thickness (mm)	1.15b	1.15b	1.97a	0.258
<i>Fruit and Nut</i>				
Fruit weight (g)	7.14b	8.31a	3.35c	0.614
Nut weight (g)	3.46b	4.23a	1.61c	0.407
Fruit length (cm)	3.93c	4.34a	4.12b	0.188
Nut length (cm)	2.79b	3.06a	2.67c	1.456
Pulp weight (g)	3.68a	4.08a	1.75b	0.411
fruit intermediate diameter (mm)	23.94b	29.84a	23.48c	0.346
Fruit upper diameter (mm)	33.69b	36.57a	32.83c	0.247
Fruit lower diameter (mm)	20.29b	24.91a	19.40c	0.212
Nut intermediate diameter (mm)	17.78b	22.29a	17.55c	0.164
Nut upper diameter (mm)	23.98b	26.84a	23.18c	0.183
Nut lower diameter (mm)	15.18b	18.57a	14.15c	0.154
Geometric fruit diameter (mm)	29.50b	33.88a	28.74c	0.184
Geometric nut diameter (mm)	22.48b	26.07a	21.79c	0.134
<i>Leaf</i>				
Leaf length (cm)	14.02c	15.31b	16.61a	0.158
Leaf width (cm)	5.33c	5.92b	9.29a	0.216
Petiole length (cm)	18.84c	20.65b	22.42a	0.134

Means carrying the same letter in each row are not significantly different

The mean values of the tree height were 6.89, 7.36 and 11.22 m in the northern Guinea savanna, southern Guinea savanna and the transition zone respectively. While the mean values of the crown diameters were 10.74, 9.83 and 12.81m respectively. In both cases, the transition zone was significantly different ($p \leq 0.05$) from the northern and southern Guinea. The mean fruit length and nut length were significantly different ($p \leq 0.05$) across the agroecological zones. The fruit length varied from 3.93 cm in northern Guinea savanna to 4.43 cm in the Southern Guinea savanna. While the mean nut length varied from 2.79 cm in the northern Guinea savanna to 3.06 cm in the southern Guinea savanna. The mean geometric diameter of fruits and nuts were significantly different ($p \leq 0.05$) between ecological zones. The geometric fruit diameter varied from 28.74 mm in the transition zones to 33.88 mm in the southern Guinea savanna, while the diameter of the nuts varied from 21.79 mm in the transition zone to 26.07 mm in the southern Guinea savanna. The agro ecology was significantly different ($p \leq 0.05$) for number of fruit, nut and pulp

weights. The analysis showed that the southern Guinea savanna had the largest mean value (8.31 g) for fruit weight, followed by northern Guinea saanna (7.14 g) and then the transition zone 3.35 g). The same trend was observed for nut and pulp weight, with the southern Guinea savanna having the largest values (4.23 g and 4.08 g), followed by the northern Guinea savanna (3.46 g and 3.68 g) and the transition zones (1.61 g and 1.75 g) respectively.

The leaf related traits were significantly different ($p \leq 0.05$) among agro ecological zones. Leaf length varied from 14.02 cm in the northern Guinea savanna to 16.61 cm in the transition zone. The same trend was observed for petiole length with the transition zone having the largest mean value (22.42 cm), followed by southern Guinea savanna (20.65 cm) and the northern Guinea savanna the least value (18.84 cm). For the leaf width, it was observed that the transition zones had the largest mean value (9.29 cm), followed by southern Guinea savanna (5.92 cm) while the northern Guinea savanna had the least mean value (5.33 cm).

Table 4: Eigenvectors, eigenvalues and proportions of variability for 4 principal components axes based on 16 tested characters for 60 *Vitellaria paradoxa* genotypes

	Traits		Eigenvectors	
	PC 1	PC 2	PC 3	PC 4
Fruit weight	0.183	-0.253	0.186	-0.344
Nut weight	0.174	-0.230	0.085	-0.388
Pulp weight	0.160	-0.230	0.255	-0.238
Fruit length	-0.105	-0.252	-0.092	-0.266
Nut length	-0.090	-0.321	0.059	-0.230
Fruit upper diameter	-0.276	0.175	0.088	0.042
Fruit intermediate diameter	-0.246	-0.228	0.051	-0.001
Fruit lower diameter	-0.273	-0.139	0.112	0.059
Nut upper diameter	-0.278	-0.136	0.067	0.129
Nut lower diameter	-0.275	-0.096	0.086	0.143
Nut intermediate diameter	-0.267	-0.120	0.125	0.055
Geometric fruit diameter	-0.275	0.184	0.086	0.034
Geometric nut diameter	-0.283	-0.122	0.097	0.112
Leaf length	0.011	-0.254	-0.491	-0.052
Leaf width	-0.142	-0.129	-0.465	0.030
Petiole length	-0.008	-0.237	-0.516	-0.076
Eigenvalue	10.068	4.043	2.533	2.157
Difference	6.025	1.510	0.377	0.736
Proportion (%)	40.3	16.2	10.1	8.6
Cumulative	40.3	56.4	66.6	75.2

Principal Components Analysis (PCA): Principal component analysis was performed to reduce the number of effective traits in group characterization. Eigenvectors, Eigenvalues and proportion of accounted variance for each variable is shown in Table 4. Axis 1 had eigenvalue of 10.067, axes 2, 3 and 4 had eigenvalues of 4.042, 2.533 and 2.156 respectively. The first four variables accounted for 75.2% of the total variability. The first principal component axis which accounted for the highest proportion (40.3%) was dominated by traits corresponding to fruit upper diameter, fruit lower diameter, nut upper diameter, nut lower diameter, geometric fruit diameter and geometric nut diameter; the second principal component axis which accounted for 16.2% of the observed variation was dominated by traits corresponding to nut length and the third principle component axis accounted for 10.1% of observed variation and was dominated by leaf length, leaf width and petiole length. The fourth principal component axis accounted for 8.6% variation and stands for fruit weight and nut weight. The configuration of the 60 shea genotypes along the first two principal component axes is illustrated in Figure 2. The ordination of genotypes on axes 1 and 2 which accounted for 56.4 % of total variation showed genotypes 24 and 26 (southern Guinea savanna), 48, 50, 51, 52 and 53 (transition zone) to be the most distinct from the other genotypes.

Single Linkage Cluster Analysis (SLCA): Using the character variation, SLCA summarised the relationship among 60 genotypes into a dendrogram (Fig. 3), starting from 100% when all the genotypes were distinct from each other to 65% level of similarity when all the genotypes occurred in a single cluster. This indicates that each genotype had at least one neighbour with about 65% similarity. The dendrogram was truncated at various levels of similarity to study the basis of the groupings. The genotypes were clustered into four groups characterised by different morphological trait values.

Group I: This group is made up of sixteen genotypes. Members of this group had the highest mean values for fruit weight, nut weight, pulp weight, nut length, leaf length and petiole length. They however showed the lowest mean value for girth, tree height, crown diameter, crown radius and bark thickness. The genotypes (1, 10, 13, 15, 20) from this group are located in the northern Guinea savanna and the genotypes (21, 23, 24, 25, 26, 27, 29, 30, 32, 35, 39) are from the southern Guinea savanna.

Group II: This group is made up of 24 genotypes. Members of this group had average values for most traits. They showed the lowest mean value for geometric fruit diameter, geometric nut diameter, trunk height, crown height, leaf length, leaf width and petiole length. The genotypes (2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 14, 16, 17, 18 and 19) from this group are located in the northern Guinea savanna and genotypes (22, 28, 31, 34, 35, 36, 37, 38, 40) are from the southern Guinea savanna.

Group III: This group is made up of seven (41, 42, 44, 45, 47, 48, 58) genotypes. Members of this group are characterized with the most extensive girth size and bark thickness. They however had the lowest mean value for fruit weight, nut weight, pulp weight and nut length. The genotypes are from the transition zone.

Group IV: This group is made up of thirteen (43, 46, 49, 50, 51, 52, 53, 54, 55, 56, 57, 59, 60) genotypes. Members of this group showed the highest mean value for geometric fruit diameter, geometric nut diameter, trunk height, tree height, crown height, crown diameter and crown radius. The genotypes from this group are from the transition zone.

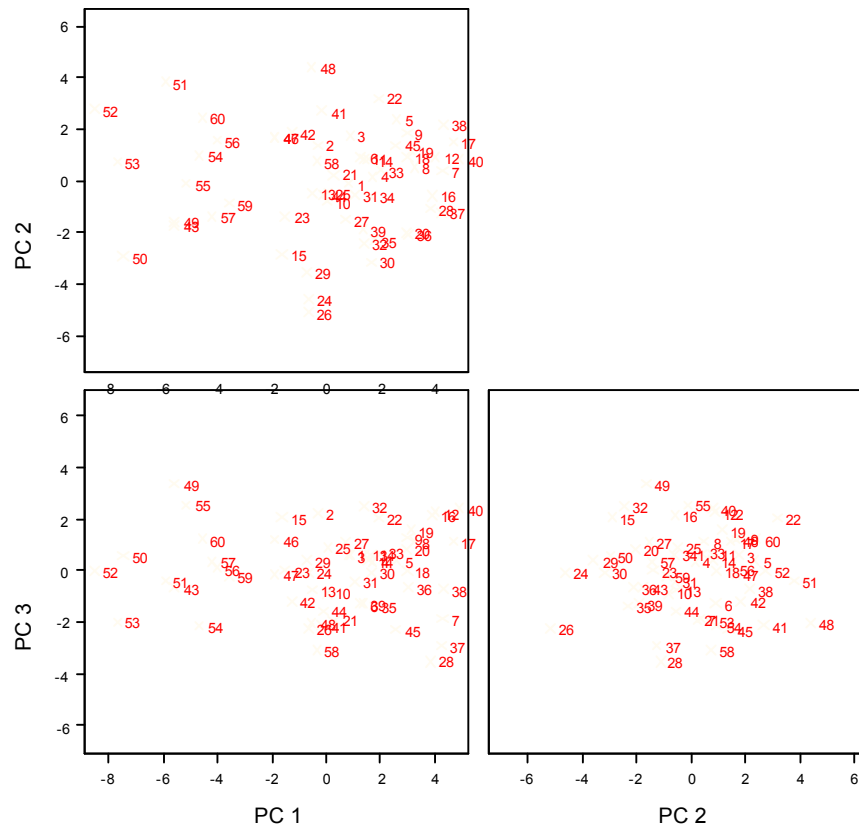


Fig. 2: Configuration of the shea genotypes under principal component axes 1 and 2

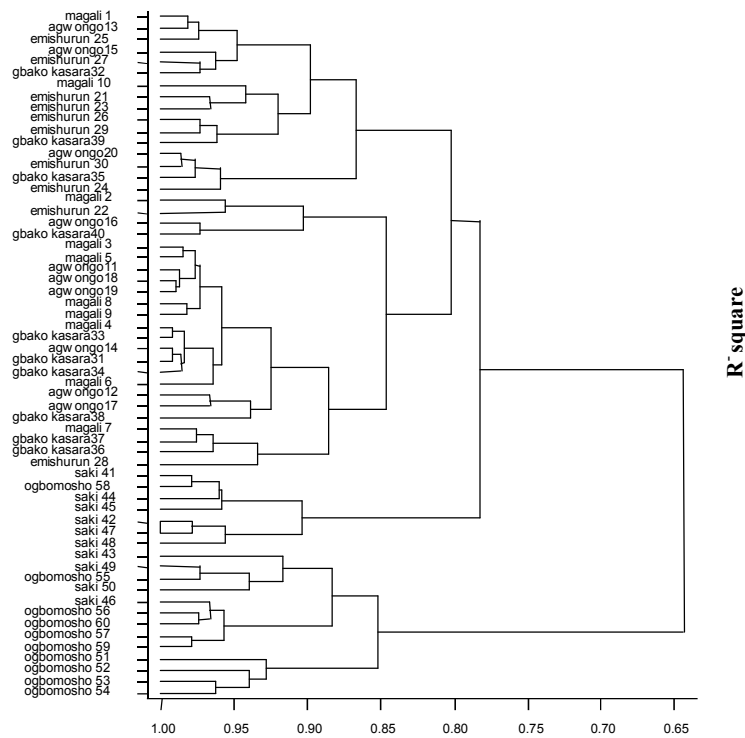


Fig. 3: Dendrogram of 60 shea genotypes using Single Linkage Cluster Analysis on *V paradoxa* across three agro ecologies in the Guinea savanna of Nigeria

DISCUSSION

Variation in the Quantitative Variables: Statistical analyses carried out on the measured variables related to the shea tree, leaves, fruits and nuts showed a very high genetic diversity among agro ecology. These results were expected because the three agro ecologies used for the trials; northern Guinea savanna, southern Guinea savanna and transition zone, represent different locations with different latitude, altitude and consequently different annual rainfall and soil type. The analysis equally revealed that each shea genotype could be used to a certain degree to describe the types of shea butter trees that exist in the Guinea savanna of Nigeria.

The distribution of variability between and within agro ecology indicated that most of the variation is present within agro ecology. This is an expected result due to the biological characteristics of shea tree. Hamrick *et al.* [15] identified those characteristics of species with high level of genetic diversity within populations and the low levels amongst populations, including: long-lived, woody perennials, gravity- and animal seed dispersal, out crossing insect pollinated-species and widespread occurrence. Such factors may explain the percentage of genetic variation found among populations of *V. paradoxa*. The status of *V. paradoxa* as a semi-domesticated species may also explain the high variability within populations [2, 16]. Since the beginning of domestication, rural populations, farmers and traders, have played a role in gene flow by transportation of fruits from village-to-village. Although seeds of shea are recalcitrant and do not maintain viability during long transportation, models of population genetics have shown that a small number of seeds could be sufficient to reduce genetic differentiation.

A study of the genetic variation among the shea tree and the discriminative nature of the characteristic features of shea tree is a necessary step for characterizing shea resources. The characteristics taken into account in this work were analyzed for each tree. These characteristics varied significantly between sampling sites. Environment (agro ecology) was highly significant for all traits in this study. Large straight-boled, high canopy individuals were common in Saki and Ogbomoso (Transition zone) where water availability was probably less of a limiting factor to survival than competition for light. Average boled trees, with spreading canopies, were frequent in open farmed parklands (southern and northern Guinea savanna) where

light was clearly not a limiting factor. The high variation for traits studied is probably indicative of the difference in tree maturity.

Organization of the Morphological Variables: In the present study, two taxonomic procedures, Principal Component Analysis (PCA) and Single Linkage Cluster Analysis (SLCA) were used. The result from the PCA identified four axes to have accounted for 75.2% of the total variation for the sixty shea genotypes evaluated. Fruit and nut diameters had high loading on the first PC axis (PC 1), which contributed 40.3% of the total variation among shea genotypes. Two-dimension ordination of the 60 shea genotypes drawn, based on combinations of the first and second principal axes revealed that genotypes 2, 22, 26, 48, 50, 51, 52, 53 and 58 were distinct from all others. One basic assumption is that numerical evaluation of overall similarity is a measure of genetic similarity [17].

Four definable groups were produced by the SLCA. In delineating the groups, certain plant attributes were found to be more important than others. For example, fruit weight, nut weight, pulp weight, nut length, leaf length, petiole length, girth size, fruit diameter and nut diameter, played remarkable roles in defining the groups. The broad grouping derived from similarity dendrogram and the subsequent merging of groups on the basis of phenetic relationships led to fewer groups than the original number of locations. Both the PCA and the SLCA clustered genotypes into the same group. For example, genotypes 2, 3, 4, 18, 19, 12, 7, 33 and 14 clustered in the same group in the dendrogram, were also clustered in the same group by PCA. Also, genotypes 15, 23, 27, 24, 29, 26, 35, 39, 32 and 30 were all in the same group in the dendrogram and score plot of PCA. Furthermore genotypes 41, 42, 45, 48 and 58, which the dendrogram placed close to one another were also together in the principal component plots. This was observed especially when the first and second components were considered in the PCA. Numerical analysis of *Dioscorea rotundata* and *Dioscorea cayenensis* accessions also showed that results of SLCA and PCA were generally in agreement [18]. The distinctiveness of genotypes 26 and 24 which made them the first to be isolated in the group, could be due to its characteristics such as the largest mean fruit, nut weight and pulp weight. Fatokun, [19] noted that among amaranth accessions, the first accession to separate had the largest seed yield. Thus accessions with extreme values are naturally the first to be isolated from others.

CONCLUSION

Genetic diversity studies are in no measure the first basic step in meaningful breeding programme and therefore require accurate and reliable means for estimation. The grouping of the dendrogram demonstrated the polymorphic nature and wide genetic base of the shea genotypes investigated. There was high genetic diversity among the shea genotypes, which facilitated the distinction of the shea genotypes into groups. This implies that a breeding programme can be initiated for the improvement of the crop

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