Genotyping Ugandan cassava breeding populations using SSR markers for resistance to Cassava Mosaic Disease

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Introduction

Cassava mosaic disease (CMD) is a very important disease often causing total yield loss in farmers' fields. Molecular tools are being incorporated in many cassava breeding systems to enhance conventional breeding for resistance to CMD. Simple sequence repeats (SSR), preferred for co-dominance, ease of application and cost effectiveness were used in Uganda to analyse local and introduced progenitors, and their progenies for resistance to CMD.

Objective

To identify polymorphic SSR markers associated with resistance to CMD in Ugandan cassava breeding population

Materials and Methods

Parental lines included susceptible Ugandan cultivars (Bamunanika, Bao, Nyaraboke, Kakwale), introduced and released CMD resistant varieties Nase10, Nase12 (recessive); TME5, TME14 (dominant) and 95/SE00036 (tolerant). Nine half-sib families, obtained via polycross mating design were assessed for reaction to CMD using severity scale of 1(no symptoms) to 5 (severe symptoms) (Plate 1). Parents were screened with a total of 140 (138 SSR, 2 SCAR) markers for polymorphism associated with resistance to CMD (Mba *et al.*, 2001). Markers were validated using bulk segregant analysis (BSA) of at least 20 progenies per family (Michelmore *et al.*, 1991). Consistently polymorphic markers were advanced to analyse the entire F_1 population (Fig. 1).

Plate 1: Photographs showing disease incidence scores at a scale of 1 (no symptoms) to 5 (total leaf mosaic)

Results and discussion

- High frequency(88%) of alleles associated with resistance to CMD (Table 1) highlights possibilities of using MAS to characterise the population for response to CMD.
- Six markers, SSRY 20, SSRY45, SSRY284, SSRY175, NS40 and NS717 identified using BSA can be advanced to map the loci conferring resistance to CMD in this population.

Reference

- Mba *et al.*, 2001. Theoretical and applied genetics 102: 21-31
- Michelmore *et al.*, 1991. Proceedings of the national academy of sciences, U.S.A

Plate 2: PAGE gel (NS158) showing allele associated with resistance (arrow)

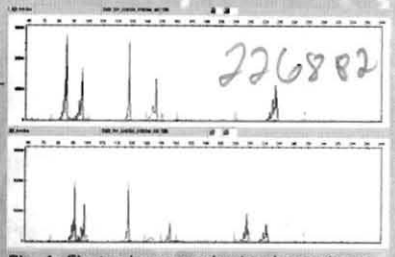

Fig. 1: Electropherogram showing three primers co-loaded in one capillary fragment analysis

Table 1: Summary of evaluation of 9 progenitors with 4 markers associated with *CMD2* (R: allele associated with CMD resistance, S: other alleles, NA: No amplification)

Lane	Progenitor	CMD resistance	NS158	NS169	RME-4	RME-1
1	Bamunanika	Susceptible	R	R	R	NA
2	Kakwale	Susceptible	R	R	R	R
3	Nyaraboke	Susceptible	R	R	R	NA
4	Bao	Susceptible	R	R	R	R
5	TME 14	*CMD2*	R	R	R	R
6	TME 5	*CMD2*	R	R	R	NA
7	NASE 10	*CMD1*	R	R	R	R
8	NASE 12	*CMD1*	R	R	R	R
9	95/SE-00036	Unknown	S	S	S	NA
10	NGA2	Tolerant	S	S	S	S
11	TME3	*CMD2*	R	R	R	R

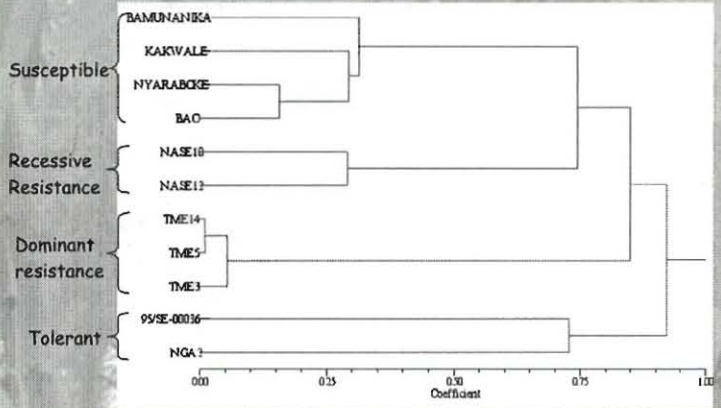

Fig. 2: UPGMA of Euclidian distances of genetic similarity in 9 Ugandan progenitors and two control lines

Conclusion and way forward

Putative SSRs associated with CMD resistance loci were identified. These will be used in linkage analysis and mapping QTL(s) conditioning resistance to CMD in the segregating population.

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