

Recent Advances in Genetic Improvement of Cassava

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Outline

- ❖ Cassava improvement
- ❖ Molecular markers in cassava breeding
- ❖ Mutagenesis for increased variability
- ❖ Inbreeding for unlocking novel recessive traits
- ❖ Bringing the benefits of modern science to farmer's fields
- ❖ Connecting the lab to field (Training)
- ❖ Acknowledgement

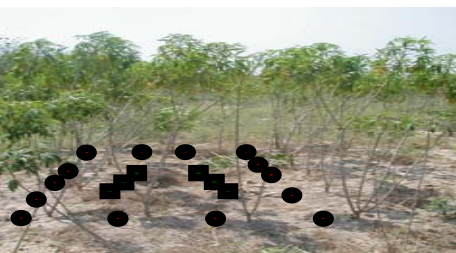
Breeding Strategy for Cassava

- ❖ Clonal propagation requires breeding methods that takes advantage of both additive and non-additive variance
- ❖ Large effective population sizes required to retain favorable dominant alleles and epistatic loci combination
- ❖ Managing such large number of progenies are beyond most breeding programs and requires new technologies to reduce in a logical manner



Cassava Breeding and Evaluation Schemes Currently Used at CIAT

Elite germplasm recombined through sexual crosses (hand or open pollinations)



Thousands of botanical seeds are produced each year

Seedlings from botanical seed are grown in screenhouses and then transplanted to the field

F1 [6000 GENOTYPES]

Plants from botanical seed are grown (avoiding selection) for 10 months and 7-8 stakes are produced from each plant

Shipment to Target Environment

Clonal Evaluation Trial [4000]

One row plot with 7 or 8 plants/plot
One replication – One location



Preliminary Yield trial [800]

2-rows plot with 10 plants
3 replications – one location

Advanced Yield Trial [300]

4-rows plot with 20 plants
3 replications – one location



Regional Trial [90]

5-rows plot with 30 plants.
3 replications – 2-3 locations

Molecular Markers in Cassava Improvement

Applications of Molecular Markers in Cassava Breeding

- ❖ Increase heritability in the identification of superior genotypes
- ❖ Select in the absence of a pathogen (the case of CMD resistance breeding at CIAT)
- ❖ Follow specific chromosome segments from unadapted wild relatives in breeding schemes
- ❖ Pyramiding multiple sources of resistance to pest and pathogens
- ❖ Reduce population sizes for more precise field evaluations

Maximizing Heritability

$$\Delta G_y = \frac{k\sigma_A^2}{y\sqrt{([\sigma_u^2 + \sigma_{wg}^2]/n) + \sigma^2/rt + (\sigma_{ge}^2/t) + \sigma_g^2}}$$

y - number of years

k - selection intensity

σ_A^2 - additive genetic variance

σ_u^2 - Environmental variance
among plants within plot

σ_{wg}^2 - Genetic variance
among plants within plot

n - number of plants within plots

σ^2 - plot-to-plot variance

r - replications

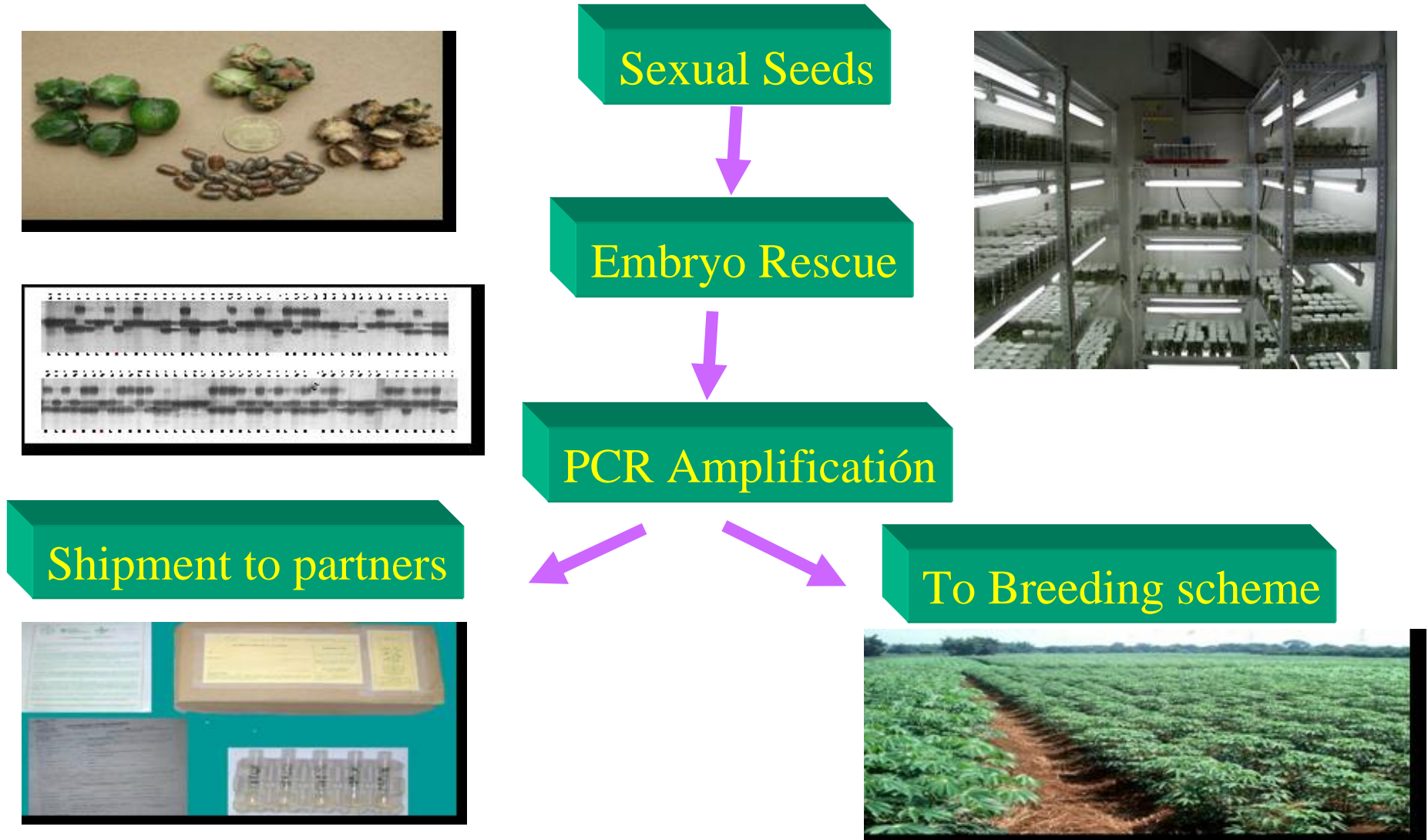
t - number of environments

σ_{ge}^2 - Genotype x environment
variance

σ_g^2 total genetic variance

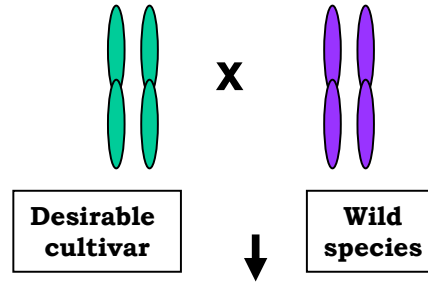
Selecting in the Absence of a Pathogen: MAS for CMD Resistance at CIAT

Progenies of TME3 x CIAT Elite parents

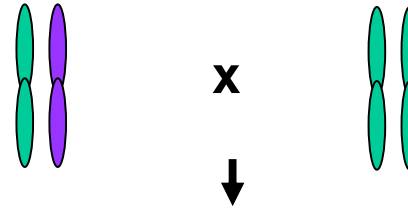


Follow Specific Chromosome Segments from Unadapted Wild Relatives: A Modified Advanced QTL Backcross Breeding Scheme

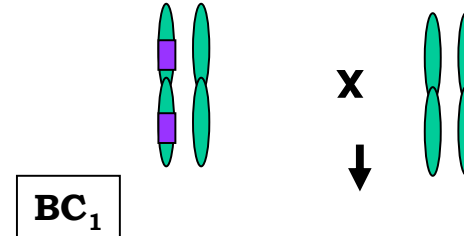
1. Produce F1 progeny



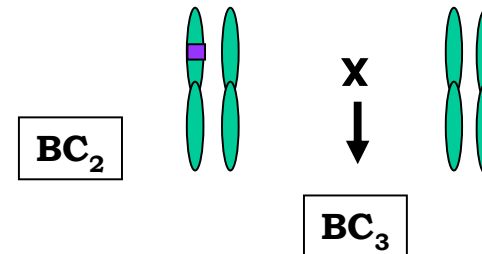
2. Select for trait



3. Produce BC₁
Select for trait and do
QTL mapping

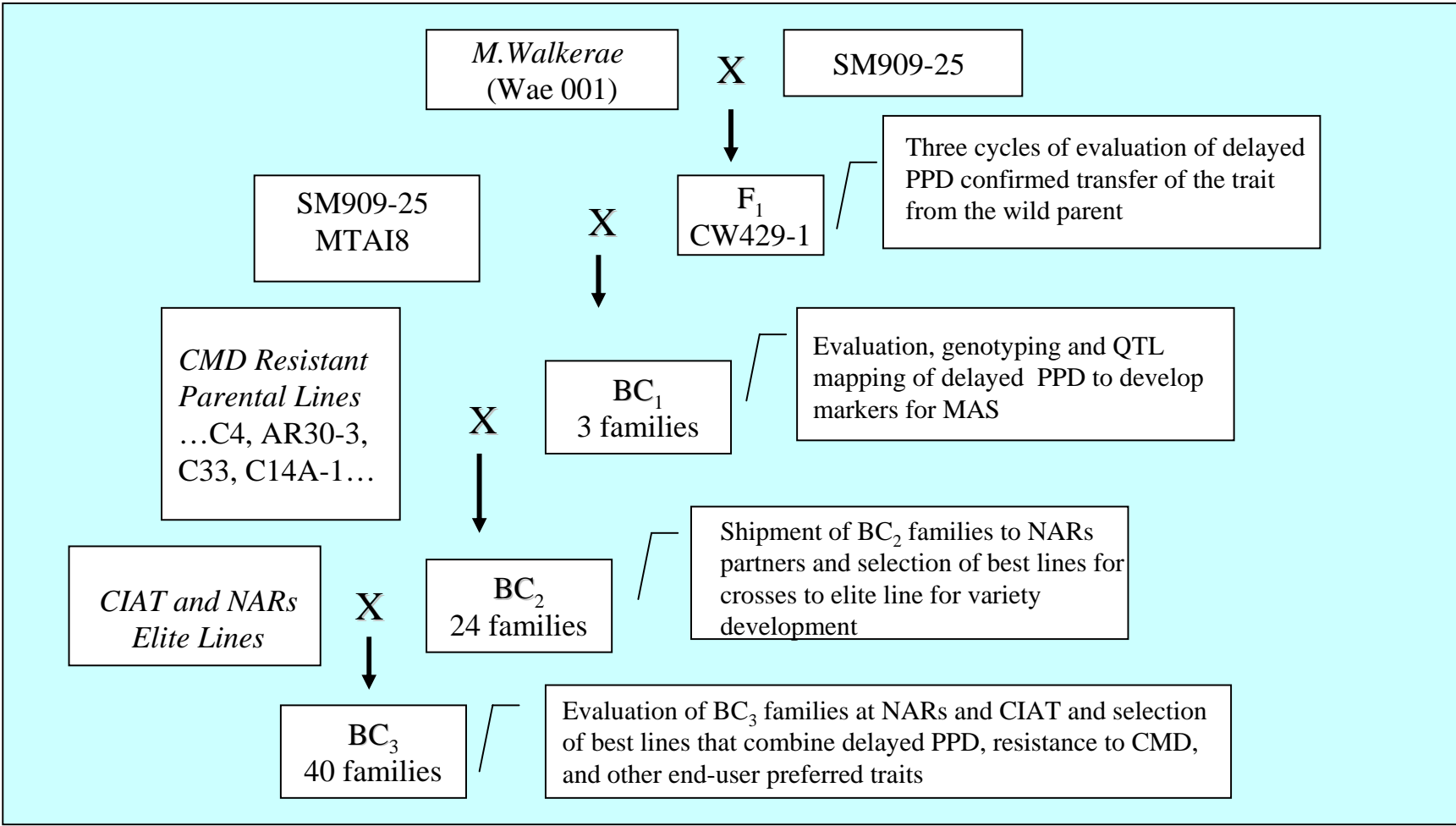


4. Produce BC₂, and BC₃
Using MAS and transfer to
Regular selection scheme



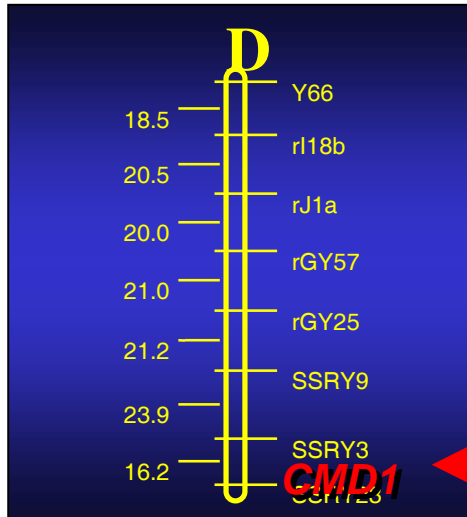
To variety development evaluation scheme

Transfer of Delayed PPD from *M. Walkerae* to Cassava Gene Pools

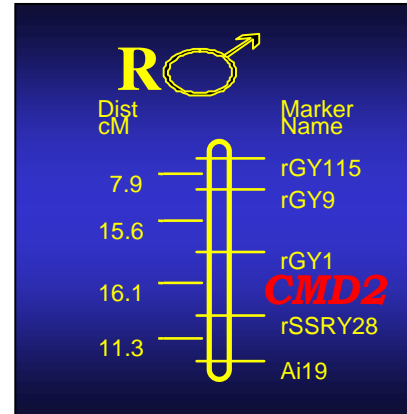


Pyramiding Multiple Sources of CMD Resistance Genes

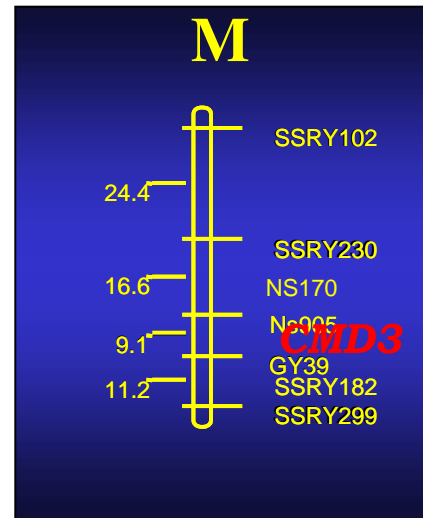
*At least 3 different CMD Resistance genes have been mapped and
Can now be pyramided using molecular markers*



Fregene et al. 2000



Akano et al. 2001



Hurtado et al. 2007

Reduction of Breeding Populations: A MAS Cassava Project in Tanzania

- ❖ Use markers linked to CMD resistance to reduce large breeding populations obtained from crossing local and neo-tropical varieties
- ❖ Evaluate F_1 s in a replicated trial over a single season and go directly to participatory variety selection (PVS) trials



With support from RF, GCP (GSS), ARI, IITA and CIAT

MASCas: MAS Resources for Cassava

Address <http://www.ciat.cgiar.org/mascas/index.htm>

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MASCas

Introduction to the Molecular Marker

Protocols for Marker Assisted Selection in Cassava

Molecular Tools Available to MASCas

Genetic Stock for Gene Mapping

Partners

Cassava Links

MASCas Molecular Marker Assisted Selection in Cassava Breeding

This project is funded by:

Rockefeller Foundation; CIAT; FAO; Generation Challenge Program (GCP).

Project leader: Dr. Martin Fregene.

Site maintained by: Ing. Fernando Rojas.

For further information contact: [Martín Fregene](#).

Last update: 14 January 2005

MASCas

Cassava is a crop that has largely been left behind by scientific plant breeding partly due to its status as an orphan crop with limited resources for research and development, its highly heterozygous nature, and its long reproductive cycle.



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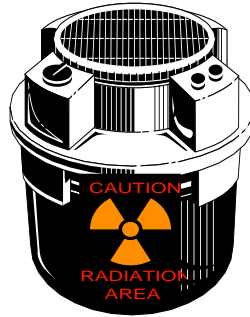
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Mutagenesis for Increased Variability

Induction of Mutations

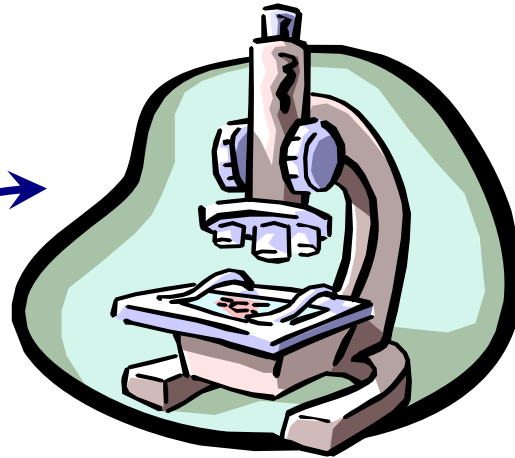
M0



M1



TILLING

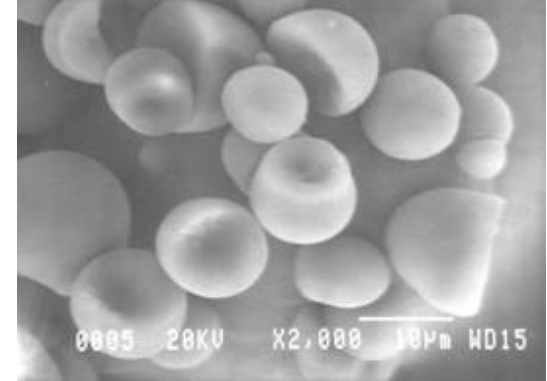
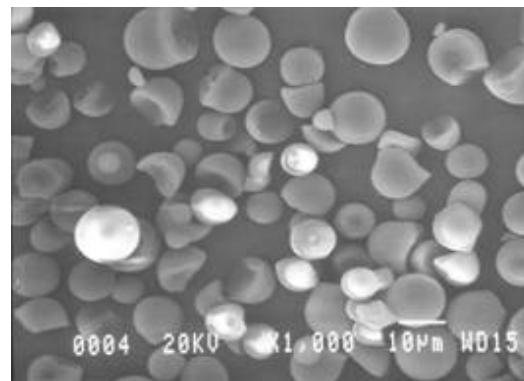
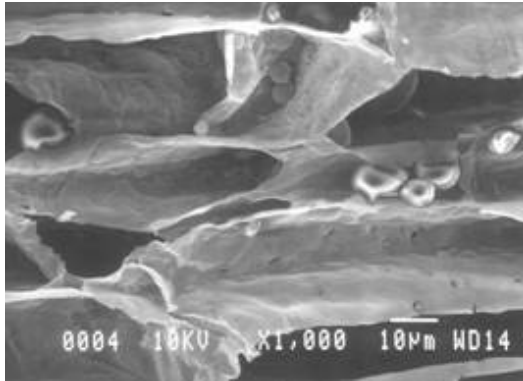


M2

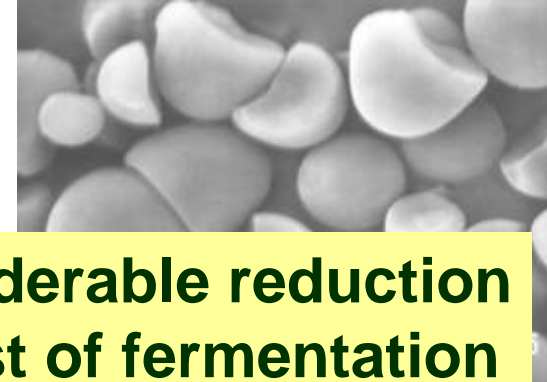
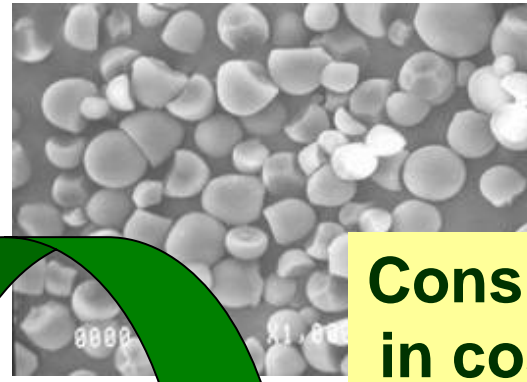
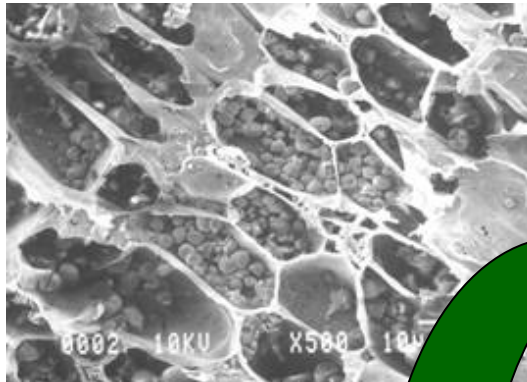
Self-pollination

Cassava Starch Mutants

“Hollow” granules

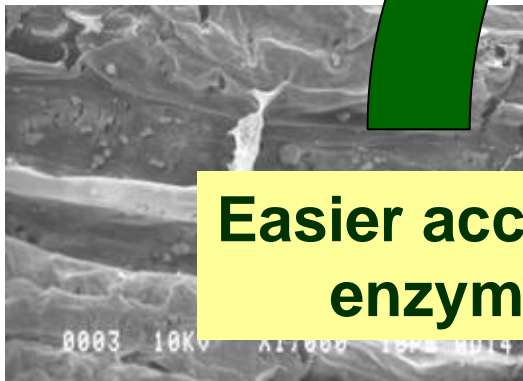


Normal starch

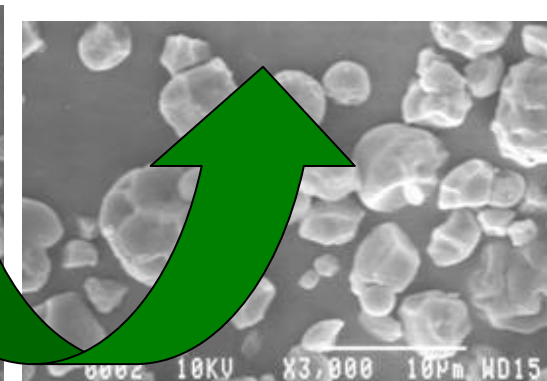
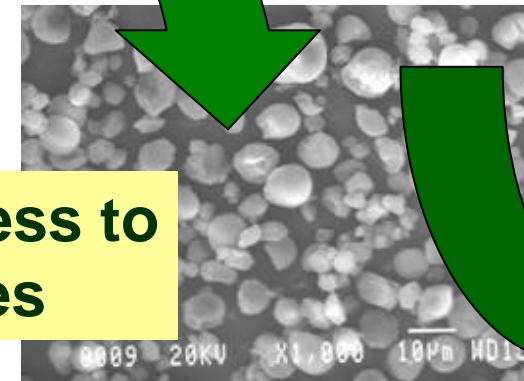


Considerable reduction in cost of fermentation

Small granules

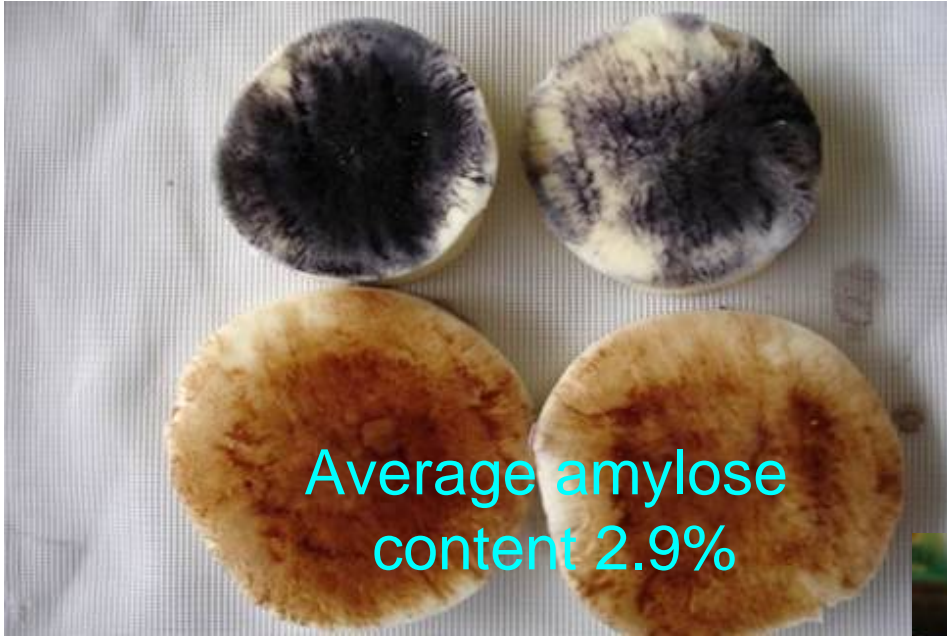


Easier access to enzymes



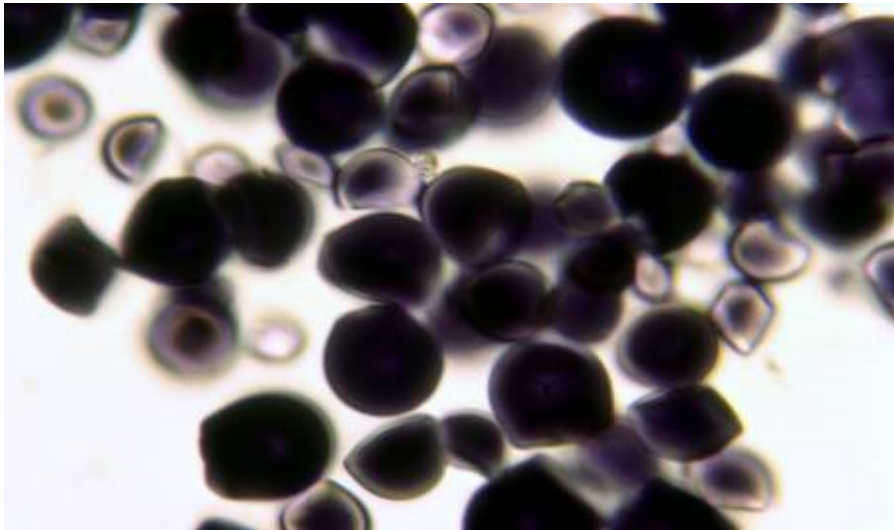
Inbreeding for Unlocking Novel Recessive Traits

Identification of a Waxy Cassava Genotype

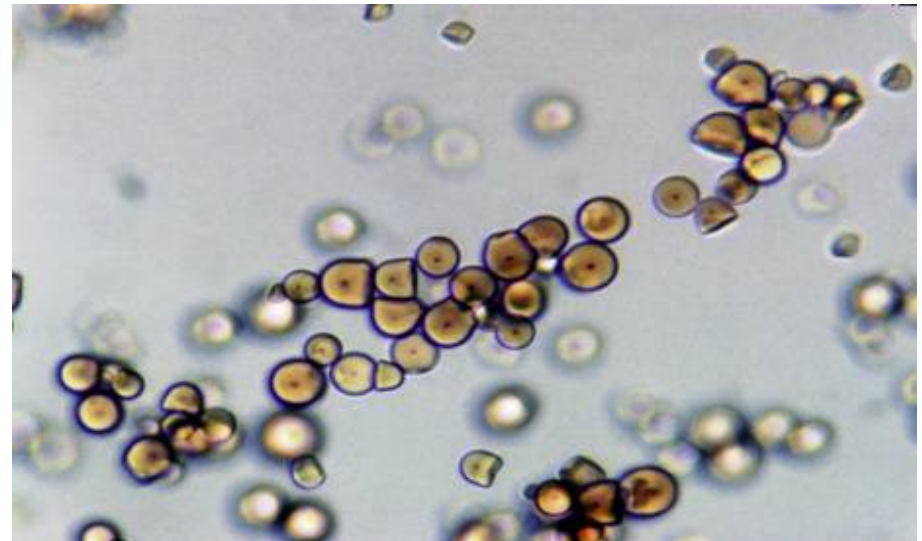


Identification of a Waxy Cassava Genotype

Light microscopy of normal...

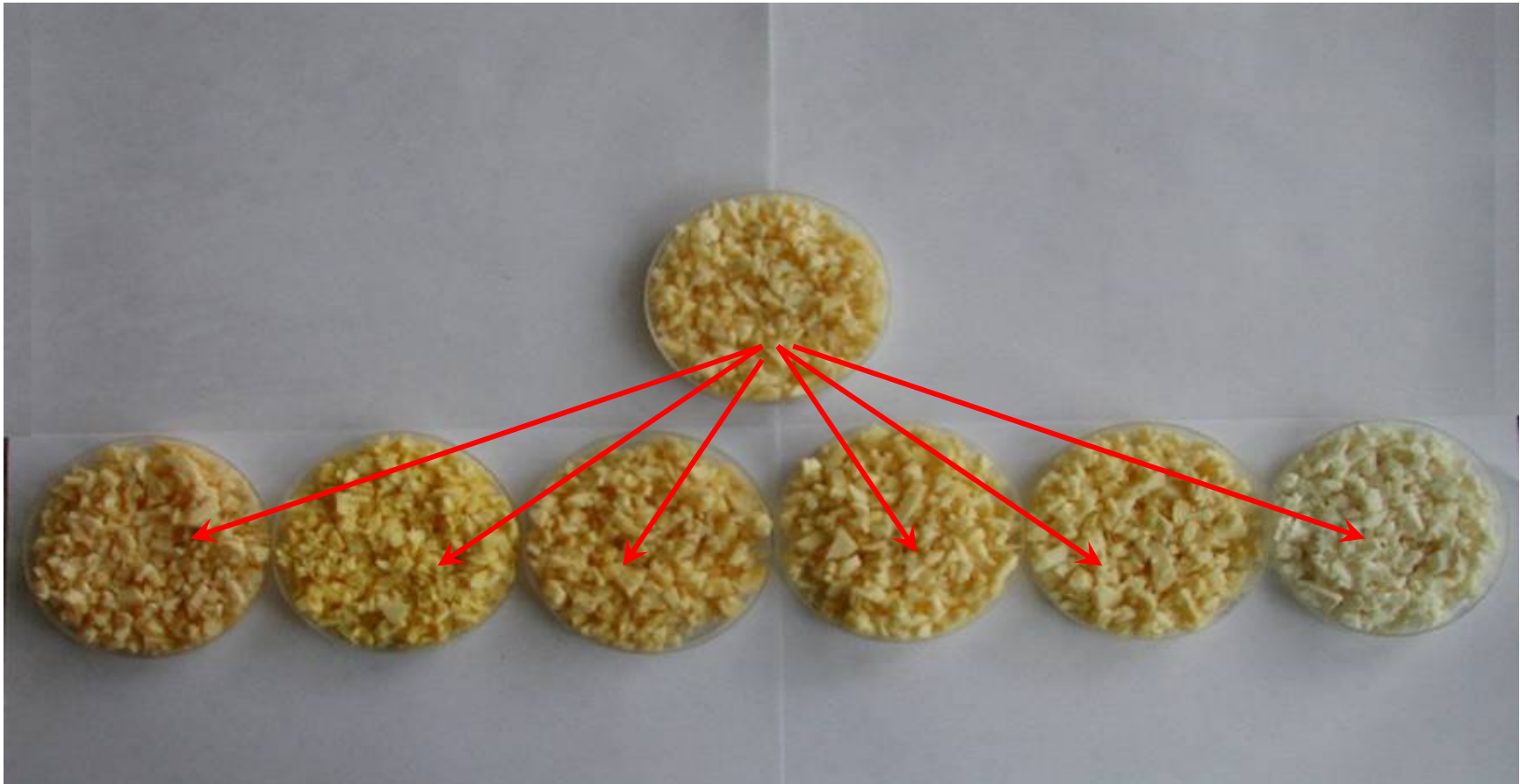


...and waxy starch



Introduction of Inbreeding

Segregation in carotene contents
in roots from clone CM4919-1



Bringing the Benefits of Modern Science to Farmer's Fields

- ❖ Demonstrate superior yield and quality to farmers and processors for accelerated adoption of new pest and disease resistant cassava varieties
- ❖ Disseminate farmer-preferred varieties by integrating formal (scientist-led) and farmer-driven multiplication of improved materials



From the Lab to the Field: Training National Program Scientists in Marker Technology

- ❖ Chikelu Mba, NRCRI, Nigeria
- ❖ Chideozie Egesi, NRCRI, Nigeria
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