

## DEVELOPING A MOLECULAR GENETIC MAP OF CASSAVA

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### Abstract

A molecular genetic map of cassava is being constructed from F<sub>1</sub> segregation data of single-dose polymorphisms of RFLP and RAPD markers. The mapping progeny is a population of 90 plants derived from a cross between two elite clones, MNGA-2 (TMS 30572), resistant to African cassava mosaic virus and bacterial blight, and CM 2177-2 (ICA-Cebucán), possessing high photosynthetic rates and tolerance of insect pests. More than 200 markers, corresponding to genomic clones selected from *Pst*I, *Hind*III, and *Eco*RI random genomic libraries (RFLPs) and polymorphisms from arbitrarily primed polymerase chain reactions (RAPDs), were monitored in this cross. Of about 900 random genomic clones, 30% detected RFLPs between the two parental cultivars. Tests of linkage between segregating RFLP and RAPD markers with respect to the male and female parents were conducted, using the MAPMAKER computer package. Segregation of the markers revealed a predominantly disomic mode of inheritance in cassava. The degree and organization of sequence duplication will be used to investigate the possible allopolyploid nature of the cassava genome. Efforts to saturate the map and to develop and characterize genetic stocks are in progress towards identifying markers linked to genes controlling traits of agronomic interest.

**Note: This manuscript was incomplete (copies of the figures were mislaid)**

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