GENETIC DIVERSITY OF CASSAVA LAND RACES IN GHANA USING SSR MARKERS

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INTRODUCTION

Cassava is a major source of energy for more than 500 million people in Africa (Jennings and Hershey, 1985). Over 200 million people in sub-Saharan Africa depend on cassava for 50% of their calorie requirements (Osiru *et al*., 1996). Cassava in Ghana is a major staple that ranks first in area under cultivation and utilization. It contributes 22% of the agricultural gross domestic product (AGDP).

The Ghana Living Standards Survey (GLSS) showed 83% of 1.73 million sampled households engaged in cassava production (MOA, 1990). The importance of cassava in sub-Saharan Africa and the need to satisfy growing demands for cassava has received attention by improving the yield genetic potential, the agronomy of production and post harvest handling methods.

However, underlying the strategy to improve cassava is an argument of how diverse cassava is in Africa, how the diversity is structured and how useful it is in crop improvement. Crop genetic diversity has resulted from many years of farmers' selection hence a great deal of useful potential in the landraces. Landraces possess genes required for adaptation to biotic and abiotic stresses, and food quality characteristics in higher frequencies compared to unadapted material.

Morphological markers are highly subjective, environmentally influenced and detect little polymorphism. Cassava landraces collected from Ghana were analysed using SSR markers for genetic diversity.

MATERIALS AND METHODS

A total of 320 cassava landraces collected from 10 regions in Ghana were used in this study(fig.1). DNA was extracted from the young fresh leaves and 36 SSR markers multiplexed were analyzed.

The PCR amplification, automated gel analysis and data collection were as described by Fregene *et al* (2001) and product from the SSR denatured and run on 5% polyacrylamide gel using DNA sequencer ABI 377. Gel data was extracted using the Gene scan and Genotype software. Genetic distance, based upon the proportion of shared alleles (PSA) was obtained from the raw allele size data using the computer microstat.

Distances between the accessions were subjected to principal component analysis (PCA) using JMP (SAS Institute 1995) to obtain a structure of relationship between the landraces. Parameters of genetic diversity and differentiation were calculated from allele data using the computer packages GENSURVEY (Vekeman *et al* 1997) and FSTAT (Goudet 1990).

fig. 1: **All ten regions where casava was sampled**

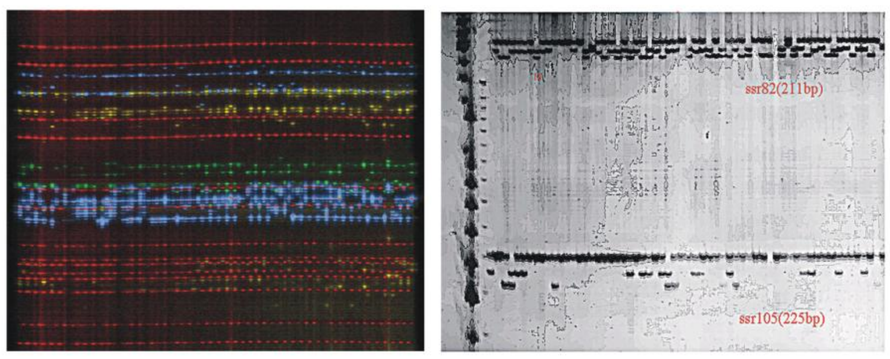

Fig. 2 CASSAVA SSR PROFILES

Table 1. Intra-population and Inter-Population estimates of genetic diversity parameters of cassava land races from different regions of Ghana

Population	n	#loc.	#loc_P	PLP	K	K_P	HO_p	HE_p	HEc_p
Ashanti	11	33	30	90.9	3.9	4.1	0.5285	0.5017	0.5262
Brong Ahafo	37	33	31	93.9	5.4	5.6	0.5012	0.5267	0.5339
Central	8	33	29	87.9	3.3	3.7	0.5082	0.4701	0.4999
Eastern	27	33	30	90.9	5.4	4.9	0.5322	0.5123	0.5223
Western	4	33	27	81.8	2.9	3.4	0.5404	0.467	0.5405
Greater Accra	10	33	29	87.9	3.7	4	0.5016	0.5065	0.5336
Volta	28	33	31	93.9	5.3	5.5	0.5133	0.5735	0.5839
Northern I	109	33	31	93.9	6.9	7.2	0.5369	0.5779	0.5806
Northern II	53	33	31	93.9	6.3	6.5	0.5479	0.5851	0.5908
Mean				90.57	4.69	4.98	0.5234	0.5245	0.5457
Std deviation				4.131	0.36	1.31	0.0176	0.045	0.0317

PLP: Percentage of polymorphic loci at the 5% level within accessions
K: Mean number of alleles per locus within accessions
K_P: Mean number of polymorphic alleles per locus within accessions
Ho_p: observed heterozygosity
HE-p: Average gene diversity
HEc_p: Average gene heterozygosity corrected for small samples sizes

Table 2. Parameters of generic diversity, Ho, Hs, Ht, Dst, Gst and Gst' (Correction for differences in sample size) by SSR locus.

LocName	Ho	Hs	Ht	Dst	Dst'	Ht'	Gst	Gst'
SSRY4	0	0.346	0.439	0.093	0.104	0.45	0.212	0.23
SSRY5	0.499	0.474	0.481	0.006	0.007	0.481	0.014	0.015
SSRY9	0.463	0.582	0.587	0.005	0.006	0.587	0.009	0.01
SSRY12	0.704	0.597	0.598	0.001	0.001	0.598	0.001	0.001
SSRY19	0.811	0.738	0.764	0.026	0.029	0.766	0.034	0.037
SSRY20	0.79	0.73	0.76	0.03	0.033	0.764	0.039	0.043
SSRY21	0.596	0.487	0.514	0.027	0.03	0.517	0.053	0.058
SSRY34	0.479	0.428	0.425	-0.004	-0.004	0.424	-0.009	-0.01
SSRY38	0.043	0.08	0.082	0.001	0.002	0.082	0.018	0.02
SSRY47	0.429	0.668	0.739	0.071	0.079	0.747	0.096	0.106
SSRY51	0.79	0.694	0.751	0.057	0.063	0.757	0.076	0.084
SSRY52	0.752	0.603	0.616	0.014	0.015	0.618	0.022	0.025
SSRY59	0.152	0.639	0.701	0.062	0.069	0.708	0.089	0.098
SSRY63	0.443	0.484	0.519	0.036	0.04	0.523	0.069	0.076
SSRY64	0.725	0.67	0.689	0.02	0.022	0.691	0.028	0.031
SSRY69	0.557	0.552	0.568	0.016	0.018	0.57	0.028	0.031
SSRY82	0.846	0.84	0.858	0.018	0.02	0.86	0.021	0.024
SSRY10	0.725	0.779	0.798	0.019	0.021	0.8	0.024	0.027
SSRY10	0.007	0.01	0.009	0	0	0.009	-0.037	-0.041
SSRY10	0.804	0.76	0.764	0.004	0.004	0.764	0.005	0.005
SSRY10	0.829	0.761	0.768	0.008	0.009	0.769	0.01	0.011
SSRY10	0.422	0.361	0.373	0.012	0.014	0.375	0.033	0.036
SSRY11	0.279	0.272	0.274	0.002	0.002	0.274	0.008	0.009
SSRY12	0.814	0.629	0.633	0.024	0.026	0.656	0.036	0.04
SSRY14	0.08	0.083	0.086	0.002	0.003	0.086	0.029	0.032
SSRY15	0.689	0.79	0.806	0.015	0.017	0.807	0.019	0.021
SSRY15	0.072	0.595	0.632	0.037	0.041	0.636	0.059	0.065
SSRY16	0.528	0.658	0.668	0.01	0.011	0.669	0.014	0.016
SSRY16	0.258	0.316	0.321	0.004	0.005	0.321	0.013	0.015
SSRY17	0.544	0.555	0.591	0.037	0.041	0.596	0.062	0.068
SSRY17	0.845	0.726	0.776	0.05	0.056	0.781	0.065	0.071
SSRY18	0.672	0.532	0.535	0.003	0.004	0.536	0.006	0.007
SSRY18	0.603	0.705	0.761	0.055	0.062	0.767	0.073	0.08
Overall	0.523	0.55	0.573	0.023	0.026	0.575	0.04	0.045

Ho Average observed heterozygosity within country
Ht Total Heterozygosity in the entire data set
Hs Gene diversity within country averaged over the entire data set
Dst Average gene diversity between populations
Gst Coefficient of gene differentiation.

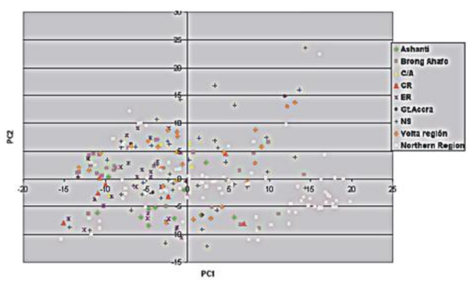

Fig.3: Principal Component Analysis (PCA) of genetic distance (proportion of shared alleles-PSA) of cassava land races from Ghana

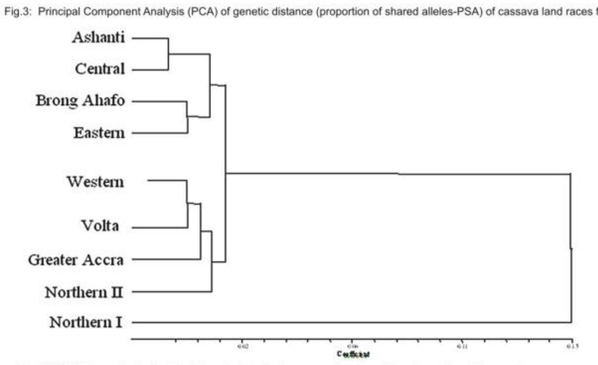

Fig. 4 UPGMA tree of pair-wise F_{ST} data calculated between samples from different regions of the country.

RESULTS AND DISCUSSION

Data from a total of 33 of 36 SSR loci primers, were used to derive estimates of the genetic diversity and differentiation. The average number of alleles for each locus was close to 5 and is similar to that found for a study of land races from Nigeria, Tanzania and 7 neo-tropical countries (Fregene *et al.,* 2001).

The probability that 2 randomly selected alleles in a given accession are different, average gene diversity, was 0.5245±0.0045 and is lower than that found for the previous study. Average gene diversity was comparable across all regions with an exception of the Volta Region and Central Region. Genetic diversity parameters, including total heterozygosity (Ht) and genetic differentiation (Gst) ranged widely across markers (table 2). Genetic differentiation, as estimated by F_{ST} (theta), was very low for samples between regions, overall 0.4, with the exception of some accessions from Northern Ghana that showed moderate to high genetic differentiation (Table 1).

The results found here support previous findings that agricultural practices and the allogamous nature of cassava produces a large pool of volunteer seedlings that natural and human selection acts upon to maintain a high level of diversity and low differentiation. Genetic distances between all pairs of individual accessions was calculated by the proportion of shared alleles (PSA) and presented graphically by PCA. PC1 and PC2 accounted for 26% and 16% of the total variance respectively. The PCA shows loose clustering of the land races by region but of note is the sub-structure of some land races from Northern Ghana (Fig. 4). This is similar to what was observed in Nigeria and Tanzania land races in an earlier study The defined sub-structure observed in the genetic relationship of cassava land races from Africa appears to be a common feature of cassava in a number of countries.

The underlying factor is yet to be understood. UPGMA cluster analysis of FST estimate of genetic differentiation amongst land races, was able to group the land races into loose clusters according to agro-ecologies, with a group of genotypes from the Northern region sub-structure being the most differentiated

CONCLUSION

The genetic diversity and differentiation in cassava land races is accessed using SSR markers as a first step to delineating heterotic pools for a more systematic improvement of combining ability via recurrent reciprocal selection.

Discovery of a sub-group within the land races, are observed from PCA of genetic distances (proportion of shared alleles) and UPGMA of pairwise FST between the different regions, that may represent heterotic groups.

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