INTRODUCTION

Wild Manihot species are a wealth of useful genes for the cultivated species Manihot esculenta Crantz, but their use in regular breeding programs is restricted by the long reproductive breeding cycle of cassava and linkage drag associated with the use of wild relatives in crop improvement. Wild relatives of cassava are important sources of genes for resistance to pests and diseases and longer shelf life. The only source of dramatically delayed PPD has been identified in an interspecific hybrid between cassava and Manihot walkerae (CIAT 2003). A unique source of resistance to the cassava hornworm was also identified in 4th backcross derivatives of M. glaziovii (Chavarriaga et al 2004). This work reports preliminary results of a study directed to identify useful genes for pest and disease resistance in wild species of Manihot and to develop low cost marker tools for their rapid introgression into cassava.

In a first phase of the project, evaluations of two Brazilian wild species (M. flabellifolia y M. peruviana) (Mueller) and commercial genotypes of M. esculenta were conducted in a screen house to identify levels of resistance to the mite, Mononychellus tanaajoa, the mealybug, Phenacoccus herreni and, the whitefly Aleurothoracillus species biotors (Fig. 1). In addition studies were conducted to develop a quick method to detect whitefly resistance, based on the number of eggs oviposited per female on a specific genotype. This will be a useful tool to evaluate resistance/susceptibility in a great number of progenies from interspecific crosses between wild Manihot species and M. esculenta genotypes.

MATERIALS AND METHODS

A. Screening for Natural Resistance:

Plants of the genotypes CMC-40, MEcu-72 from M. esculenta; MFLA 444-002 from M. flabellifolia and MPER 417-003, MPER 417-005 from M. peruviana, were propagated. Four, 40 day old plants of each genotype, were placed individually in a fine nylon mesh screened cage. Infestations of M. tanaajoa, P. herreni and A. socialis, obtained from greenhouse/screenhouse colonies were introduced on individual plants on the following manner:

1. Upper leaves of the five genotypes were infested with 200 M. tanaajoa mites.
2. P. herreni ovisacs were placed in the axil of upper plant leaves. First damage/population evaluation were made ten days after infestation and continued every ten days for eight weeks.
3. The five genotypes were infested with 200 recently emerged (12h) A. socialis adults. Evaluations were initiated after five days and continued every ten days, for eight weeks.
4. Population and damage scales were employed for evaluating each of the pest species. These scales are based on a 1 to 6 rating where 1 indicate no pest population and no plant damage; while 6 indicate very high pest population (i.e. for whiteflies 6=> 4,000 nymphs and pupae per leaf) and severe damage.

B. Rapid Selection Method for A. socialis:

Ten plants of progenies from the interspecific cross of M. esculenta x M. flabellifolia, CW235-72, CW259-3, CW259-43, CW257-10, CW258-7, CW268-10 and commercial cassava variety, CMC-40 were sown in plastic pots. Five plants of each genotype, at 40 days after germination, were placed in nylon mesh cages (1mx1mx1m) for whitefly (A. socialis; obtained from CIAT reared colonies) infestation. Ovipositional preferences was determined by introducing ten pair of recently emerged A. socialis adults (reared on CMC-40) into small leaf cages (2.5 cm diameter x 2.0 cm depth) attached to the underside of upper leaves of each genotype (Fig. 2A). After five days adults were removed and the number of eggs oviposited recorded (Fig. 2B). Eggs were allowed to hatch and nymphs allowed to develop for ten days in order to estimate development to the third instar (Fig. 2C).

RESULTS

M. tanaajoa: The mite infestation on the M. flabellifolia genotype (MFLA 444-002) and the M. peruviana genotypes (MPER 417-003 and MPER 417-005) were significantly different (Tukey P< 0.005) from the M. esculenta genotypes (MECU-72 and CMC-40). Leaf damage on the three wild Manihot genotypes was significantly different from the two M. esculenta genotypes (Fig. 3).

CONCLUSIONS AND ONGOING RESEARCH

The wild species genotypes MFLA444-002, MPER 417-003 and MPER417-005 displayed immediate level of resistance to M. tanaajoa and high levels of resistance to A. socialis.

The genotypes MFLA 444-002 y MPER 417-003 showed moderate levels of resistance to P. herreni.

The ovipositional rate (No. of eggs) of A. socialis on a given genotype is a good indication of the level of resistance of determined genotype.

A project to develop low cost marker tools for accelerated marker-aided introgression of useful genes into cassava gene pools in being funded under the GCP/Generation Challenge Programme) with participation of IARCa (CIAT, Cali, Colombia) and NARS in Brazil (CNPMF/EMBRAPA, Cruz das Almas, Bahia) and in Africa in Ghana (CRI, Kumasi), Nigeria (NRARI, Umadike) and Uganda (NAARI, Namulonge).

REFERENCES
