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BACKGROUND

Cassava is a major source of carbohydrates to over 60 % of Ugandans. However, during the 1990s, production was devastated by a pandemic of severe cassava mosaic virus disease (CMD), and is being restored through use of CMD resistant varieties. Lately, it has become apparent that the large *B. tabaci* populations that was associated with the epidemic especially occur on some of the improved CMD-resistant genotypes. For instance > 40 % yield loss due to damage by *B. tabaci* was recorded on Nase 12 (Legg, Unpublished data). In mitigation, the Cassava Programme of Uganda in collaboration with NRI and IITA has initiated research to identify resistance to African *B. tabaci* amongst the local & introduced germplasm. This would provide the twin benefit of preventing physical damage and reducing frequency of virus transmission.



Fig.1. *B. tabaci* feeding damage on shoot



Fig.2. Massive nymphs on leaf

MATERIALS AND METHODS

B. tabaci adult numbers were counted on genotypes in a breeder's clonal evaluation trial and local germplasm characterization trial planted in single row plots (10 plants/row) in two replicates at Namulonge. The clones were crosses between a landrace (Tongolo=T) and a *Tropical Manihot esculenta* line (TME4) and Ugandan selection (SS4). *B. tabaci* adults were counted on top 5 open leaves on each plant after every three weeks. Three successive records from clones that were unaffected by CMD were subjected to repeated measured analysis using GENSTAT.



Fig. 3. The cassava entomologist gives Ugandan farmers hope as they lament the destruction by whitefly of Nase 12, ones of their premium cassava varieties



Tolerant clone

RESULTS AND DISCUSSION

Differential varietal reactions to *B. tabaci* was observed amongst the CMD resistant clones and the landraces (Table 1, Fig. 4). The results indicated apparent existence of resistance sources. Clones TSS4-2 and SS4T-29 and the landraces Nabwire 1, Mutesa, Mercury and Magana had least numbers of whiteflies. Their apparent resistance will be confirmed in additional experiments alongside other genotypes that have emerged as promising (data not presented) from over 450 CMD improved genotypes screened in Uganda at two different agro-ecologies.

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Table 1. Mean no. of adult *B. tabaci* (\pm SE) on 125-day old CMD resistant cassava clones at Namulonge, Uganda, 2003

clones	Mean Adult no./ top 5 open leaves
TTME4-97	97.4 \pm 13.9 a
TME4T-79	96.3 \pm 8.2 a
SS4T-42	85.4 \pm 10.2 ab
Nase 10	84.9 \pm 7.4 ab
TSS4-20	72.0 \pm 13.8 bc
TTME4-86	68.9 \pm 6.9 bc
SS4T-50	68.6 \pm 13.3 bc
TSS4-10	56.2 \pm 8.9 c
TSS4-41	54.2 \pm 11.0 c
SS4T-5	54.2 \pm 4.7c
TSS4-7	47.7 \pm 7.4 cd
TSS4-1	47.0 \pm 3.9 cd
TSS4-2	29.7 \pm 4.2 d
SS4T-29	28.3 \pm 2.2 d

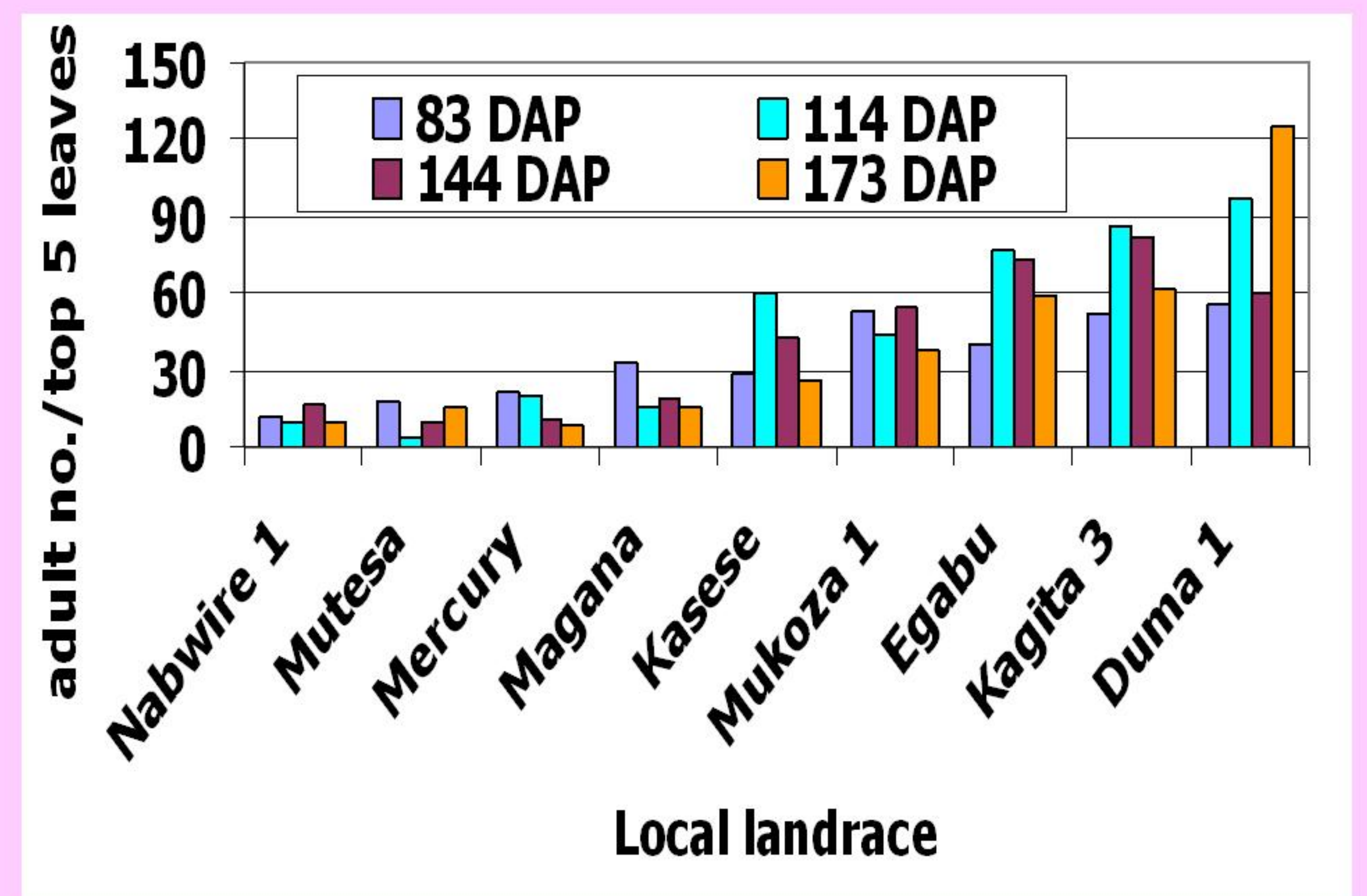


Fig.4. Mean *B. tabaci* adult no. on landraces grown at Namulonge, Uganda, 2002.

CONCLUSION AND FUTURE PERSPECTIVES

The study has revealed the potential of resistance to African *B. tabaci* in landraces and improved cassava genotypes. The rich cassava genetic diversity in Uganda will be exploited further to identify genotypes with high level of resistance. Identification of genes responsible for the resistance would be fundamental in the management of *B. tabaci* on cassava.