



ASSESSMENT OF GENETIC VARIABILITY OF LOCAL CASSAVA CULTIVARS IN UGANDA USING SIMPLE SEQUENCE REPEAT MARKERS

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Background:

Cassava is a valuable staple food crop in Africa, and of considerable importance in East Africa. In Uganda, a total of 3.5 million tonnes of cassava was being produced annually from c.450,000 hectares of land before the cassava mosaic epidemic became severe in the country after 1990¹.

In this study we use simple sequence repeat markers to (i) assess the genetic diversity and differentiation of cultivars within and between different agroecologies in Uganda and (ii) also determine how Uganda cassava compares with the total genetic diversity of the species within Africa and the cassava collection maintained at the International Centre for Tropical Agriculture (CIAT, Spanish acronym).

Materials and methods:

Collection of cassava cultivars was done in 18 districts in 2002. A total of 224 accessions were collected labelled and planted at Namulonge Agricultural and Animal production Research Institute, Uganda.

DNA extraction was by the CTAB method². 35 simple sequence repeat markers with high polymorphic information content and widely distributed on the cassava genome were used in DNA analysis following Mba et al. 2001³.

For reference purposes, 20 Tanzanian cultivars were included from a previous study of diversity in Tanzaniaplus 20 from Ghana, 22 from Nigeria, 20 from Guatemala and 18 holdings from CIAT and IITA forming 9 groups based on country of origin-Guatemala being split into two populations.

Parameters of genetic diversity and differentiation were estimated from allele data using GENESURVEY⁴, FSTAT⁵ and NTSYS-PC⁶.

Results:

Table 1: Genetic diversity within groups of cassava landraces classified according to Uganda agroecologies.

Population	sample size.	No. Pol. Loci	% pol.	Mean no. alleles/ pol. Locus	HO _p	HEc _p
NORTHERN	10	35	82.9	3.6	0.5524	0.4884
BANANA/COFFEE	106	35	94.3	5.1	0.5475	0.5395
BANANA/MILLET	42	35	94.3	4.4	0.5439	0.5338
COTTON						
MONTANE	13	35	97.1	4.2	0.5948	0.5940
PASTORAL	21	35	94.3	4.2	0.5654	0.5606
TESO	3	35	88.6	2.6	0.5476	0.5448
mean	6 pop.		91.90	4.01	0.5586	0.5435
std			5.24	0.84	0.0192	0.0346

H_e: average expected heterozygosity within population corrected for small sample size
H_o: average observed heterozygosity
% Pol.: percentage polymorphism
Pol.: polymorphic

Figure 1. Principal Component Analysis of SSR marker diversity in the cassava accessions grouped according to country of origin

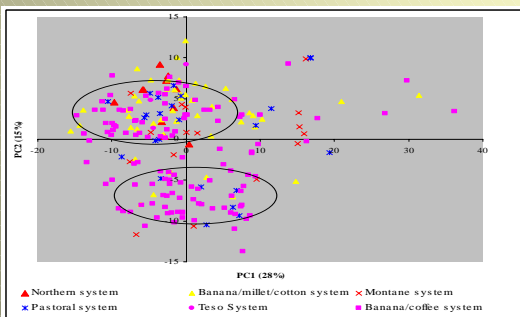


Figure 2. Principal Component Analysis of SSR marker diversity in the cassava accessions grouped according to Uganda agroecologies

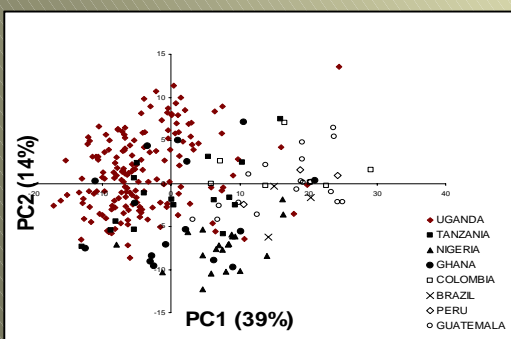


Figure 3. Map of Uganda showing cassava collection positions in the different agroecologies

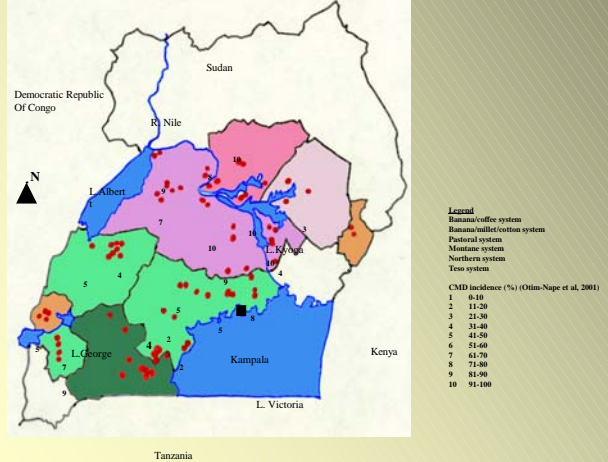


Table 2: Genetic diversity within groups of cassava landraces classified according to country of origin.

Population	Sample Size	No. of loci	Percent Of pol ^a . Loci ^b	Mean no. Alleles /locus	Mean no. alleles/ pol ^a .locus	H _e ^c	H _o ^c
UGANDA	198	35	94.3	5.2	5.4	0.5530	0.5468
COLOMBIA	5	35	94.3	3.3	3.4	0.5081	0.5963
BRASIL	3	34	97.1	2.8	2.8	0.5735	0.6304
PERU	3	35	94.3	2.7	2.8	0.5810	0.6619
GUATEMALA1	7	35	94.3	2.5	2.6	0.5290	0.4219
GUATEMALA2	11	35	97.1	3.8	3.9	0.5274	0.5906
TANZANIA	19	35	91.4	3.9	4.1	0.5658	0.5536
NIGERIA	20	35	94.3	3.9	4.0	0.5002	0.5131
GHANA	19	35	94.3	4.2	4.4	0.5429	0.5694
Mean			94.59	3.59	3.71	0.5423	0.5649
Std			1.70	0.86	0.89	0.0285	0.0698
			H _e	H _o	D _s	G _{st}	
Mean			0.6305	0.5635	0.0670	0.1078	
Std			0.1696	0.1606	0.0332	0.0502	
95%CI			0.5713	0.5083	0.0566	0.0916	
99%CI			0.6827	0.6135	0.0767	0.1235	

H_e: average expected heterozygosity within population corrected for small sample size
H_o: average observed heterozygosity
% Pol.: percentage polymorphism
Pol.: polymorphic

Conclusions:

•Uganda cassava landraces cluster together with the other African landraces but are distinct from the other Neotropical landraces.

•Uganda generally has a high diversity of cassava landraces but low differentiation between them.

•The cultivars grown by farmers in the banana/coffee system belong to two groups while the majority of the cultivars grown in the other agroecologies belong to one of these.

• We see the negative influence on diversity especially in the regions that were most affected by CMD.

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