

Phenotyping cassava (*Manihot esculenta*) resistance to whitefly (*Aleurotrachelus socialis*)

Bohorquez A., Tohme J., Parsa S. and L.A. Becerra López-Lavalle

CIAT, Agrobiodiversity and Biotechnology Project, AA6713, Cali, Colombia

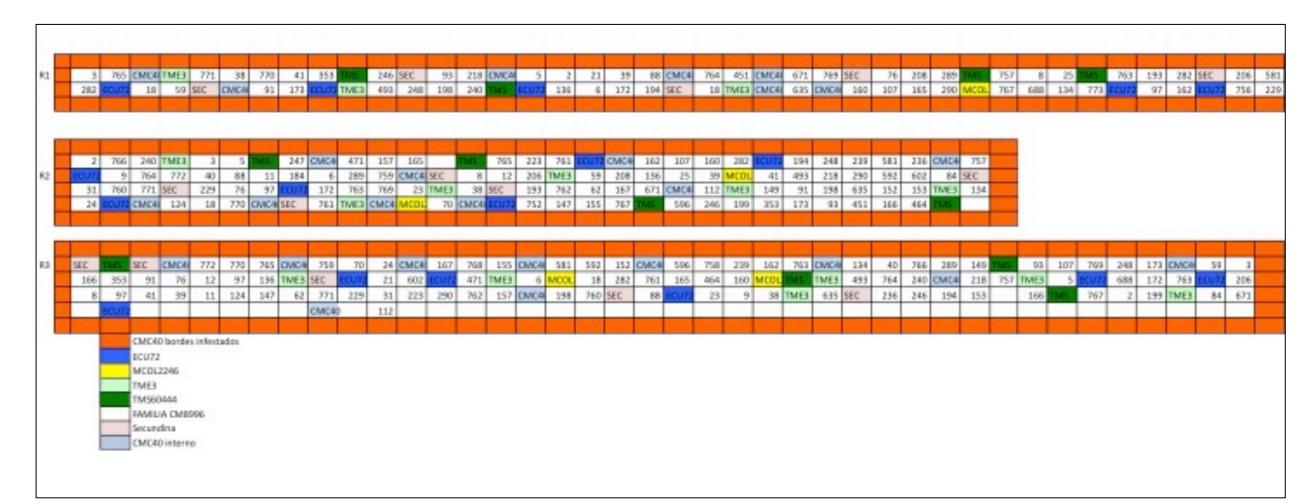


Introduction

Whiteflies as direct feeding pests constitute a major problem in cassava production in Central and South America and the Caribbean Region. There is a large complex in the neotropics, where 11 species are reported. The major species causing yield losses in the northern region of South America (Colombia, Venezuela and Ecuador) is *Aleurotrachelus socialis*. Generally, sources of natural resistance to whitefly attack are very rare or inexistent; however in the genus *Manihot*, wild (*M. flabellifolia*) and cultivated (*M. esculenta* MEcu72 and MPer415) cassava display resistance to *A. socialis*, both in greenhouse and field trials (Bellotti & Arias, 2001). On whitefly resistant cassava, *A. socialis* deposit fewer eggs, establish fewer feeding sites, and experience delayed nymph development increasing overall mortality. The progress in transferring resistant widely to other cultivars is being hindered by the lack of a rapid reliable biological assay. A rapid and reliable greenhouse-based assay is needed to advance the understanding of the plant's responses to the whitefly attack and its resistance mechanisms. Such whitefly resistant assay must eliminate the chance of escapes and ensure an accurate expression of host plant resistance. It must give consistent and reproducible pest attack reaction that correspond with known resistance levels among cassava cultivars and be highly correlated with field observations under natural infestation.

Methodology

CIAT cassava Genetics Laboratory multiplied in vitro forty-day-old plants corresponding to CM8996 progeny (105 genotypes) of MEcu72 \bigcirc (Resistant) x MCol2246 \bigcirc (Susceptible), the susceptible check CMC40 and others important genotypes (TME3, Secundina). Those plants utilized in greenhouse experiments were grown in plastic bags with 1.0 kg of sterilized soil and were maintained at 30±5°C and RH of 60±10% (Fig. 2A, B). *A. socialis* adults were obtained from the CIAT's entomology group (Fig. 2C). To determine whitefly resistance levels against *A. socialis* attack in the CM8996 segregating population, we use the randomized complete blocked experimental design (Fig. 1). In this design we use CMC40 infested plants as borders. Three plants of each genotype (CM8996 progeny) and five plants of each checks were placed on tables of 2 mt. x 10 mt. covered with mesh. Each table corresponds to a replica or block. The first and second leaves open were screened in each plant taking pictures, to count the total number of nymphs and the number of emerged nymphs (the adult) (Fig. 3). The parameters used to measure antibiosis were: duration of the life cycle of *A. socialis* for each genotype compared regarding to checks susceptible and resistant. To measure antixenosis, data were taken total population of nymphs and oviposition in each genotype.



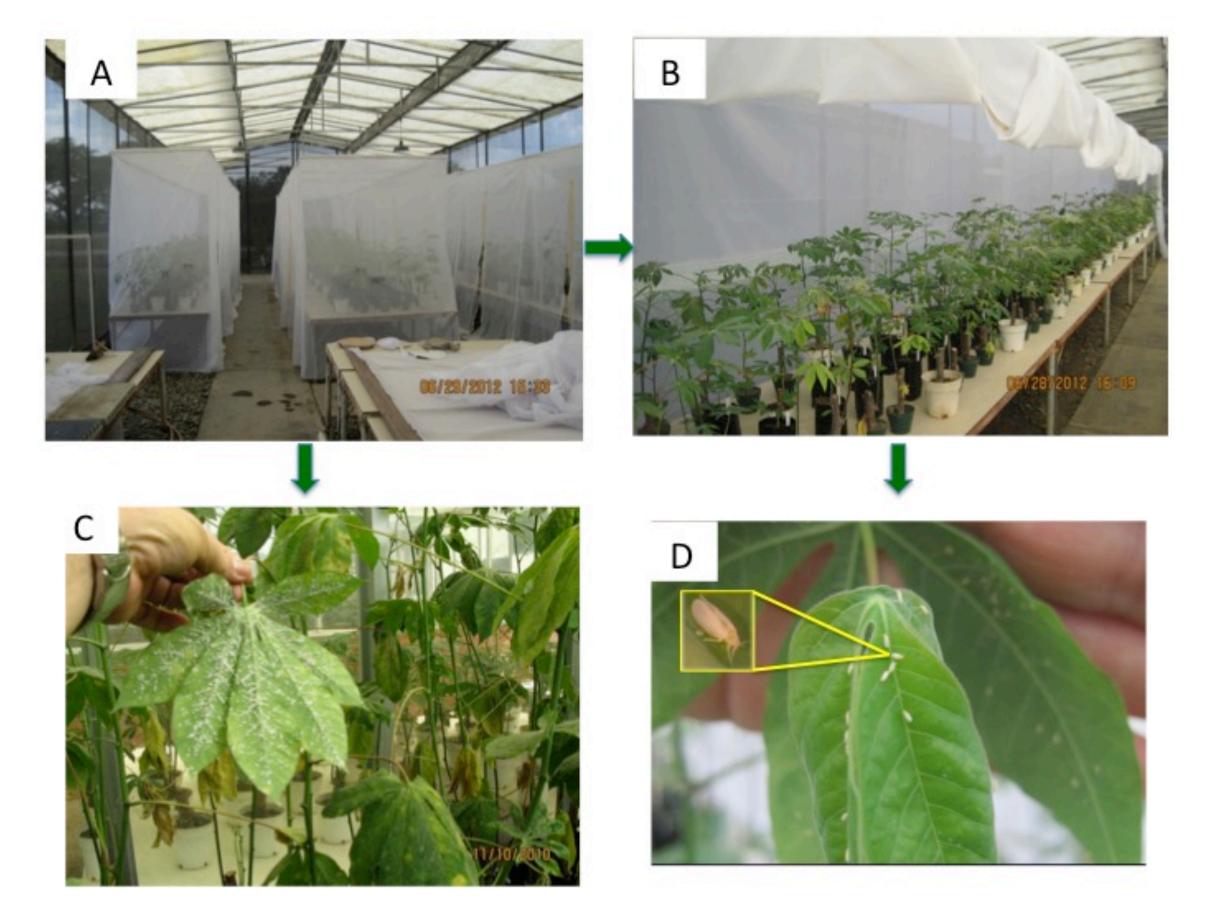
Research

Program on

Roots, Tubers

and Bananas

Fig. 1. Experimental design used in the white fly resistance phenotypification.

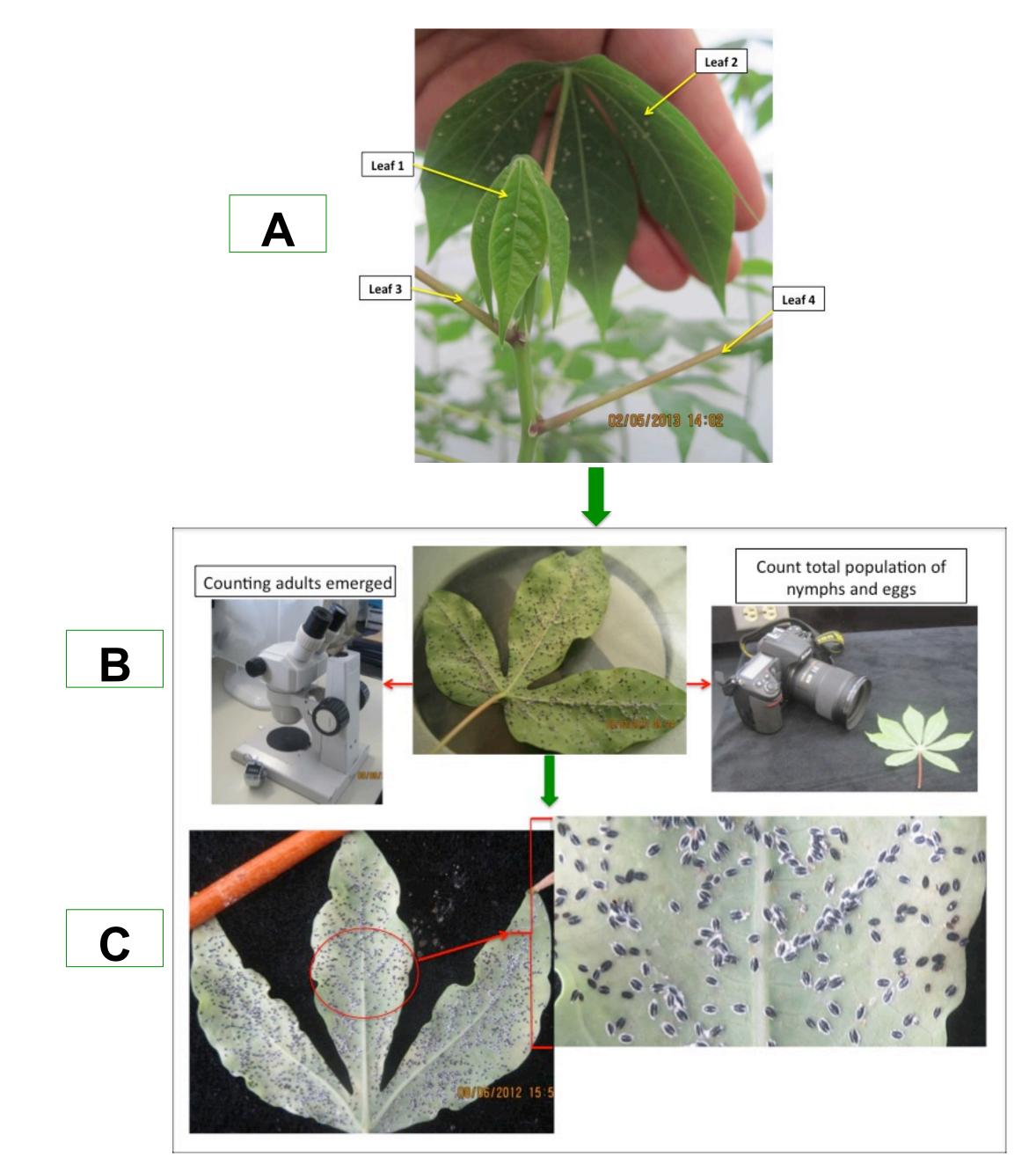


Results and Discussion

The ANOVA showed significant differences (<0.0001) in all genotypes evaluated for insect preference towards the leaf 1 (Data not shown). Likewise, the ANOVA showed significant differences between genotypes in terms of the traits evaluated: percentage of adult emergence and total population of nymphs on leaves 1 and 2. Subsequently performed comparison test of means of Dunnet which allowed all genotypes compare against each check. These results were plotted on a scatter graph (Fig. 4). Our results show that the proposed experimental design, we can to obtain a rapid and reliable greenhouse-based assay. The analysis clearly separated resistant genotypes from the susceptible type when compared against the two parental checks ECU72 (Resistant) and MCOL2246 and the susceptible standard CMC40.

% Emergency (Adults)

Fig. 2. A Cages used in the experimental design in the Greenhouse. **B** Details of the arrangement of the plants within the cages. **C** CMC40 plants infested with *A. socialis*, used as inoculum to infest genotypes experiment. **D** Plants infested with adults of *A. socialis* within experimental cages.



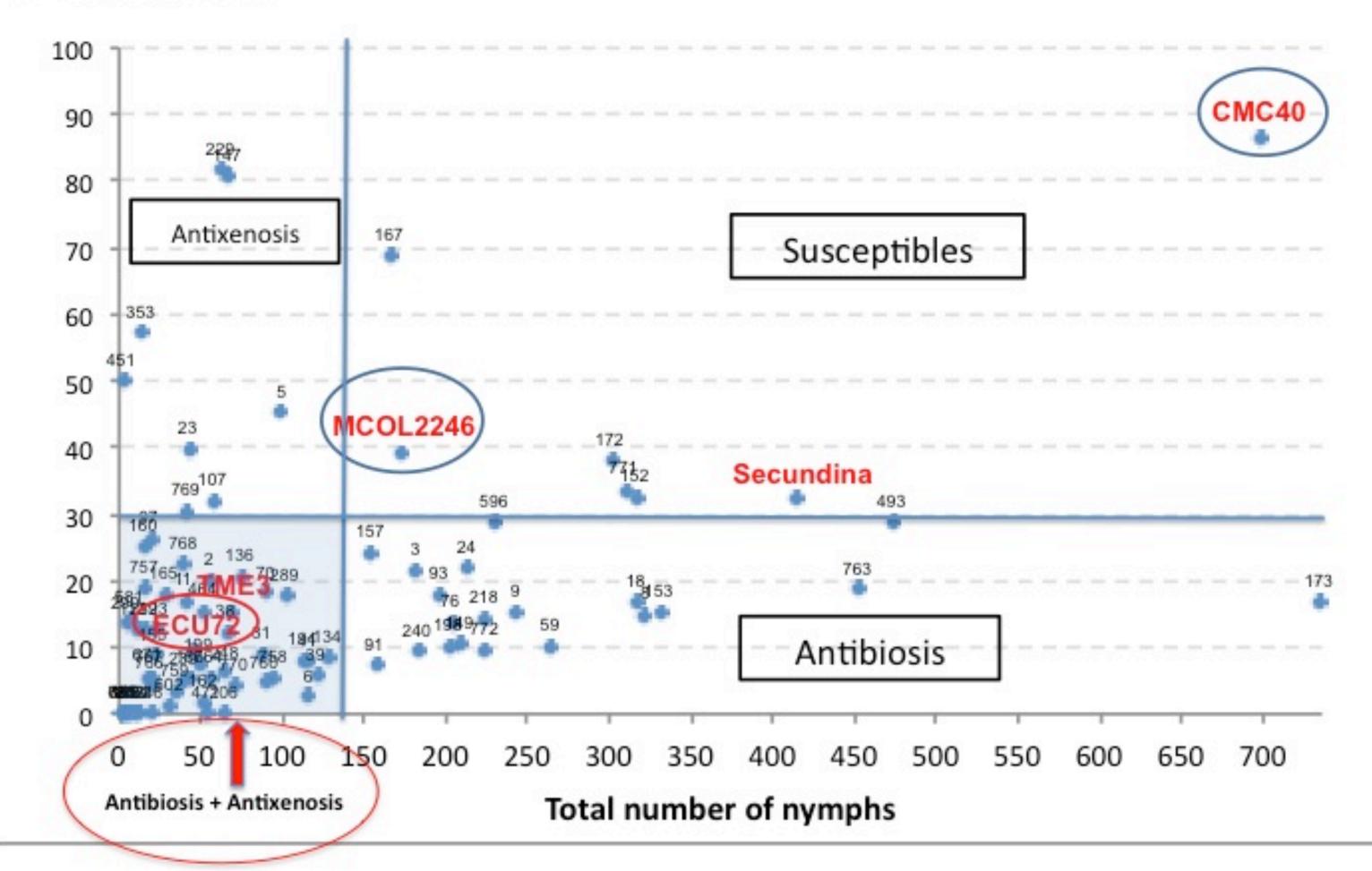


Fig. 4 Graphic showing the location of the genotypes evaluated considering parameters: X axis averages the total number of nymphs and the Y-axis percentage of adult emergence of *A. socialis*. (Dunnet p<0.0001). The genotypes considered with antibiosis, are those with adult emergence rates significantly low compared to the susceptible check CMC40. On day 35 post-infestation more than 80% of the nymphs had emerged in CMC40, on the same day, were considered resistant genotypes emergency percentages less than 20%, which means a lengthening of the cycle of life and/or death nymphs. Likewise, antixenosis genotypes were those with low populations of nymphs and therefore low rates of oviposition. The best genotypes were similar to the check and parental ECU72, which presents a combination of two mechanisms of resistance: antixenosis and antibiosis (Bellotti & Arias, 2001).

Fig. 3. Data collection methodology for measuring resistance to cassava whitefly. **A** At the time of infestation with whitefly adults are selected leaves 1 and 2 open after of shoot tip, which are preferred by adults to oviposition and feeding. **B**, **C** The leaves 1 and 2 pictures were taken from each genotype after 34 days post-infestation. These photos were used to count the total nymphs. At the same time were counted in the stereoscope the emerged nymphs.

Conclusions

The first high-throughput screening method is available to assess whitefly resistance levels in cassava germplasm, as well as, a accurate system to study the mechanism of this resistance to whitefly in the genus *Manihot*.

Future perspective

The availability of this fast accurate methods to measure the levels of whitefly attack in cassava will allow us to design accurate assays to investigate and elucidate at the genomic and metabolomic level the mechanism of resistance to whitefly attack.

References

Bellotti AC, & Arias B. 2001. Host plant resistance to whiteflies with emphasis on cassava as a case study. *Crop Protection* 20:813-823