

Marker Assisted Selection: A Paradigm for Germplasm Transfer and Genetic Improvement of Cassava in Africa

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BACKGROUND

Cassava is one of the most important food staples in sub-Saharan Africa. Increasing productivity to meet food and industrial needs are key challenges for African NARs. Many pathogens still take their toll and occasionally, epidemics affect farmer fields significantly, therefore, new sources of variation are needed to genetically enhance productivity in Africa. However, cassava's long growth cycle makes breeding very slow requiring 8-10 years to release improved varieties. The International Center of Tropical Agriculture (CIAT), Colombia developed molecular markers which has been used to map genes for pest and disease and nutritional quality traits. Under a GCP competitive grant project "Development of Low Cost Technologies for pyramiding useful genes from wild relatives of cassava into elite progenitors", led by CIAT and involving NRCRI, Nigeria and CRI, Ghana, these markers are being used in MAS to develop pest and disease resistant, high performance genotypes for release in both countries. We report the results and achievements recorded under this project.

MARKER ASSISTED SELECTION (MAS)

Cassava improvement through conventional breeding (including use of wild species) is relatively slow and inefficient. MAS can be applied to support existing conventional breeding programs to increase breeding efficiency. By moving from phenotype based to genotype based selection, the potential benefits of using markers linked to genes of interest in breeding programmes will accelerate the release of improved germplasm. The existence of a strong breeding program is a prerequisite for the application of advanced molecular technologies such as MAS. In situations where the infrastructure and capacity are insufficient to support a successful conventional breeding programme, MAS will not provide a short cut to genetic improvement. In view of this factor, MAS laboratories were for the first time established under this project, at NRCRI and CRI (Fig. 1). These laboratories are strategically important for MAS activities.



Fig. 1 MAS laboratory at NRCRI

GERMPLASM TRANSFER TO NARS

Although considerable diversity exists within the African *M. esculenta* accessions, this can be improved by using the vast germplasm base from Latin America where cassava originates. The current cassava and *Manihot* collection, held in trust at CIAT, has provided access to useful economic traits in Latin America (LA) and Asia. CMD, the most important cassava disease in Africa, has been a hindrance in fully utilizing this vast genetic resources in Africa. Under the current GCP project, marker assisted introgression of CMD resistance in LA germplasm was used to deploy adapted germplasm to Africa (Fig. 2). Given the need to fully exploit the germplasm in Latin America for the benefit of African breeding programs, CIAT transferred thousands of *in vitro* culture plants from 2005-2006 representing over 200 genotypes to Africa (NRCRI and CRI). Before introduction to Africa, all parental lines of the genotypes were evaluated with eight markers—simple sequence repeats (SSRs) or sequence-characterized amplified regions (SCARs)—that were associated with the *CMD2* gene. These were NS158, SSRY28, RME1, RME2, RME3, RME4, RME5, and RME6. At least two markers, polymorphic in the parents and flanking the resistance gene, were used to evaluate the progenies. After PQS inspection, the *in vitro*

plants were hardened and then transplanted to the field. The introduced genotypes were evaluated in Nigeria and Ghana. They were evaluated for CMD as described by Akano *et al.* 2002. Another set of 600 F₁ seedlings generated from parents selected for high beta carotene (pre-cursor of *Vit. A*) was also introduced from CIAT to NRCRI and CRI for the improvement of nutritional quality traits in cassava.

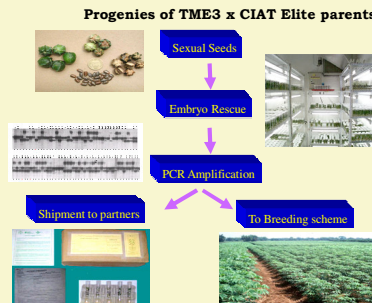


Fig. 2 MAS for CMD resistance

GENETIC IMPROVEMENT

MAS can rapidly increase genetic gain and result in economic benefits to farmers from genetic improvement of their plants. In this project new hybrids have been developed by introgressing useful genes from exotic germplasm into local varieties in Africa and then used to select for desirable traits based on genotypic data. In the GCP project, CIAT genotypes were crossed with farmer preferred local cassava at NRCRI and CRI. These activities resulted in the development of 11,000 hybrid seeds at NRCRI, and 3,000 seeds at CRI. These progenies will be used in MAS activity to select pest and disease resistant genotypes. The dynamic evolution of the CMD virus has resulted in various variants and other hybrid combinations which could pose a serious threat to cassava. As part of efforts to develop stable and durable CMD disease resistance in Africa, activities to identify new sources of CMD resistance were initiated. Four segregating crosses involving parents selected from NRCRI germplasm were used under the Genotyping Support Services to map new CMD genes based on bulk segregant analysis approach. This activity is important in pyramiding different sources of CMD resistance genes into elite cassava varieties

ACHIEVEMENTS

The major achievement of this project till date is the nomination of three entries, CR 14A-1, AR 38-3 and CR 41-10 for the Nationally Coordinated Research Project (NCRP) which is a multi-locational evaluation trial of elite genotypes for their adaptation response and general performance across Nigeria as a first step towards their release. CR 14A-1 is already at the On-farm trial stage. This clone has been distributed to 13 states in Nigeria. Ten clones from this project, which could not be immediately absorbed into NCRP trials are already at the uniform yield trial in NRCRI breeding scheme. Seven of the clones had yield above 35 t/ha with highest yield being 54 t/ha (Table 1). NRCRI is currently seeking improved varieties with root yield in the range of 35-40 t/ha which is a top criteria being emphasized by the release committee in Nigeria as part of measures to double yield output. A total of 146 genotypes with CMD resistance and good vigor have so far been identified and are at various stages of yield evaluation at NRCRI (Fig. 3). They represent 65 families and 10 of the families have no less than 4 genotypes. Under the Genotyping Support Service, two new CMD resistance genes from NRCRI germplasm were identified. This will provide an important opportunity to pyramid these genes into elite germplasm at NRCRI. A total of 23 genotypes have also been identified for CMD disease resistance at CRI and are being evaluated for yield. Twenty clones from the NCRP and UYT have been sent to Ghana and most of the materials are doing well in reaction to CMD.



Fig. 3 Latin American cassava genotypes with resistance to CMD integrated into Nigeria breeding programme.

Table 2: Yield potential of CMD - resistant cassava genotypes undergoing pre-varietal release trials in Nigeria.

Genotype	CMD (12 MAP)	Root Yield (tons/ha)	Fresh Shoot yield (tons/ha)	Harvest. index
AR1-82	1.0	43.4	37.8	0.5
AR37-108	1.0	39.2	85.9	0.4
CR12-45	1.7	54.3	54.2	0.5
CR14A-1	1.7	47.4	48.1	0.5
CR26-1	1.3	37.1	26.0	0.6
CR36-2	1.3	28.2	22.2	0.6
CR36-5	1.0	39.8	31.8	0.6
CR42-4	1.0	39.4	28.3	0.6
CR52A-25	1.0	35.3	16.7	0.7
CR52A-41	1.0	29.9	12.4	0.7

FAST TRACK DELIVERY

Novel breeding strategies is being used in this project to accelerate the release of improved varieties in a short period. The strategy is that Neo-tropical cassava genotypes are pre-selected for CMD resistance with markers and evaluated for one or two years in the breeding scheme at CIAT before being shipped to Africa. The Neo-tropical genotypes selected for good performance from a two year evaluation in Africa are then rapidly evaluated in multiple location trials for another two years and subsequently released as varieties. Within 5 years of evaluation, African farmers can have access to elite clones from exotic germplasm (Fig. 4).

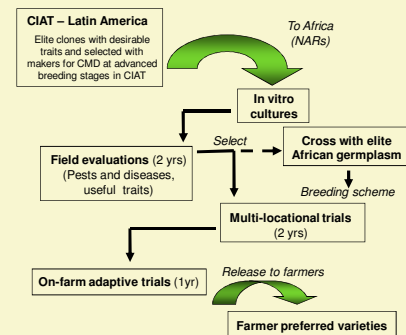


Fig. 4: A five-year scheme for fast delivery of best bet cassava varieties from LAC to African farmers.

ACKNOWLEDGEMENTS

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REFERENCES

Akano, *et al.* 2002. *Theor. Appl. Genet.* 105: 521-525.