Molecular Marker-Assisted and Farmer Participatory Improvement of Cassava Germplasm for Farmer/Market Preferred Traits in Tanzania

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INTRODUCTION

Tanzania is the fourth largest producer of cassava in Africa with average yields of about 8 t/ha (FAO, 2001). This is well below the continent´s average of 10 t/ha and the average yield of 14 t/ha of Africa´s and the world´s larger producer, Nigeria. The low yield is caused by many factors including susceptibility of commonly grown varieties to major diseases and pests such as cassava mosaic diseases (CMD), cassava bacterial blight (CBB), cassava green mites (CGM), cassava mealy bug (CM) and nematodes.

A Farmer participatory, molecular marker-assisted, decentralized, breeding scheme has recently been approved for funding by the Rockefeller Foundation to speed up the process of improving local cassava germplasm for resistance to pests and diseases in Tanzania. The proposed breeding project will take farmer preferred germplasm by agro-ecology and cross them to improved introductions that have resistance to Cassava Mosaic Disease (CMD), Cassava Green Mites (CGM), and Cassava Bacterial Blight (CBB). Given the fairly large number of parents that will be used, molecular markers associated with pest and disease resistance will be employed to reduce, in a logical manner, the number of progeny to a manageable number. The progeny selected by MAS will be evaluated in a single season in the corresponding agro-ecology and then evaluated over two cycles in collaboration with end-users (rural communities and cassava processors). The project will be carried out in a total of six years divided into 2 three-year phases. A principal objective of the project is the development of capacity for participatory plant breeding and marker-assisted breeding.

MATERIALS AND METHODS

The collection and evaluation of local germplasm, and the introduction of improved progenitors for use as parents in the breeding project have been carried out. Improved progenitors were designed to have resistance to CMD, CBB and CGM as well as molecular markers associated with these genes. The Rockefeller funded project "Molecular Mapping of Genes Conferring Resistance to Cassava Mosaic Disease (CMD) in African cassava germplasm" has led to the identification of 3 SSR and 2 RAPD markers tightly linked to a novel source of CMD resistance controlled by a single dominant gene designated *CMD2* (Akano et al 2002; Moreno and Fregene unpublished data). Resistance to CGM have also been observed in F1 inter-specific hybrid families obtained by crossing the cassava clones CG487-2, CG501-16, MCol2215 and CM2766-5 to a genotype of M. esculenta sub spp *flabellifolia* (Belloti and Fregene 2002, unpublished data; CIAT 2002). Bulk segregant analysis (BSA) was quickly used to identify several SSR markers associated with CGM resistance in the MCol2215 cross (CIAT 2002). The inter-specific hybrids of *M. esculenta* sub *flabellifolia* that carry the novel CGM resistance were crossed extensively to elite parents of cassava gene pools from the 5 agro-ecologies, a number these parents have the SG107-35 source of CBB resistance. Progeny from the above crosses were established from embryo axes of mature sexual seeds, multiplied and kept *in vitro* (Fig. 1). Two *in vitro* plants were used for marker evaluation to identify CMD, CBB and CGM resistance. More than 300 genotypes that combine resistance to CMD, CBB and CGM and high productivity have been shipped to Tanzania, at least 10 plants per genotype were shipped.

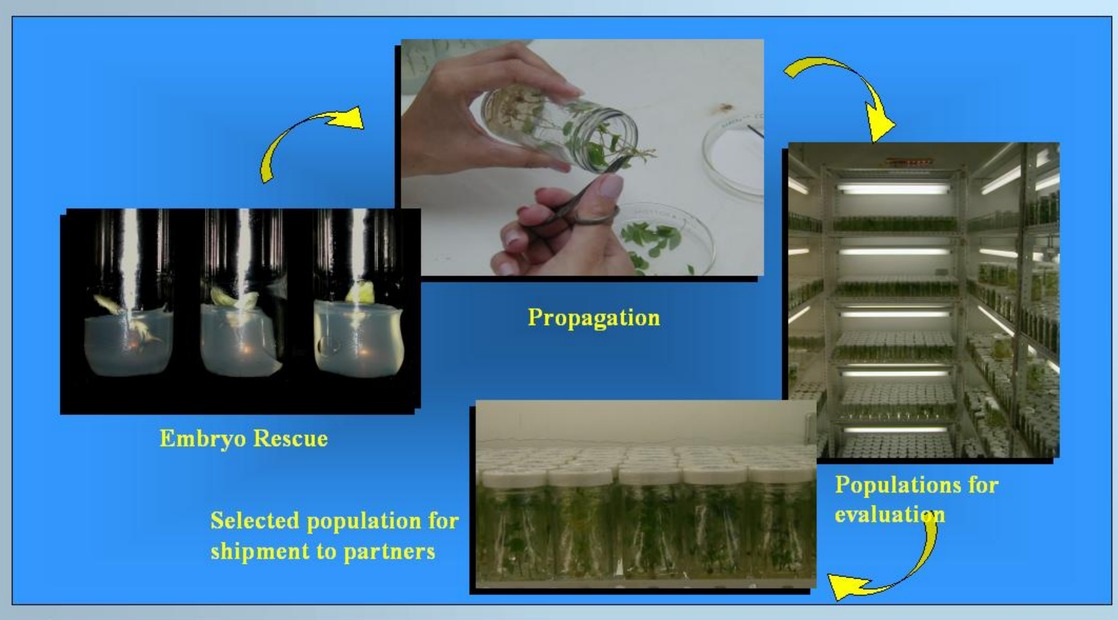

Fig. 1. Embryo rescue for the establishment of molecular breeding populations

RESULT AND DISCUSSIONS

Progenies of inter-specific hybrids crossed to parent of cassava gene pools adapted to the sub-humid, acid savannah, mid-altitude and semi-arid agro-ecologies, with good resistance to CBB were crossed to CMD2 donor parents to obtain more than 1600 BC2 progenies. Embryo rescue and multiplication of the BC2 families were done to obtain 10 plants per genotype, about 5 *in vitro* plants per genotype was used in MAS using markers associated with CMD and CGM (Fig. 2). A special format in Microsoft excel was developed to display results of the molecular marker-assisted evaluation of the BC2 progenies. Plants selected by molecular marker analysis were further multiplied to obtain more than 20 plants per genotype and these were shipped to Tanzania. On arrival in Tanzania, at least 8 plants were hardened in the screen house and inspected by plant phyto-quarantine authorities. The remainder plants, 2 per genotype, will be multiplied and kept *in vitro* as backup. After 2 months the screen house plants will be transferred to the field in a single row trial experiment for evaluation and selection. At least 30 genotypes of the 200 improved introductions will be selected for crosses to the selected local varieties that have also been recently collected. Selection parameters will include harvest index, pest and disease resistance and root quality. See Fig 3 for molecular breeding scheme.

The local land races and introductions will be used as female parents to achieve a wide base of cytoplasm, therefore open pollinated and controlled pollinated sexual seed will be harvested from both. Between 10,000 and 20,000 seeds are expected from crosses for each agro-ecology.

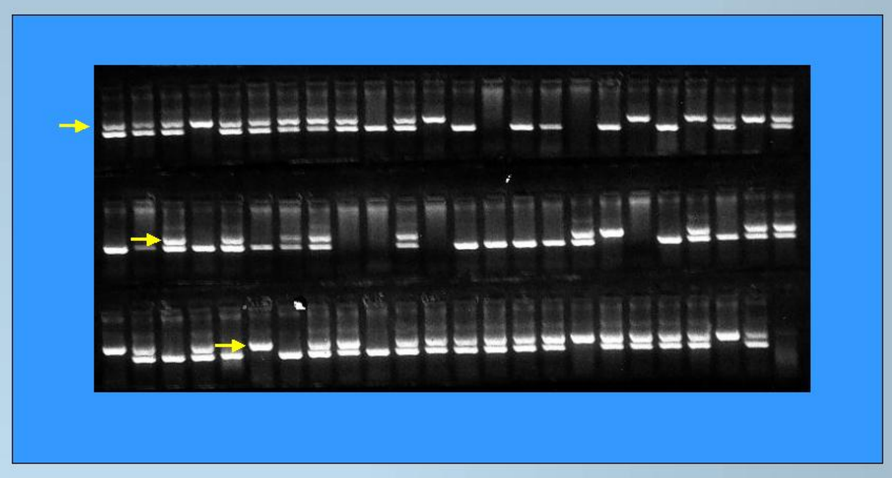

Fig. 2. Molecular markers associated with CMD resistance

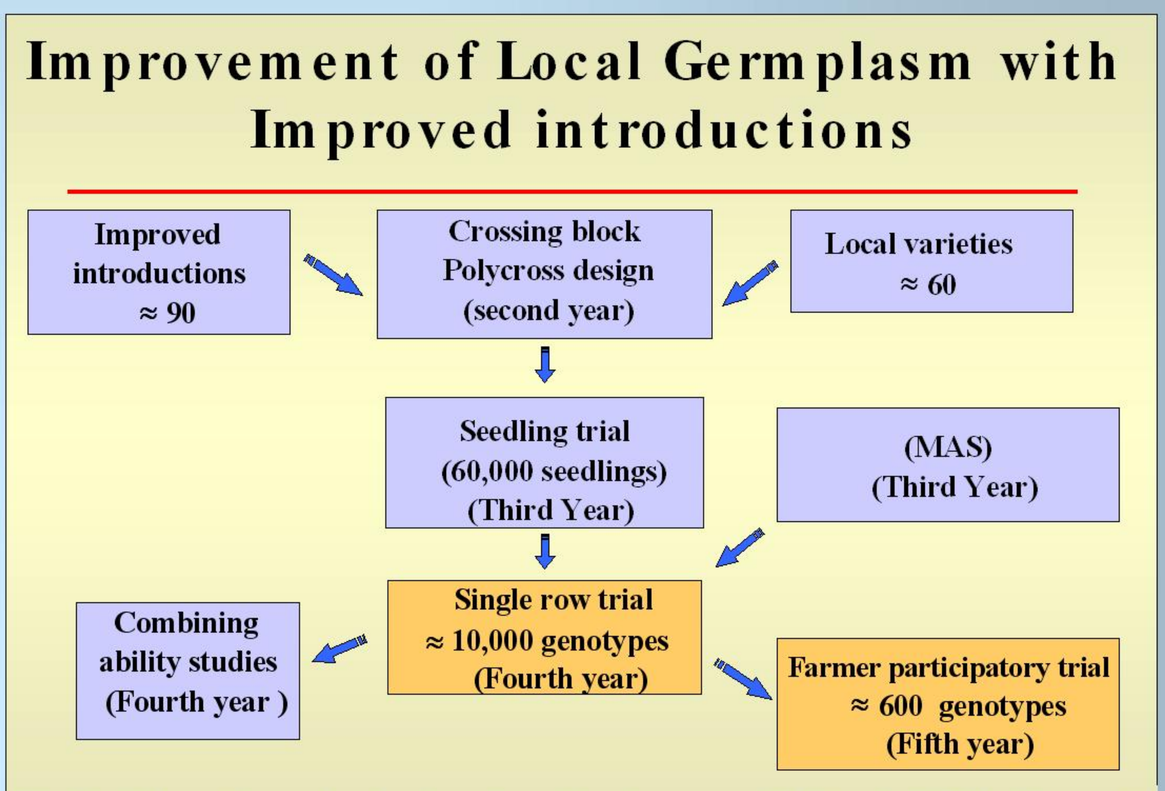

Fig 3. Scheme for molecular breeding of resistance to CMD and CGM in Tanzania

CONCLUSIONS AND ONGOING WORK

A molecular marker-assisted breeding project to develop improved germplasm for small cassava farmers have been initiated. The first years will be spent in the establishment of parents and generating broad-based breeding populations for subsequent selection by molecular markers and in collaboration with farmers. The project is a first and experience gained is expected to guide the application of molecular markers in cassava breeding.

REFERENCE

Akano A., Barrera E., Mba c., Dixon A.G.O., Fregene M (2002) Generic Mapping oa a dominant gene confering resistance to the Cassava Mosaic Disease (CMD). Theoretical Applied Genetics.

CIAT (200). Annual Report Project SB2, Assesing and utiloizing agrobiodiversity through Biotechnology, CIAT, Cali, Colombia, pp 239-241.

FAO (2001) FAO production yearbook for 2000, Rome, Italy: FAO Muhanna and Mtunda 2001 a repot on a survey of cassava in Tanzania. Ministry of agriculture and food security, Tanzania.

ACKNOWLEDGEMENTS

This project will not have been possible but for the farmers of Mtawara and Lindi districts who shared their cassava germplasm with ARI and CIAT researchers in the summer of 1999 that was subsequently analyzed with molecular markers to estimate genetic diversity. The broad and unique diversity in that collection is the basis of this project. Funding for this project is from the Rockefeller foundation for which we thank Drs Gary Toeniessen and Joe DeVries.

Fig. 4. Farmers and cassava researchers pose for a picture in Nachingwea, south eastern Tanzania