

Identification of molecular markers linked to genes conferring resistance to whitefly in cassava



A. BOHORQUEZ, B. Arias, A. BELLOTTI, M. FREGENE AND J. TOHME

Centro Internacional de Agricultura Tropical (CIAT), AA6713, Cali, Colombia.

INTRODUCTION

Whitefly as direct feeding pests and virus vectors constitute a major problem in agricultural production in the world. There are almost 1200 reported species with a wide range of hosts including legumes, horticultural crop, vegetables, fruit trees and ornamentals where they can cause major economic losses.

In cassava (*Manihot esculenta* Crantz), the whitefly (*Aleurotrachelus socialis*) is reported causing up to 80 percent of root losses. The principal symptoms in the plant are: total chlorosis of the leaves, curling of the apical leaves; yellowing and drying of the basal leaves; and stunting of the plant's development. The adult insects are found primarily in the apical zones of the plant where they extract large quantities of the sap from the conductive vessels, causing a considerable damage by loss of vigor. This of course leads to reduced yield. The honeydew which they excrete as a result of the copious sap intake serves as a substrate for sooty mold fungi, which can also damage hosts by preventing photosynthesis.

MATERIALS AND METHODS

Different sources of resistance to Whitefly has been reported (CIAT, 1995). The most important sources of the resistance genes are: MBra-12 and Ecu-72. These two genotypes have been used as parentals in the generation of new genotypes. One of the offspring, CG489-34 is considered one of the most resistant progeny to this pest. MCol 2026 and MCol 2246 were identified as two of the most susceptible genotypes. Different breeding populations have been obtained from crosses between the resistant and susceptible genotypes. The cross CG489-34 X MCol-2026 produced 131 individuals

We are using Amplified Fragment Length Polymorphism (AFLPs) and Simple Sequences Repeat (SSR) combination with the Bulk Segregant Analysis (BSA) method to find markers associated to resistance for mapping and ultimately cloning of the resistant genes.

The more contrasting individuals (resistant and susceptible clones) (Fig. 1), in the field for each family were selected. DNA was extracted from the different individuals and each group with the parental was mixed in a bulk.

RESULTS

The resistant and susceptible bulks were evaluated using AFLPs markers. Sixty-four different combinations from the AFLPs Gibco Kit were evaluated, and 15 combinations were found to be highly polymorphic. Among these, 22 polymorphic bands were obtained, i. e. they were only found in the resistant bulk. When the bulk was opened, the bands segregated in all the resistant clones (Fig. 2 and 3). Every combination was then evaluated in the progeny. These data are being analyzed with the data from the glasshouse and the field in order to identify possible linkage between the gene (s) of resistance and the markers (Fig 4)

The resistant parental Ecu-72 and CG489-34 and susceptible parental MCol 2026 and MCol 2246 were also evaluated with 186 cassava SSR markers (Mba et al, In preparation). Approximately 90 SSRs were found to be polymorphic (Fig. 4). These SSR's are being evaluated on the F1 population (Fig. 5)



Fig. 1. Cassava leaves infected with second whitefly instar nymphs. A) Susceptible genotype var. Mcol 2026; B) Resistant genotype CG 489-34.

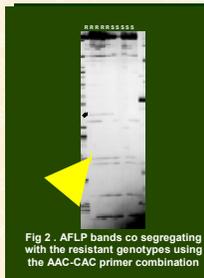


Fig 2. AFLP bands co segregating with the resistant genotypes using the AAC-CAC primer combination



Fig 3. AFLP bands co segregating with the resistant genotypes using the AAC-CTA primer combination

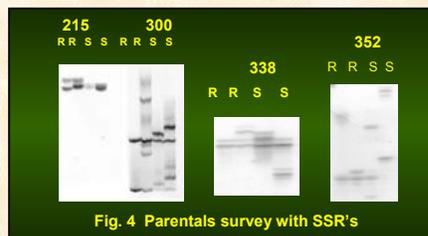


Fig. 4 Parentals survey with SSR's

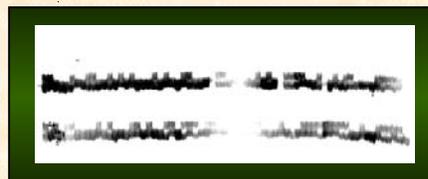


Fig. 5 SSR survey on the 215 F1 genotypes of the mapping population

CONCLUSIONS AND ONGOING WORK

- Using AFLPs, we found bands co segregating with resistance to white fly. These bands are being sequenced to generate SCARs markers. The new SCARs markers will be used for the identification of resistant materials in breeding programs.
- A linkage map for resistance to white fly is being constructed using the AFLPs and SSRs markers.
- Development of a second mapping population using Ecu-72 as the resistant parent and MCol 2246 as the susceptible parent. MCol 2246 has good attributes as tolerance to other pests like mites and thrips, but is very susceptible to white fly.

REFERENCES

- Arias B. 1995. Estudio sobre el comportamiento de la "Mosca Blanca" *Aleurotrachelus socialis* Bondar (homoptera: Aleyrodidae) en diferentes genotipos de Yuca, *Manihot esculenta* Crant'z. Tesis.
- Brown, J. K., D. R. Frolich, and R. C. Rosell. 1995. The sweetpotato or silverleaf whiteflies: biotypes of *Bemisia tabaci* or a species complex. Annu. Rev. Entomol. 40: 511-534.
- Butler, G. D., Jr. and T. J. Henneberry. 1994. *Bemisia* and *Trialleurodes* (Hemiptera: aleyrodidae), pp.325-352. In G.A. Matthews and J. P. Turnstall, Insect pests of cotton. CAB, Wallingford, U.K.
- CIAT, 1995. Cassava program annual report. 54p.
- Fregene, MA.; Angel, F.; Gomez, R.; Rodriguez, F.; Bonierbale, M.; Chavarriaga, P.; Roca, W. and Tohme, J. (1997). A Molecular Genetic Map of Cassava. Theor. Appl. Gen. 95:431-441

ACKNOWLEDGMENTS

We wish to thank Dr. Gail M Timmerman-Vaughan (Crop & Food Research Institute, New Zealand), Dr. Pamela Anderson (CIAT) for valuable discussions related to the project, and Fernando Calle for his valuable contribution in the establishment of plants in the field.

This work is supported by funds from the New Zealand Ministry of Foreign Affairs and Trade (MFAT).