

Full Length Research Paper

Morphological characterization of cashew (*Anacardium occidentale* L.) in four populations in Malawi

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An assessment of the genetic diversity in cashew (*Anacardium occidentale* L.) would assist in planning for future selection of good high yield germplasm that will produce nuts of high quality and fetch high prices on the market. The genetic diversity and relationship among 40 accessions of cashew collected from 4 populations (Liwonde, Nkope, Kaputu and Chikwawa) was characterized using quantitative and qualitative traits. The study results have revealed similarity values between 35 to 66%. Analyses of genetic similarity based on unweighted pair group method of arithmetic averages (UPGMA) grouped the 40 accessions into 4 clusters with 14 sub-clusters and the principal component analysis revealed that apple length, apple nut ratio, nut weight, kernel weight, out turn percent and flower sex ratio accounted for most of the variation. The variation could be attributed to genetic history, ecogeographic origin and selection for desired agronomic traits by farmers. Accessions LW41, NE2, NE4, CH18 and PAL26 showed potential for selection in nut and kernel weight and out turn percent suggesting that this could be a valuable source of variation for tree improvement programme in cashew nuts. The findings suggest availability of broad genetic base that could be exploited for future cashew selection and breeding in Malawi.

Key words: Accessions, *Anacardium occidentale*, clusters, population, UPGMA.

INTRODUCTION

The cashew nut (*Anacardium occidentale* L.) belongs to Anacardiaceae family which also includes the mango, pistachio and poison ivy (Nakasone and Paull, 1998). *Anacardium* contains 8 species all of which are native to the coastal parts of north eastern Brazil (Azam-Ali and Judge, 2000). Cashew nut tree provides food, employment, income and the wood is used for carpentry mainly in the construction of boats and ferries while other products derived from it include firewood and charcoal (Akinwale, 2000). Cashew resins are also used in the manufacture of insect repellents and natural insecticides, while different tree parts have medicinal value as they are used to cure various diseases (Cavalcante et al., 2003).

The cashew tree is a sprawling broad-leaved ever-green, well adapted to poor soils and dry sandy locations, drought resistant, but grows best on well drained sandy soils with pH of 4.5 to 6.5 (Aliyu, 2007). It favors temperatures between 15 to 35°C and rainfall over 400 mm with elevation of up to 2000 m above sea level. Flowering for cashew is similar to the close relative mango in that both male and perfect flowers are borne on the same inflorescence. Trees with more of the perfect flowers bear more fruits and the number of inflorescence produced per plant is one of the major factors determining productivity (de Azevedo et al. 1998).

The Malawi cashew industry has a cultivation history of about 50 years and is dominated by commercial farmers with very little participation by smallholder farmers (Kachule et al., 1998). Cashew is grown in the lake shore districts of Mangochi, Salima, Nkhotakota, NkhataBay and Karonga and some upland districts of Machinga,

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Chikwawa and Nsanje. Cashew production in eastern and southern Africa is constrained by numerous problems ranging from unavailability of good quality planting material, high susceptibility to pests and diseases, inadequate knowledge on management of cashew among others (Shomari, 2002). To improve the productivity of the nuts there is need to select desirable genotypes from the existing gene pool and use superior materials for tree improvement programme. Genetic improvement is limited by the lack of knowledge of genetic diversity of the existing germplasm. Breeding of cashew is mostly based on selection of useful phenotypic and agronomic traits such as nut size, nut weight, colour of apple, size of the fruits, tree canopy, length of panicle and overall yield production (Mneney et al., 2001). Traditionally, genetic diversity evaluated in crop species is based on differences in morphological characters and qualitative traits (Schut and Stam, 1997). In many cases morphological characters have been used as a powerful tool in the classification of cultivars and as such morphological traits continue to be the first step in the studies of genetic relationships in most breeding programmes (Van Beuningen and Busch, 1997). Therefore, it becomes imperative to quantify the extent of variation among the cashew germplasm in Malawi by using morphological traits. The objective of this study was to assess the genetic relatedness of cashew accessions from four distinct populations in southern and central Malawi using quantitative and qualitative traits.

MATERIALS AND METHODS

The study was conducted in smallholder and commercial farmers' orchards forming 4 populations namely; Liwonde in Machinga and Nkope in Mangochi district both at smallholder farmers' orchards while Kaputu and Chikwawa in Salima district represented commercial farmers orchards (Figure 1 and Table 1).

Sampling and data collection

Ten trees were selected from each of the 4 populations in 2 districts of southern and central Malawi. Each sample was given an accession number as described by Muchugi et al. (2008) based on historical performance as provided by the farmers. Characterization of vegetative, reproductive parts, apple, nut and kernel traits was assessed based on the cashew descriptor list of the international board for plant genetic resources (IBPGR, 1986). Fourteen quantitative and 4 qualitative traits were assessed from June 2007 to September 2008 (Table 2 and 3).

Determination of parameters

The nut-in-shell was recorded according to Masawe (2006). Nuts were shelled and weighed to calculate percent out turn. Nuts per panicle were counted randomly on selected 10 clusters per individual tree in all the 4 populations. Plate 1 shows a representative sample of nuts assessed during the study.

The different flower types were identified according to Masawe et al., (1996). Each tree had its diameter at breast height (dbh) measured using a caliper while height was measured using a calibrated pole. Leaf samples were obtained to determine leaf area

according to the procedure by Chavez and Mariscal (2006). Apple measurements of weight, thickness, length, width, fluid and astringency were determined following IBPGR (1986) protocols. Plate 2 shows some of the apples assessed during the study.

Statistical analyses

Data on the quantitative and qualitative traits was subjected to cluster analysis to conduct similarity estimates using unweighted pair group method of arithmetic averages (UPGMA) in multivariate statistical package (MVSP) 3.1 (Kovach, 2007) and the principal component analysis (PCA). The data on quantitative traits were also subjected to analysis of variance in MINITAB 15.0.

RESULTS

The quantitative and qualitative morphological traits of cashew accessions were classified using similarity coefficients and the dendrogram from Euclidean distance of complete linkage clustering method divided the 40 cashew accessions into 4 clusters with an average similarity level of 66% (Figure 2).

Cluster I

This cluster comprised of 3 accessions NE1, NE4 and NE2 all from Nkope population in Mangochi district with mean yield of 15.3 kg per tree and kernel weight ranging from 0.5 to 1.7g, shelling percent of 16 to 25.5 (mean 21.7%). This group was an early bearing type with short harvesting period of 92 days.

Cluster II

This was the largest group and comprised of 24 accessions from all populations. At 87% level cluster II divided into 9 sub-clusters and each population contributed 6 individuals. The group registered kernel weight ranging from 0.7 to 2.2 g with highest out turn of 17 and 29.4% for accessions LW46 and LW48 respectively.

Cluster III

It was composed of 6 accessions divided in 2 sub-clusters of 3A with 4 accessions (NE3, PAL33, LW41, PAL32) and 3B with 2 accessions (LW40 and PAL1) and included all the 4 populations. These sub-clusters were divided at phenon level 86%. The group was characteristic of average nuts weighing between 5.3 and 10.1 g with mean 6.5 g, apple weight ranging from 18.2 to 62.2 g mean 46.3 g.

Cluster IV

Cluster IV was made up of 3 sub-clusters at level 85%



Figure 1. Southern and Central Malawi showing collection sites of *A. occidentale*

(4A, 4B, 4C) comprising of 7 accessions from 3 populations and characterised by powdery mildew and insect attack except Nkope population. The group exhibited kernel weight range of 1.0 to 1.9 g (mean 1.5 g) and out turn of 19.5 to 32.6% (mean 24.3%). The apple weight ranged from 13.7 to 81.1 g (mean 49.9 g). In this group out of all the accessions characterized PAL26 recorded the highest out turn of 32.6%.

Principal component analysis

Results of principal component analysis (PCA) (Figure 3) show that 92.1% of the total variation can be explained by the 3 PCA based on first-second and third eigen-vectors. The first 2 principal components accounted for 70.1% of the total variation. The nut and apple traits such as weight, shell weight, apple length and ratio of kernel to

Table 1. Localities and climatic data for four cashew populations in Malawi.

Population	Locality		Mean annual rainfall (mm)	Altitude (m asl)	Mean temperature (°C)
	Latitude °S '	Longitude °E			
Liwonde	15° 02.879'	035° 14.750'	812	478	25.7
Nkope	14° 12.181'	035° 01.933'	743	489	25.7
Chikwawa	13° 31.971'	034° 18.449'	906	525	25.3
Kaputu	13° 45.497'	034° 27.867'	965	508	25.3

Table 2. List of accessions of cashew trees from four populations.

ID	Accession	Population	Age	ID	Accession	Population	Age
1	LW42	Liwonde	12	21	PAL27	Kaputu	12
2	LW43	Liwonde	12	22	PAL32	Kaputu	12
3	LW45	Liwonde	12	23	PAL33	Kaputu	12
4	LW48	Liwonde	12	24	PAL26K	Kaputu	12
5	LW49	Liwonde	12	25	KA5	Kaputu	12
6	LW40	Liwonde	20	26	KA6	Kaputu	20
7	LW41	Liwonde	20	27	KA7	Kaputu	20
8	LW44	Liwonde	20	28	KA8	Kaputu	20
9	LW46	Liwonde	20	29	KA9	Kaputu	20
10	LW47	Nkope	20	30	KA10	Kaputu	20
11	NE2	Nkope	12	31	CH15	Chikwawa	12
12	NE3	Nkope	12	32	CH16	Chikwawa	12
13	NE6	Nkope	12	33	CH17	Chikwawa	12
14	NE9	Nkope	12	34	CH18	Chikwawa	12
15	NE10	Nkope	12	35	CH100	Chikwawa	12
16	NE1	Nkope	20	36	PAL1	Chikwawa	20
17	NE4	Nkope	20	37	PAL17	Chikwawa	20
18	NE5	Nkope	20	38	PAL36	Chikwawa	20
19	NE7	Nkope	20	39	CH12	Chikwawa	20
20	NE8	Nkope	20	40	PAL38	Chikwawa	20

shell account for most of the variation. The spread of the accessions across the PCA axes was not in total agreement with UPGMA as there was considerable amount of overlap of some accessions with more accessions in group 2 are diffused into group III however cluster I of the dendrogram agrees with grouping of accessions NE1, NE2 and NE4.

Variation of quantitative traits

Means of characters per population in Table 4 were significantly different ($p \leq 0.05$). Nkope population had highest variation in perfect flowers, flower sex ratio, apple nut ratio and apple length. Nut weight and thickness was prominent in Liwonde, Kaputu and Chikwawa populations while kernel weight and out turn percent were prevalent in Chikwawa, Kaputu and Liwonde. Out turn trait had the lowest variation across the population while flower sex ratio was the highest.

DISCUSSION

The cashew accessions have shown morphological differences which could be attributed to several factors including differences in geographical origin, ecological adaptation to sites and selection by humankind. A wide range of variation was observed in nut, kernel characteristics and other traits. Natural and human selection has strong forces in shaping cashew populations in Malawi leading to high phenotypic variability. Apple and nut traits as well as size and ratio of kernel to shell are critical in separating the cashew accessions. The similarity of the 4 populations ranged from 35 to 66% and this is in agreement with Samal et al. (2003) who reported on Indian cashew germplasm. The 4 groups with sub-clusters observed gives variation that a breeder can use for improvement of yield and quality of cashew. The categories in 4 groups with varying number of sub-clusters suggest polymorphism amongst accessions. The clustering pattern confirms the origin of the accessions as

Table 3. List of some quantitative and qualitative descriptors assessed in *A. occidentale*

Trait type	Character assessed	Acronyms
Vegetative	Tree crown spread (m)	TCS
	Lead size (cm ²)	LSA
	Leaves per twig	LPT
Inflorescence	Number of flowers per panicle	FPP
	Number of male flowers per panicle	MFP
	Number hermaphrodite flowers	HFP
	Flower sex ratio	FSR
Apple	Apple weight (g)	AWT
	Apple fluid weight (g)	AFW
Nut in shell	Nut weight	NWT
	Nuts per panicle	NNP
	Total nut yield per tree (kg)	TYT
Kernel	Kernel weight (g)	KWT
	Out turn percent (%)	OTP
Qualitative traits	Apple juice astringency	AJA
	Disease incidence	DII
	Secondary flowering	SEF
	Apple skin colour	ASC



Plate 1. Cashew nut-in shell of some accessions.



Plate 2. Plates of a sample of cashew apples from Nkope population.

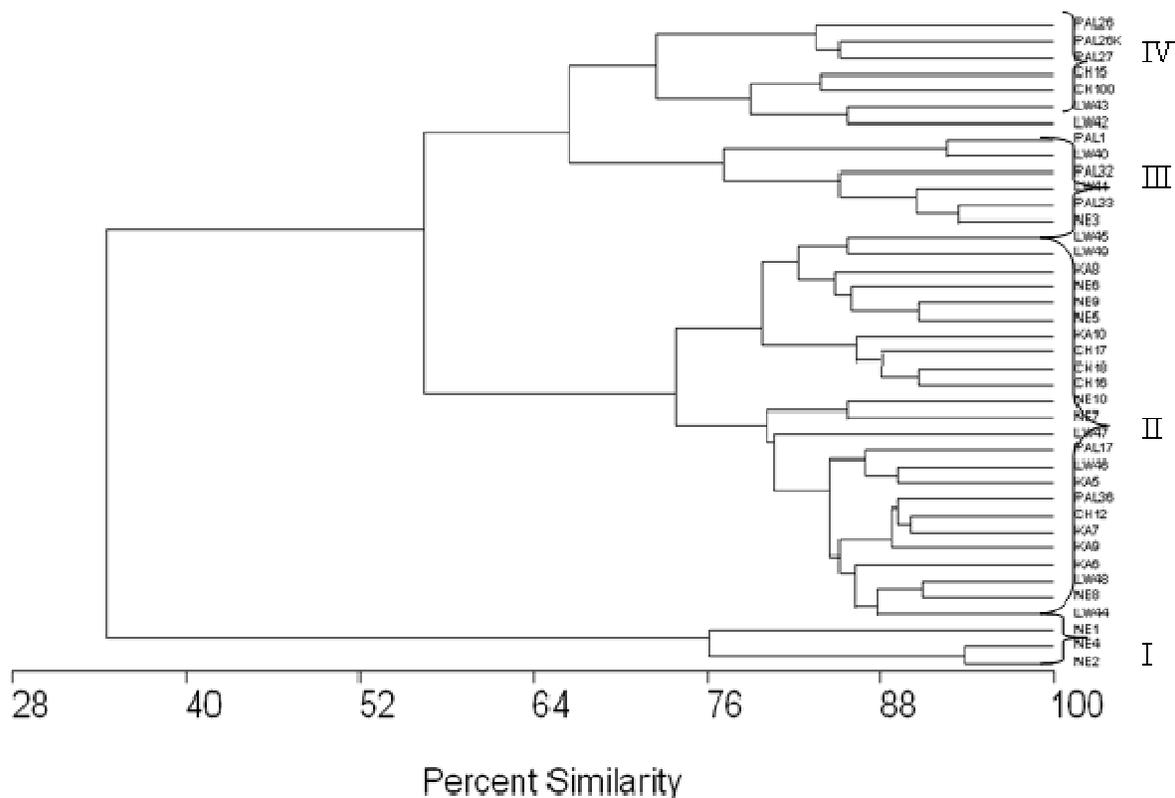


Figure 2. UPGMA showing the relationship among the forty cashew accessions

either being within the populations or other populations, a development which could be associated with farmers being responsible for seed dispersal. It has generally been noted that accessions have been dispersed in different clusters of the dendrogram with accessions NE1, NE2 and NE4 completely separately from the rest of the groups. The three accessions recorded highest nut

yield, kernel to nut ratio and can be described as unique group and might be genetically different from the rest of the accessions. The clustering pattern of accessions probably reflects the genetic history, ecogeographic origin and or agronomic affinity of selection. Cluster II exhibits different accessions from the 4 populations which suggest high genetic similarity among the populations

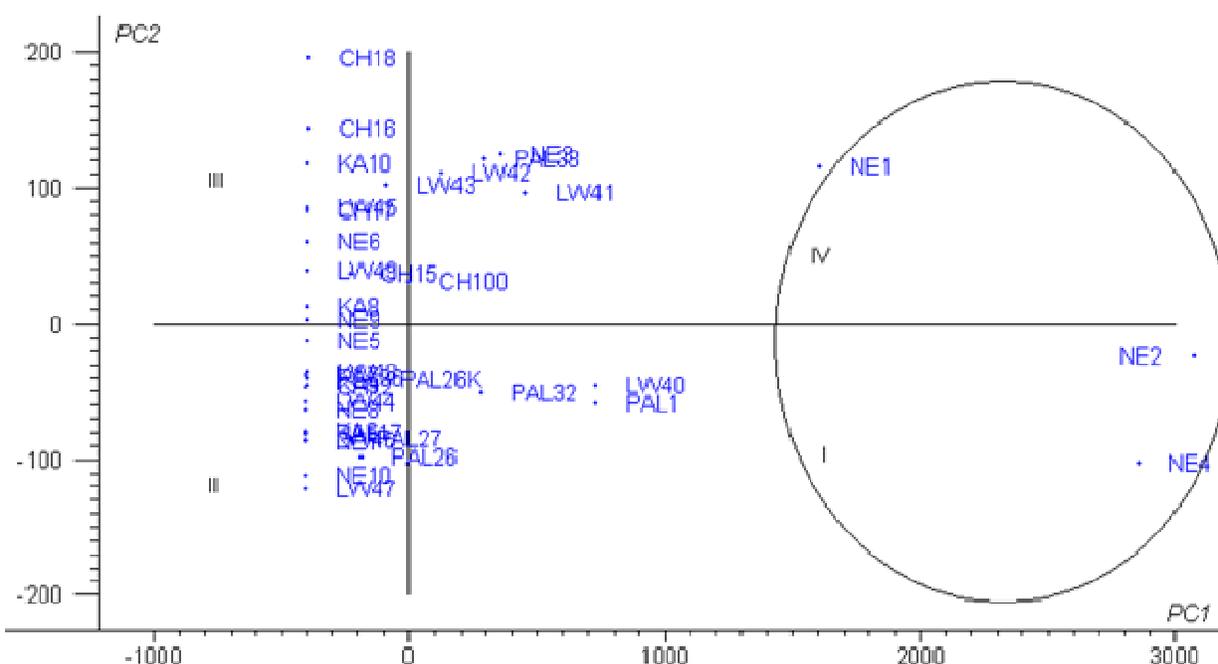


Figure 3. Principal component analyses of populations of cashew using quantitative and qualitative traits.

Table 4. Variation in cashew quantitative traits among 4 populations.

Trait	Population				CV (%)	SE	LSD
	Liwonde	Nkope	Kaputu	Chikwawa			
Apple length	31.8 ^b	62.7 ^a	32.3 ^b	35.6 ^b	37.5	15.21	3.790
Apple nut rat	6.0 ^b	10.7 ^a	7.6 ^b	7.82 ^b	35.1	2.82	2.559
Nut wt (g)	6.2 ^a	4.1 ^b	5.5 ^a	5.9 ^a	22.2	1.21	1.097
Nut thickness	8.1 ^a	5.5 ^b	7.5 ^a	8.2 ^a	21.7	1.59	1.440
Kernel wt (g)	1.6 ^a	1.0 ^b	1.1 ^b	1.6 ^a	26.5	0.35	0.316
Out turn (%)	25.3 ^a	22.7 ^{ab}	20.2 ^b	24.6 ^a	14.0	3.25	2.952
Flower sex rat	0.10 ^b	0.25 ^a	0.13 ^b	0.13 ^b	57.5	0.09	0.080
Perfect flowers	11.4 ^b	24.2 ^a	12.7 ^b	15.1 ^b	40.4	6.40	5.810

Values in the same row followed by the same letters are not significantly different from each other ($p \leq 0.05$).

and this can be attributed to wide seed dispersal across the cashew growing areas in Malawi.

Most of the germplasm for the country has come in through project activities where commercial farmers have obtained their planting material from similar source. This corroborates with findings of Kachule et al. (1998) who reported the history of Malawi cashew industry in which Agricultural Development Marketing Corporation (ADM ARC) a parastatal organisation had been co-ordinating activities of cashew production including distribution of selected germplasm to both commercial and small holder farmers. The variability found in the present study is in agreement with that reported for the cashew nuts distribution range from India as reported by Archak et al. (2003). The grouping of the accessions could also provide preliminary guide to the identification of parental

lines in terms of seed. The mean yield of 15.3 kg per tree (range 0.5 to 26 kg per tree) is higher than the findings by Samal et al. (2003) but lower than those reported by Aliyu (2004) and Marlos et al. (2007). The wide variation in yield is an indication of the potential of genetic base in relation to nut yield that can be used to improve production of cashew in Malawi. The quality characteristics of nut weight for accession NE2 (cluster 1), CH18 (2), and LW 41 (3) with 7.5, 7.7 and 10.1g respectively is regarded as high by IBPGR (1986) and this can form the basis for selection of planting material for improvement, however most of the qualitative and quantitative traits are in the same range for data of cashew nuts from Brazil.

The variation shows mean values of some traits being higher than reported by many authors; for example breeders could take advantage of superior traits for apple

weight, nut weight, out of turn percentage for tree improvement. The significant difference ($p \leq 0.05$) in the population trait means indicate variations amongst the populations but the variation is quantitative and qualitative traits is high among within population. Nkope population produced more flowers and nuts per panicle than those reported by Heard et al. (1990). This suggest that there is a scope for selection of superior genotype and that perfect flowers can be used as a reliable criterion for selection as trees with more perfect flowers bear more fruits. The flower sex ratio in Liwonde, Kaputu and Chikwawa populations agrees with those reported by Archak et al. (2003). The nut and kernel weights in Liwonde and Chikwawa populations are in similar range as reported by Faluyi (2006) and this suggests that the 2 traits need to be considered together when selecting accessions for improvement. There is considerable variation amongst the populations in flower sex ratio, perfect flowers, apple length, apple nut ratio, and kernel and nut weight suggesting high potential for selection.

Conclusion

The different clusters of cashew accessions obtained using quantitative and qualitative traits suggest that there is genetic variation in the 4 populations. Most of the morphological variation is attributed to differences in apple, nut, floral, fruiting, tree habit and leaf characteristics. The study provided information for assessing genetic relatedness of the cashew accessions and the information will help in tree improvement programmes. Highly diverse population like Nkope would be suitable for collection of germplasm that could be used to produce valuable clones after vegetative propagation. Accessions LW41, NE2, NE4, CH18 and PAL 26 have revealed good traits of nut and apple weight, fluid weight, nut yield, and out turn percent that could be selected for and be vegetatively propagated for establishment of orchards for evaluation and further selection. The study has shown existence of potential genetic base that can be used to improve production of cashew in Malawi. However, to confirm whether the variation is genetic in nature there is need to characterize the four populations using molecular markers such as amplified fragment length polymorphism (AFLP) DNA markers, simple sequence repeats (SSRs) or microsatellites.

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