Molecular Marker-Assisted Selection (MAS) for Improvement of Local Cassava Germplasm in Tanzania for Pest and Disease Resistance

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INTRODUCTION

Centralized breeding cassava program in International Agricultural Research Centers (IARCs) and National Programs is a multi-stage evaluation lasting 8-10years with farmers being introduced at the very end of the scheme. The low adoption of improved cassava genotypes coming from centralized breeding programs in many African counties have led to the proposal of a decentralized breeding scheme involving molecular marker-assisted selection (MAS), to quickly reduce the size of breeding populations derived from crossing local varieties to improved introductions, followed by participatory plant breeding (PPB) (CIAT, 2005). A project to test this idea was initiated in Tanzania in October 2003 with support from the Rockefeller Foundation and is in its fourth year. Improved varieties with good resistance to the cassava mosaic disease (CMD) and the cassava green mites (CGM) were introduced from CIAT and evaluated for resistance to pest/diseases and other traits of agronomic interest. Selected introductions were then crossed to local farmer preferred genotypes collected in the Eastern, Southern, and Lake regions of the country. We describe here generation of crosses, establishment of the seedling nursery, evaluation for pest and disease resistance, and molecular marker-assisted selection for resistance to CMD.

MATERIALS AND METHODS

Genetic crosses and establishment of seedling nursery
Eighty introductions from CIAT resistant to CMD and CGM were crossed (controlled and polycross) to 51 local varieties resistant to CBSD and possessing farmer-preferred traits. The seeds were planted in the field at Chambezi.

Field evaluation of resistance to CMD, CBSD and CGM
Evaluations were carried out at 3, 6 and 9 months after planting. Leaves were collected from healthy plants for MAS using available markers linked to *CMD2* gene.

MAS for *CMD2*
A SCAR marker, RME-1 and two SSR markers, NS158 and SSRY28 were used for molecular evaluation of the parents and progenies without field symptoms. Positive control was the source of *CMD2*, the genotype TME-3.

RESULTS AND DISCUSSION

Genetic crosses and establishment of seedling nursery
At Chambezi, 57,463 crosses were made and 27,107 seeds were collected. Another 24,566 seeds from open pollination were collected from the controlled crossing block. A total of 26,592 seedlings eventually were transferred to the field at Chambezi in March 2006.

Field evaluation of resistance to CMD, CBSD and CGM
Among the 44 families evaluated for CMD in the first batch, there was a mean severity score of 2.15 (range 1.60 - 2.85) on family basis at 3 MAP and a mean score of 2.33 (1.71 – 2.98) at 6 MAP.

MAS for CMD2: Selection of families
Based on the evaluation of the parents, families with 1 or 2 of the 3 markers being polymorphic in the parents were selected for MAS (Table 1 and Fig 1). Additional markers are being developed from BAC contigs to evaluate families for which polymorphic markers in the parent are yet to be identified.

Table 1: Number and proportion of families selected for MAS based on polymorphism of markers associated with *CMD2* in the parents.

	RME-1		SSRY28		NS158	
	# Families	%	# Families	%	# Families	%
Controlled crosses	73	36.1	44	21.8	10	4.9
OPs from Polycross block	26	61.9	19	45.3	26	61.9
OPs from controlled crossing block	45	71.4	25	39.7	45	71.4

Harvest of the first batch is currently ongoing and will be completed in May 2007. F1 plants show good fresh root yield and high dry matter content (Figure 2). Evaluation for resistance to cassava brown streak disease (CBSD) also reveal that over 50% of the progenies show good resistance to the disease.

Criteria for selections will be field resistance to CMD, including molecular data from MAS, CBSD, CGM, and the ability to produce 10 stakes. About 8000 clones are expected to be established in the CET. Selections will be immediately established in a replicated (2 reps of 4 plants each) clonal evaluation trial (CET) station at Chambezi and Naliendele, two locations with strong CBSD and CMD pressure.

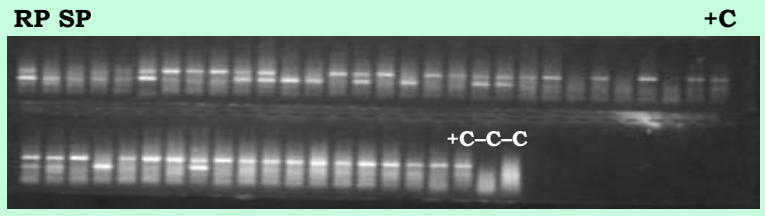

Fig. 1: Gel image of PCR product of the SCAR marker RME-1 evaluated in 49 progenies of the family KHC16 (controlled cross). First well shows the resistant parent (RP) CR27-24 (CIAT accession), second well shows the susceptible parent (SP) Nachinyaya (Tanzanian local variety), wells labeled as +C represent the positive control *CMD2* donor parent TME-3, wells labeled as –C represent the negative controls, the remaining wells correspond to progeny of KHC16.

Selection based on single plants will also be made and 500 of the best genotypes will be selected for participatory variety selection (PVS). Site for PVS will be 10 villages in Coastal and Southern Tanzania. Experimental design will 2 reps of 4 plants, genotypes will be evaluated at 3, 6, and at harvest with harvest.

The CET will be evaluated for field resistance to CMD, CBSD, and CGM as well as yield components such as harvest index, number of roots, and total plant biomass, and farmer-preferred characteristics. Selections from the CET will be re-evaluated on-station in a preliminary yield trial (PYT) and on-farm in farmer participatory trials according to the original PPB and MAS scheme. About 5% of the 8,000 clones will be selected for on-farm trials in 2008 and 2009.

Fig. 2. Storage roots of F1 progeny between CIAT Introductions and local Tanzanian varieties

CONCLUSIONS AND ONGOING WORK

The Tanzanian MAS-PPB project seeks to improve local varieties for disease and pest resistance and provide a proof of concept for the MAS-PPB paradigm in cassava breeding but more importantly it is expected transfer useful variability from the crop's center of diversity of cassava to Africa. The concept has already been extended to three other NARs in Africa, namely Nigeria, Ghana, and Uganda, under the auspices of a Generation Challenge Program (GCP) competitive grant project 'Development of Low-cost Marker Technologies for Pyramiding Useful Genes from Wild Relatives of Cassava into Elite Progenitors'.

The second and most important phase of the project is the farmer participatory evaluation of cassava genotypes that have resistance to CMD, CGM, and CBSD. Detailed records of why farmer select certain genotypes, including perceptions of disease response, yield, dry matter content, cooking quality and taste will be made and used to guide future germplasm transfer to NARS cassava breeding program.

ACKNOWLEDGEMENTS

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REFERENCES

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