

## Final Technical Report

### Tropical Whitefly IPM Project – Sub-Project 5 – “Sustainable management of whiteflies as vectors of viruses of cassava and sweetpotato in sub-Saharan Africa”

#### Background

##### *The Project Context*

During the first phase of the Tropical Whitefly IPM Project, which ran from 1997 to 1999, extensive diagnostic surveys of viruses of cassava and sweetpotato and their whitefly vectors were conducted in nine countries in sub-Saharan Africa. These included: Ghana, Benin, Nigeria, Cameroon, Uganda, Kenya, Tanzania, Malawi and Madagascar. The most important whitefly vectored virus disease problems, cassava mosaic disease (CMD) and sweetpotato virus disease (SPVD), were found throughout their respective survey areas (sweetpotato surveying was restricted to East and Southern Africa), but the ‘hotspot’ common to both was the Lake Victoria Basin area of southern Uganda and north-western Tanzania. This region was therefore targeted for the more detailed research studies of the second phase of the project. A key aspect of this work was complementation with allied Crop Protection Programme (CPP) supported promotional projects, targeting CMD and SPVD management in broadly the same geographical area. Through this complementation, it was anticipated that the prospects for impact would be greatly enhanced.

##### *The Crops and their Virus Diseases*

Cassava and sweetpotato are major sources of food and income for families in East Africa. CMD is caused by cassava mosaic geminiviruses (CMGs) (Family *Geminiviridae*: Genus *Begomovirus*), which are transmitted either by the feeding activity of the whitefly vector, *Bemisia tabaci*, or through planting infected cuttings. CMD was first reported from Africa more than a century ago (Warburg, 1894). Whilst it subsequently spread to affect cassava throughout the continent, the impact on yield has typically been moderate to mild. During the 1990s, however, an epidemic of unusually severe CMD, initially reported from Uganda, spread throughout the country (Otim-Nape et al. 1997) and subsequently into neighbouring Kenya, Tanzania, Sudan and the Democratic Republic of Congo (Legg 1999), and Rwanda (Legg et al. 2001). Spread of this severe form of CMD led to the virtual abandonment of cassava cultivation in many areas, had a major impact on food security in the region, and caused financial losses estimated at in excess of US\$60 million per year (Otim-Nape et al. 1997). The epidemic affected the lives of millions of people in Uganda, and had a similar impact in north-western Tanzania. Although the situation stabilized in Uganda after the late 1990s, the epidemic has continued to spread through north-western Tanzania.

Sweetpotato is a key food security crop in the Great Lakes zone of East and Central Africa, and Uganda is Africa's number one producer. The crop is grown mainly by women to provide daily food for their families, with any surplus sold to provide cash for other requirements. Sweet potato virus disease (SPVD), caused by co-infection of sweetpotato by the aphid-borne *Sweetpotato feathery mottle virus* (SPFMV) (Family *Potyviridae*: Genus *Potyvirus*) and the whitefly-borne *Sweetpotato chlorotic stunt virus* (SPCSV) (Family *Closteroviridae*: Genus *Crinivirus*), is one of the major constraints to production in East Africa, and it is particularly severe in the Project's target zones of north-western Tanzania and southern Uganda. Farmers perceive SPVD to have increased in prevalence in the last few years, perhaps as a result of increased sweetpotato production to replace cassava production lost to CMD.

#### *Management initiatives*

In East Africa, the CMD problem has been addressed in part through the introduction of varieties known to be resistant to CMGs from IITA-Ibadan, in Nigeria, West Africa. These were evaluated under Ugandan conditions, and those exhibiting the greatest CMD resistance were identified for mass multiplication and distribution. By the late 1990s these varieties were beginning to have an impact at farm level, and it is currently estimated that more than one quarter of all cassava cultivated in Uganda (> 100,000 ha) is under improved CMD-resistant varieties. Recent work financed by USAID's Office for Foreign Disaster Assistance has built on these successes and introduced resistant germplasm to the neighboring countries of Kenya and Tanzania. In the current project, it was proposed to strengthen the management of CMD through developing alternative CMD/CMG vector control strategies that complement the resistant variety-based approach already in place. Alternative strategies considered included: whitefly resistance, augmented biological control, crop management practices and phytosanitation.

The identification of SPVD-resistant varieties of sweetpotato, which give superior yields in severely SPVD-affected areas and their subsequent dissemination offers promise for the rapid control of SPVD. SPVD devastated sweetpotato crops in central Mpigi District (Uganda) in the 1960s but is now a minor problem there due to the natural appearance and spread of the resistant variety, New Kawogo (Aritua et al. 1998). By contrast, there were no similar locally-occurring, high yielding SPVD-resistant varieties in the southern Uganda target zone of this Project. However, the CPP-funded, NRI executed SPVD control projects, R7492/R8243, have had considerable success in identifying and beginning to popularize SPVD resistant varieties in southern Uganda, and the proposed second phase of the Tropical Whitefly IPM Project set out to build on these successes in strengthening SPVD management. Key targets were the enhancement of biological control and the determination of guidelines for the effective use of phytosanitation. An additional objective was the development of a combined approach to the management of whitefly-transmitted virus diseases for these two crops, and through collaboration with allied project, the development and dissemination of training materials.

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## Outputs

- B. Hotspots characterized
- C. Principles of pest and disease dynamics understood
- D. IPM component research validated and IPM packages promoted
- E. Training materials developed

## Activities

### B1. African hot spots characterized

*Molecular characterization and dynamics of cassava mosaic geminiviruses in Tanzania – Mr. J. Ndunguru, LZARDI, Tanzania and Dr. C. Fauquet, ILTAB, USA*

#### **Introduction**

Virus infection constitutes the most formidable threat to cassava production and can be observed wherever cassava is grown in Africa. Cassava mosaic virus disease (CMD), caused by CMGs, is the most important disease of cassava in Africa. Prior to 1997, only two CMGs were recognized: *African cassava mosaic virus* (ACMV) and *East African cassava mosaic virus* (EACMV) (Hong *et al.*, 1993). A total of 8 distinct CMG species have now been identified. Recently, however, a geminivirus variant, which appears to be a recombinant hybrid of EACMV and ACMV, was detected in Uganda (EACMV-UG; Deng *et al.*, 1997; Zhou *et al.*, 1997) and is associated with the severe CMD pandemic currently causing serious damage to cassava in Uganda, Kenya, Tanzania, Sudan, D.R. Congo and Rwanda (Legg, 1999). Appropriate CMD control measures can only be developed on the basis of a sound understanding of the identity and characteristics of the causal viruses, and the interactions between them. This project therefore was aimed at defining the genetic diversity, distribution and identity of CMGs occurring in Tanzania and determining their molecular characteristics and effects of their interactions on disease.

#### **PhD course work**

Course work was undertaken at the Department of Microbiology and Plant Pathology, at the University of Pretoria, Pretoria, South Africa from January to June 2002. Courses taken during the training included Plant Molecular Genetics, Advanced Microbiology and Biostatistics. All the course exams were successfully completed and passed.

#### **Collection and identification of geminiviruses infecting cassava in Tanzania**

This work involved collection of cassava mosaic diseased samples from the major cassava growing areas in Tanzania and to identify the viruses using PCR and RFLP. Information generated was used to map the geminivirus distribution in the country. RFLP analysis of the CMGs revealed more molecular variability in *East African cassava mosaic virus* (EACMV) genomes than in *African cassava mosaic virus* (ACMV) and N-terminal partial sequence comparison of the replication associated gene (AC1) strongly reinforced this observation. In addition to the previously characterized EACMV- [Tanzania] (EACMV- [TZ]), eleven EACMV-like virus types, designated here as EACMV- [TZ1] to- [TZ11] were identified following restriction analysis of PCR products using *EcoRV* and *MluI* endonucleases. These viruses were associated with distinct symptoms on different cassava cultivars, and had a non-overlapping and overlapping geographical distribution with most of them occurring in the coastal regions of the country. Of these, EACMV- [TZ1] was the most widespread followed by EACMV- [TZ2]. EACMV- [TZ4], EACMV- [TZ5] and EACMV- [TZ8] were the most virulent types and were associated with severe to very severe mosaic symptoms in

cassava in the field. Two previously undescribed CMGs were detected in the Mara Region of the Lake Victoria zone. There were provisionally designated *East African cassava mosaic Tanzania-Mara* {EACMV-[TZ-Mara]} and an ACMV-like isolate, ACMV- [Tanzania] (ACMV- [TZ]). The EACMV-UG2 associated with the pandemic of severe cassava mosaic disease (CMD) has expanded its range into Tanzania covering most of the Lake Victoria region. Co-infection frequently involved ACMV and EACMV-UG2 mainly at the front of the CMD pandemic and plants displayed more severe symptoms than those infected by either of the two viruses alone. ACMV was not found in any of the coastal regions or in the south of the country. A scientific paper reporting this work is awaiting resubmission to the *Annals of Applied Biology* journal.

### **Sequence analysis of DNA particles ‘A’ and ‘B’ of CMG collections**

CMD-infected cassava cuttings collected from Tanzania were planted in growth chambers at the Donald Danforth Plant Science Center to reproduce the field symptoms. These materials together with field samples were used as a source of viral DNA for cloning and sequencing of CMGs. A total of 15 virus isolates were cloned and their DNA sequenced. Partial and full-length DNA A and DNA B sequences are available and a scientific paper is being prepared to publish these results. Some strains of EACMV occurring in West Africa were found to be present in Tanzania

### **Determination of molecular factors in ACMV and EACMV involved in symptom severity**

In addition to the CMGs, two novel single-stranded DNA satellite molecules have been discovered for the first time associated with CMD in cassava from Tanzania. These DNA molecules, though different from the CMGs, have the capacity to enhance symptoms and even break resistance in highly CMD resistant cassava landraces. A scientific paper to publish this work is to be submitted to *Science*.

Critical analysis of the CMGs from Tanzania has revealed the presence of a truncated DNA A component of EACMV in some CMD-diseased plants. This defective genome is replicated by the helper virus (EACMV) and has the capacity to modulate disease symptoms. Again this finding will be reported in a scientific paper that is under preparation

Based on the geminivirus sequences, different primers have been designed to help in the PCR detection of different CMG strains that are found in Tanzania. This will aid subsequent CMD/CMG monitoring work, allow the development of an improved distribution map of the complex mix of CMGs in Tanzania and help control practitioners to determine priority regions for intervention in CMD management programmes. Improved understanding of the nature and interaction mechanisms of the CMGs will also help breeders in their efforts to identify, incorporate and deploy new sources of resistance and to manage existing resistance-based control approaches.

### **Construction of infectious clones for infectivity assay and virus interaction studies**

Infectious clones have been constructed for selected virus isolates. Interactions between different virus species have been studied in a model plant *Nicotiana benthamiana* as well

as in cassava in the greenhouse using biolistic gun inoculation. Southern blot analysis of virus replication revealed different levels of virus replication depending on types of virus combination. Interestingly the EACMV-UG2 associated with the severe CMD pandemic interacts with the novel satellite DNA molecules resulting in enhanced symptoms compared to when present in a single infection. This has important implications for existing CMD management efforts and further studies are required firstly to confirm if this phenomenon is more widely occurring, and secondly to determine what the implications are likely to be for resistant germplasm that currently comprises the primary component being used in CMD management programmes.

### **Additional achievements**

1. To simplify the sampling, storage and characterization of CMG DNAs, the efficacy of the FTA card technology (developed by Whatman) has been investigated and a protocol established that enables rapid sample collection and simple DNA retrieval for CMG detection and characterization. Viral DNA eluted from FTA cards has been found to be suitable for all the downstream analyses such as PCR, cloning and sequencing, and species or strain differentiation. A poster on this work was presented at the Sixth International Scientific Meeting of the Cassava Biotechnology Network (CBN), CIAT, Cali, Colombia, in March 2004.
2. A tool is being developed to differentiate between mild and severe isolates of EACMV-UG2/ACMV commonly found infecting cassava in Tanzania.

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*Molecular variability of Bemisia tabaci and its effects on the epidemiology of cassava mosaic geminiviruses in Uganda – Mr. P. Sseruwagi, IITA-ESARC, Uganda and Prof. J. Brown, University of Arizona, USA*

## **Background**

*Bemisia tabaci* (Gennadius)(Hemiptera: Aleyrodidae) is the key vector (Fishpool *et al.*, 1994) of cassava mosaic geminiviruses (CMGs), which are the causative agents of cassava mosaic disease (CMD) (Geddes, 1990): the most important production constraint to cassava in the Africa. Over the past decade, severe outbreaks of *B. tabaci* in many parts of sub-Saharan Africa have become more frequent and crops colonised by *B. tabaci* have suffered major losses with yield reductions ranging from 20% to 100% due to a pandemic of severe CMD (Thresh *et al.*, 1994). In order to ensure the sustainable control of CMD and the future development and expansion of cassava production in Africa, the molecular variability of cassava *B. tabaci* and its effects on the epidemiology of cassava mosaic geminiviruses (CMGs) in the pandemic affected zones of East and Central Africa would have to be established. Raised populations of *B. tabaci* continue to be reported in areas recently affected by the CMD pandemic, and a definitive answer is needed on the existence or otherwise of a ‘pandemic biotype’. This will facilitate biotype ‘tracking’ and will aid in forecasting patterns of spread of the CMD pandemic and support on-going efforts to control the CMD pandemic in the affected zones. The work reported here is part of the Tropical Whitefly IPM Project of the System-wide Programme for Integrated Pest Management (SP-IPM) and aimed to:

- 1) Identify the CMGs occurring in the ‘post-epidemic’ situation in Uganda
- 2) Establish the molecular variability of the principal *B. tabaci* genotypes on cassava through comparison of sequences of portions of the mitochondrial DNA cytochrome oxidase I (*mtCOI*) gene.
- 3) Describe the geographical distribution of the mtCOI-based ‘local’ and ‘invader’ *B. tabaci* haplotypes in the ‘post-epidemic’ situation in Uganda and the relationship between their distribution and that of the CMGs affecting cassava in the country.
- 4) Gather information on mating and fecundity characteristics of the *B. tabaci* haplotypes associated with the CMD epidemic in Uganda
- 5) Determine the degree of ‘cassava restriction’ of cassava *B. tabaci* haplotypes and the colonization of alternative crop and weed hosts.

## **Training in background courses in molecular biology/biotechnology**

As part of a PhD training programme, background courses in molecular biology were undertaken at the School of Molecular and Cell Biology, the University of the Witwatersrand, Johannesburg, South Africa between February and June 2002 under the supervision of Prof. M.E.C Rey. Key biotechnology themes including: eukaryotic tissue culture, plant biotechnology and tissue culture, fermentation and bioprocessing, gene manipulation, heterologous expression of proteins and proteomics, pharmaceuticals/drugs design and genomics/bioinformatics comprised the five months coursework component leading to a Postgraduate Diploma in Science - Biotechnology. Also, part of the coursework component included relevant topics in biosafety, commercialization, public

awareness, intellectual property and biotechnology, business ventures and trade and research and technology transfer. The coursework component was divided into three facets: formal coursework, external visits to biotechnology-related enterprises and a “hands-on” techniques course. On completion of the course, the award of Postgraduate Diploma in Science – Biotechnology of the University of Witwatersrand, Johannesburg, South Africa was conferred on 8<sup>th</sup> April 2003.

### **Establishment of the genetic variability and distribution of cassava mosaic geminiviruses in the ‘post-epidemic’ Uganda**

The molecular variability of CMGs in the ‘post-epidemic’ Uganda was investigated and the results reported in a scientific paper (Sseruwagi *et al.*, 2004a) now in press in the *Annals of Applied Biology* journal. The molecular characterization of the CMGs was conducted in the Department of Plant Science, University of Arizona, Tucson, Arizona, USA, under the supervision of Prof. J.K. Brown between Oct. 2002 and June 2003. The study established the occurrence of two previously reported CMGs: *African cassava mosaic virus* (ACMV) and *East African cassava mosaic virus-Uganda variant* (EACMV-UG2) in the ‘post-epidemic’ Uganda. EACMV-UG2 was the predominant virus and occurred in all the surveyed regions. It was detected in 73% of the severely and 53% of the mildly diseased plants, while ACMV was less widespread and occurred most frequently in the mildly (27%) diseased plants. Mixed infections of ACMV and EACMV-UG2 were detected in only 18% of the field samples. Unlike previously reported results, however the mixed infections occurred almost equally in both the mildly (21%) and severely (16%) diseased plants indicating a lack of the synergism associated with dual infections in previous studies. The widespread occurrence and distribution of EACMV-UG2, the strain associated with the epidemic of severe CMD in Uganda confirmed that the current situation in the country is one of a ‘post-epidemic’ nature. It was concluded that EACMV-UG2 is still a major production constraint to cassava production in Uganda.

### **Establishment of *B. tabaci* variability and distribution in the ‘post-epidemic’ Uganda**

The genetic variability and geographical distribution of *B. tabaci* haplotypes in the ‘post-epidemic’ Uganda were established. The results have been written up in a scientific paper (Sseruwagi *et al.*, 2004b), which has been submitted to the journal, *Molecular Ecology*. This work was conducted concurrently with the virus work in the Department of Plant Science, the University of Arizona, Tucson, Arizona, USA in Prof. J.K. Brown’s laboratory. In summary, the study used the mitochondrial cytochrome oxidase I (mtCOI) molecular marker to investigate the genetic variability of the cassava *B. tabaci* populations associated with the CMD epidemic in Uganda in 2002. The occurrence of two previously described haplotypes: a ‘local’ and ‘invader’ (Legg *et al.*, 2002) in the ‘post-epidemic’ Uganda was confirmed. Comparison of the pairwise nucleotide identity of the partial sequences of mitochondrial cytochrome oxidase I (mtCOI) DNA revealed that the two populations were ~ 8% divergent and shared very close sequence similarity (98 - 99.9%) with their closest relatives. The ‘local’ haplotype predominated (83%) and was more widespread than the ‘invader’ (17%). Unlike the late 1990s at the height of the spread of the epidemic of severe CMD in Uganda when a clear association was



established between the *B. tabaci* haplotypes and the CMGs, in the current ‘post-epidemic’ situation there was no clear association between the two. It was concluded that the widespread occurrence of the ‘local’ haplotype and the lack of a clear association between the *B. tabaci* haplotypes and the CMGs in the ‘post-epidemic’ Uganda is a new development whose significance in the epidemiology of the CMD pandemic still needs to be established. As part of the work recommended for future study, are the components described in activities described below.

#### **Establishment of the bionomics and mating compatibility of the *B. tabaci* haplotypes associated with the CMD epidemic in Uganda**

As a preliminary step to investigating the bionomics and mating compatibility of the *B. tabaci* haplotypes associated with the CMD epidemic in Uganda, new whitefly collections were made in September 2003 in the areas identified through the whitefly haplotype survey work. The colonies have been established at the Natural Resources Institute (NRI), UK and the work will commence as soon as the genetic identities (based on the KDR nuclear marker) of the colonies are obtained from Prof. J.K. Brown. The data will be reported in a proposed scientific paper as indicated under the output section on journal publications.

#### **Establishment of cassava restriction of cassava *B. tabaci* haplotypes and colonization of new alternative crop and weed hosts**

The occurrence of alternative hosts for cassava *B. tabaci* could be of epidemiological significance to the continued spread of the CMD pandemic in the affected region in East and Central Africa. Therefore, in order to establish the occurrence of alternative host plants for the cassava *B. tabaci* haplotypes in Uganda, adult female whiteflies and nymphs were collected from potential alternative crop and weed hosts in the field in September 2003 for mtCOI characterisation at NRI, UK.

About 90% of the work has been completed and the sequence data is being analysed. Based on the preliminary results, the *B. tabaci* populations clustered in four main clades: the B-like types, non-B-like types, Ivory Coast Okra-like types and the cassava like types. This is the first time the putative B and/or non B-like and the Ivory Coast Okra-like types have been identified in Uganda. Additional work is to be conducted in order to confirm whether the putative B and/or non-B or the Ivory Coast like types are capable of inducing silverleaf symptoms (SSL) in the squash test plants, which is diagnostic for the B and/or non B biotypes inducing silvering. All the cassava types clustered with the ‘Local’ haplotype reported in Legg *et al.* (2002). In order to confirm whether the *B. tabaci* populations that clustered with the cassava type are indeed the cassava types colonizing other plants, analysis of the field-collected nymphs from the potential alternative host plants will be conducted using the mtCOI marker. Should the results of the adult whiteflies match those obtained from the analysis of the nymphs, this will be the first time new alternative weed and crop hosts for the cassava *B. tabaci* will have been reported in the ‘post-epidemic’ Uganda. The data will be reported in the proposed scientific paper/s indicated in the output section on journal publications.

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- C1. CMD epidemics studied in African hotspots
- C2. CMD epidemics forecast

*Emergency mitigation of the CMD pandemic in East and Central Africa – Dr. J. Legg and research and extension partners in target countries*

The monitoring of the CMD pandemic and the use of monitoring data to forecast future patterns of development have been addressed through collaboration with the project, 'Cassava Mosaic Disease Pandemic Mitigation in East and Central Africa', funded by the Office for U.S. Foreign Disaster Assistance. This project, initiated in 1998 and targeting Uganda, Kenya and Tanzania at the outset, is currently in its sixth one year phase, and now incorporates emergency CMD management work in Kenya, Tanzania and Burundi, although work has also been done in the Republic of Congo, Cameroon and most recently, Rwanda. In its target areas of southern Uganda and north-western Tanzania, the Project has provided an important complement to the more research-oriented approach of the Tropical Whitefly IPM Project and the farmer field school based work of the allied CPP-funded roots and tubers projects on CMD and SPVD. A project outline and summary of the monitoring, diagnostics and epidemic forecasting work is provided below in an excerpt from a presentation given at the Project's regional stakeholders meeting held in Bukoba, Tanzania, in September 2003.

**Overview of the Project 'Cassava Mosaic Disease Pandemic Mitigation in East and Central Africa' and development of the African CMD pandemic – J. P. Legg**

A pandemic of unusually severe CMD spread through Uganda and into western Kenya and western Tanzania during the 1990s devastating cassava production. By 1999, virtually all of Uganda had been affected, Western and Nyanza provinces in western Kenya and Kagera region in Tanzania. Rwanda, Burundi and eastern Democratic Republic of Congo were threatened. Losses in Uganda, Kenya and Tanzania alone were estimated at US\$ 100 million annually and the CMD pandemic represented a major threat to regional food security.

In order to address this problem, major programmes to develop and disseminate resistant germplasm were initiated in Uganda as early as 1993, and these had considerable success, particularly in the eastern part of the country. By contrast, little was being done in the neighbouring and similarly affected countries. A proposal was therefore submitted to the US Agency for International Development's (USAID) Office for Foreign Disaster Assistance (OFDA) for a project which aimed to tackle the CMD problem in the most recently affected zones of Uganda as well as the newly-affected zones in western Kenya and Tanzania. Contacts were made through the co-ordination office of the System-wide Programme on Integrated Pest Management's (SP-IPM) Tropical Whitefly IPM Project, through USAID's Washington office, a concept note for the planned CMD project was submitted, and in mid 1998, USAID approved funding for a first project phase to run from October 1998 to September 1999. Subsequent to the successful completion of this phase, further funding was received for follow-on projects running from 1999-2000 and from 2000-2001, and in mid 2001 a fourth grant for the period October 2001 to

September 2002 was approved which also incorporated emergency CMD management activities for the Republic of Congo (ROC). Reports of increasing CMD-associated problems in Burundi in 2002 led to the incorporation of this additional country into the 2002-2003 grant, increasing the number of participating countries to five.

In this report, a brief summary is provided of the principal elements of the fifth phase of the project (2002-2003) and some results are presented illustrating the pattern of expansion of the CMD pandemic during this period.

**The five objectives of the project were as follows:**

*1. Monitoring and diagnostics*

To establish the extent of spread of the CMD pandemic, to use risk assessments to guide interventions and to use farmer-based early warning systems to facilitate rapid responses to pandemic expansion

*2. Multiplication of CMD resistant varieties*

To accelerate the multiplication and distribution to cassava producers of high yielding CMD resistant varieties thereby mitigating the effects of production loss resulting from the effects of the CMD pandemic

*3. Germplasm diversification and exchange*

To provide cassava producers with a diversity of cassava varieties combining multiple pest-disease resistance with preferred quality characteristics and to facilitate regional germplasm exchange leading to the establishment of strategic stocks of CMD resistant varieties in East, Central and Southern African countries

*4. Training and technology transfer centres*

To enhance the understanding and management practice of CMD amongst cassava producers through training, and to strengthen the process of technology transfer through the establishment of technology transfer centers

*5. Project management, monitoring and impact assessment*

To strengthen networks at local, national and regional levels for the enhanced implementation of Project activities

**Project Partners**

Partners for the project in 2002/3 were slightly changed from those of previous phases of the Project, reflecting the incorporation of activities in Burundi. In Uganda, IITA-ESARC co-ordinated the programme from Kampala, the IITA-executed East African Root Crops Research Network (EARRNET) provided germplasm development support, the Cassava Programme of the National Agricultural Research Organization (NARO) was the local co-ordinating research partner and the Community Enterprise Development Organization (CEDO) supervised much of the multiplication work at district level. CEDO worked closely with the extension service. In western Kenya, the Kenya Agricultural Research Institute (KARI) ran the programme in partnership with the Ministry of Agriculture and

Rural Development's extension service. A number of NGOs contributed to the multiplication and distribution work at the secondary and tertiary levels. In Tanzania, the co-ordinating partner was the Lake Zone Agricultural Research and Development Institute (LZARDI), from its research station bases at Ukiriguru and Maruku. Multiplication and distribution work was supported in Kagera region by the Kagera Agricultural and Environmental Management Project (KAEMP) and Norwegian People's Aid (NPA) and in Mara region by the Mara Farmers Initiative Project (MARA-FIP). CARE, World Vision and a number of other NGOs contributed to this work at secondary level. Plant quarantine services in both Kenya (Plant Quarantine Station, Muguga, Nairobi) and Tanzania (Plant Protection Department, Dar-es-Salaam) supervised open quarantine facilities at Alupe, western Kenya and Maruku, Kagera region, Tanzania, respectively, and support for the molecular characterization of epidemic-associated whitefly populations was provided by the University of Arizona. Research co-ordination in ROC was provided by the Délégation Général à la Recherche Scientifique et Technologique (DGRST), with logistical support from the office of FAO. Multiplication work was done in collaboration with FAO and partners in the Ministry of Agriculture. The programme in Burundi was led by the Institut des Sciences Agronomiques du Burundi (ISABU) which also conducted germplasm evaluation and the first station-based phase of the germplasm multiplication work.

### **CMD Pandemic Development: 2002-2003**

Monitoring and diagnostics surveys were conducted in Kenya, Tanzania, ROC and Burundi in 2003. In addition, surveys were conducted in southern and eastern Cameroon and throughout Gabon in order to assess the extent of the westwards spread of the pandemic.

In Kenya, the two trends apparent in the previous year were repeated. Severe CMD and the pandemic-associated virus, EACMV-UG, continued to spread further to the south, and the pandemic can now be considered to have covered virtually the whole of Western and Nyanza Provinces. Set against this was the continued amelioration of the situation in the part of Western Province near to the Uganda border. Although overall incidence for western Kenya remained unchanged from the previous year at about 52%, there was a significant increase recorded in the percentage of fields growing CMD-resistant varieties derived from the management programme; up to 20% from 15% the previous year.

In Tanzania, a survey was conducted in mid-2003. Results of this are reported in detail later in these proceedings. In general, very high levels of whitefly-borne infection were recorded and whitefly populations were higher overall than they have been in any of the previous surveys. Areas newly affected by the high levels of whitefly-borne infection, severe symptoms and raised whitefly populations characteristic of the pandemic front included Kasulu district, Mwanza district, parts of Magu district and Tarime district. The pandemic therefore appears to be spreading south-westwards into Kigoma region towards Lake Tanganyika, southwards into Shinyanga region (through Bukombe district), eastwards through Mwanza region, and southwards from Kenya into Mara region. Significantly, Mara, Mwanza and Kigoma regions all rely heavily on cassava as the

primary staple food (in contrast to Kagera where bananas are more important). Urgent efforts will therefore be required to address this increasingly grave situation.

A second diagnostic survey for ROC was conducted in February 2003. This survey covered the main cassava-growing regions (nine) of the country, in comparison with the four of the 2002 survey. There was little change recorded in overall incidence, with the 2003 mean value of 86% only slightly greater than that recorded in 2002 (82%). In most regions, cutting infection predominated and whitefly populations were moderate to low. One area in which it appears there is a significant increase in the importance of CMD is the Pool region, where areas previously affected only by ACMV, were newly-affected by the pandemic virus, EACMV-UG.

Ten districts were surveyed in Burundi in 2003. Three zones were distinguished (figure 1). The first, the pandemic spread zone in the north-east was characterized by high incidences of whitefly-borne CMD, predominance of EACMV-UG and high whitefly populations. EACMV-UG was present but less frequent in the second zone of districts to the south and west and incidences and severity were moderate. To the south and far west in the third zone, incidence and severity were both low and only ACMV was present. This pattern suggests that the pandemic is currently spreading through Burundi towards the south and west, threatening the rest of the country. A follow up survey in 2004 should allow the rate of spread to be assessed.

Surveys conducted in southern and eastern Cameroon and throughout Gabon revealed the sole occurrence of ACMV, together with high incidence of mild CMD in much of the area. EACMV-UG, associated with severe whitefly-borne infections was detected in eastern Gabon, however, an area that borders the Plateaux region of central ROC (Figure 2). It was therefore concluded that eastern Gabon represents the westernmost 'front' of the CMD pandemic and that the pandemic has yet to reach Cameroon. Since much of central Gabon and southern and eastern Cameroon is covered by dense primary rainforest, it is likely that further spread westwards will occur slowly. The more likely route for pandemic spread into West Africa may be through the savannas of Central African Republic and Central Cameroon.

2003 has provided a comprehensive set of data on the state of the pandemic in many of the worst affected countries. A number of gaps in knowledge have been highlighted, however. The gravity of the pandemic's spread in Burundi suggests that the situation in Rwanda may be similarly severe. The last survey conducted in Rwanda was in 2002 and indicated that at that time the pandemic was confined to the north-eastern region. Informal reports received in July 2002 suggested that parts of south-eastern Rwanda were affected, but up to date information is required. A survey is therefore planned for 2004 within the framework of the next phase of the OFDA project. Similarly, informal reports have also been received from southern Sudan about the occurrence of severe CMD, and published data have also confirmed the co-occurrence of ACMV and EACMV-UG. Insecurity has precluded the implementation of diagnostic surveys in previous years, but as this situation continues to improve, there may be opportunities to carry out a survey in 2004, and this will be another target of the next phase of the Project.

A key facet of the recent dynamics of the CMD pandemic has been the apparent spread from East to Central Africa. Based on the evidence of the occurrence of the pandemic as far west as Gabon, summarized above, there is considerable concern about the possibility of further westwards spread towards the major cassava producers of West Africa, the most significant of which is Nigeria, the world's largest cassava producer. The dense rainforests of Central Africa seem likely to offer a substantial impediment to spread from Gabon and ROC into Cameroon. A more likely route for spread would seem to be the savannas of Central African Republic (CAR). FAO has reported severe CMD from eastern regions of CAR, but there is no diagnostic data available for the country on CMD incidence, severity and infection type, and on virus occurrence. A further target for 2004 therefore will be the assessment of CMD in CAR, which should allow more accurate assessments to be made of the threat of the westwards expansion of the pandemic into Cameroon and Nigeria.

Data summarizing the status of the pandemic in 2003 are presented in Figure 3.

A comprehensive set of reports of the activities of this project are available as follows:

*Quarterly Reports*

1998: Quarter 1 (October to December)

1999: Quarters 1-4

2000: Quarters 1-4

2001: Quarters 1-4

2002: Quarters 1-4

2003: Quarters 1-4

*Stakeholder Workshop Proceedings*

1999: Proceedings of the Regional Stakeholders Workshop, Kampala, Uganda

2000: Proceedings of the Regional Stakeholders Workshop, Kampala, Uganda

2001: Proceedings of the Regional Stakeholders Workshop, Bukoba, Tanzania

2002: Proceedings of the Regional Stakeholders Workshop, Kisumu, Kenya

2003: Proceedings of the Regional Stakeholders Workshop, Bukoba, Tanzania

Many of these are available for downloading from the Tropical Whitefly IPM Project website: [www.tropicalwhiteflyipmproject.cgiar.org/wf/](http://www.tropicalwhiteflyipmproject.cgiar.org/wf/)

Hard copies can also be obtained from Dr. J. Legg, IITA-ESARC, c/o Lambourn and Co. Ltd., Carolyn House, Dingwall Rd., Croydon, CR9 3EE, UK.

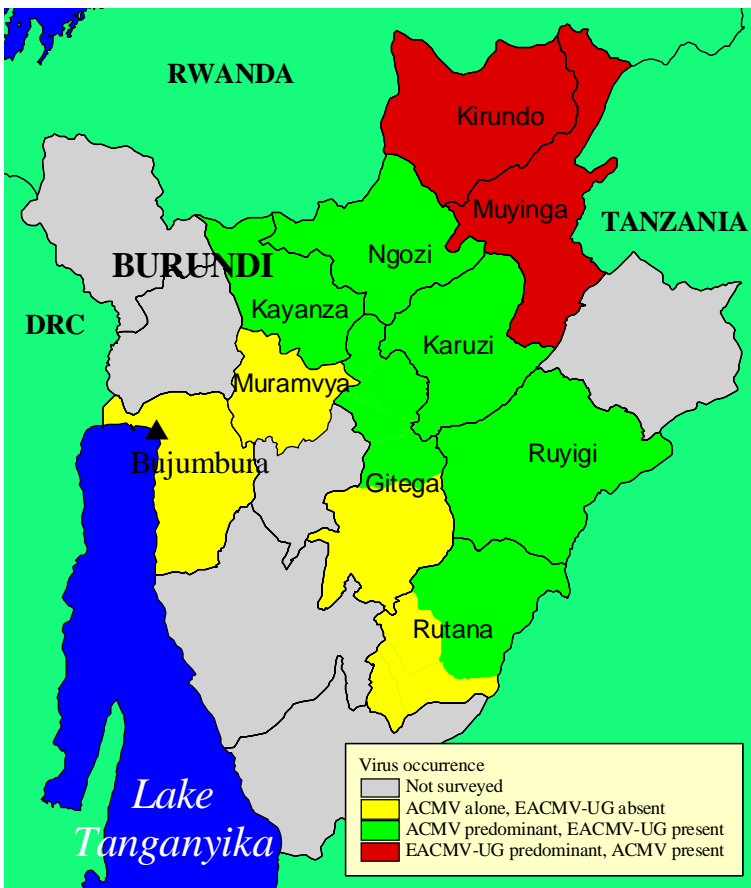


Fig. 1. Pandemic spread, Burundi, 2003

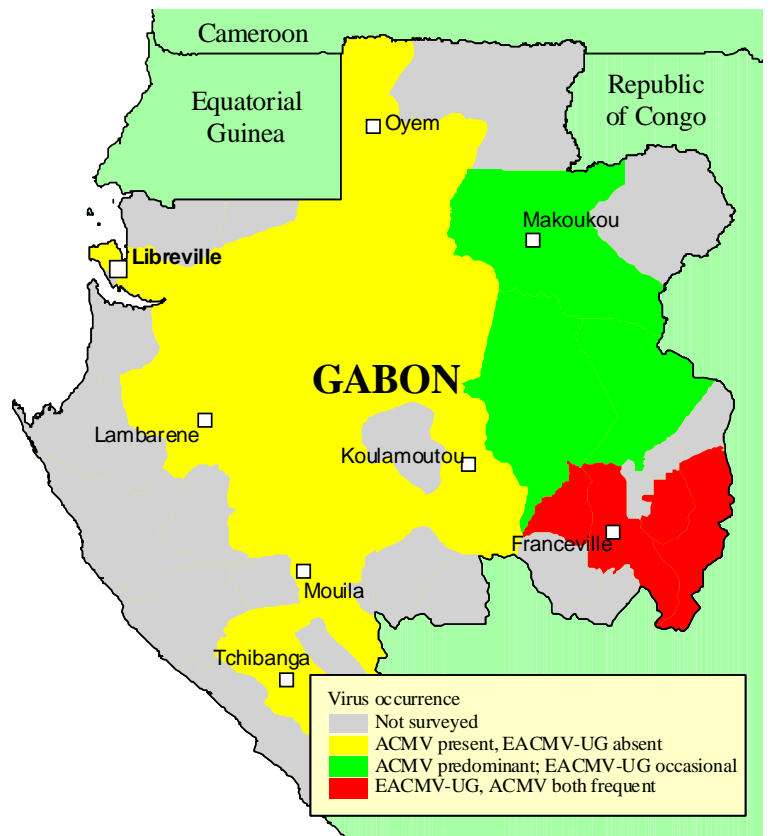


Fig. 2. Pandemic spread, Gabon, 2003

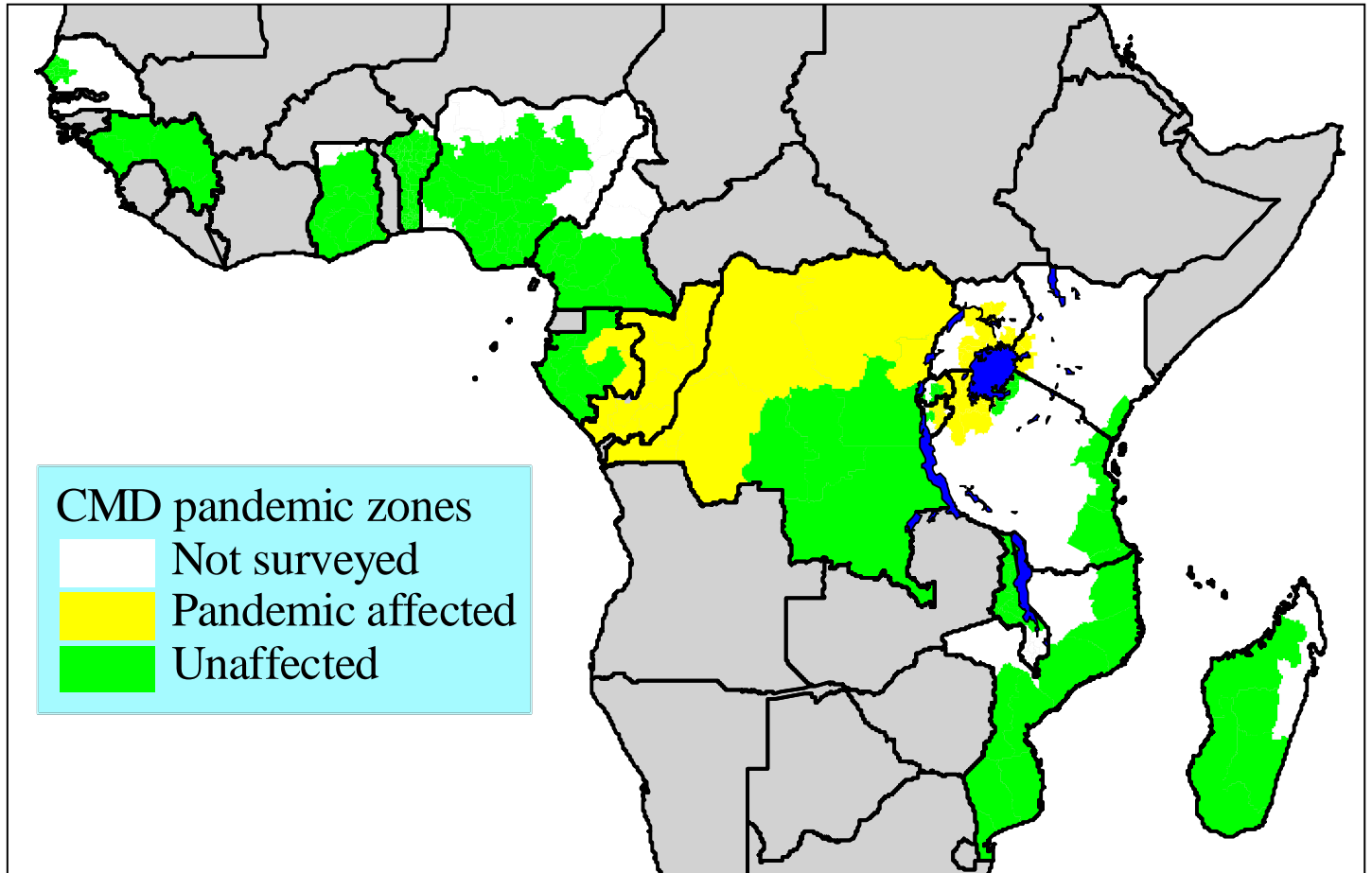


Fig. 3. The African CMD Pandemic, 2003



### D1-3 SPVD and CMD management guidelines developed and integrated

#### *Management of sweetpotato virus disease in East Africa – Dr. R. Gibson, NRI*

Studies on the epidemiology and management of sweetpotato virus disease (SPVD) have been conducted through the Makerere University MSc research programmes of Mrs. Ephrance Tumuboine, Ms. Milly Nambogga, Mr. Innocent Ndyetabura and Mr. Richard Ssemaganda, the last two of which were funded directly through the Tropical Whitefly IPM Project (and are described in this FTR). Dr. Richard Gibson, of NRI, UK, has played a key advisory role for each of these studies, the highlights of which are summarized in this report.

A common feature of control strategies is the use of isolation to control virus spread. Maize is a common intercrop for sweet potato in the Lake Victoria Zone of Tanzania and intercropped sweet potato has been reported to have a lower incidence of sweet potato virus disease (SPVD). It is a non-host of *B. tabaci* and may be interfering with their movement. A trial at Namulonge Research Institute Farm showed there were fewer whiteflies on intercropped plots (Table 1). Other trials have also demonstrated that intercropping an SPVD-susceptible sweet potato variety (Tanzania) with a very resistant variety (New Kawogo) considerably reduce the progress of SPVD in the susceptible variety.

**Table 1.** Nymphs, adult whiteflies and infected plants in sole and maize-intercropped sweet potato during 2002a and b growing seasons

Treatment	Number of whiteflies:		SPVD-affected plants (%)
	nymphs	Adults	
2002a			
Sweet potato	5.9	49.6	0.39
Sweet potato + maize	4.0	26.0	0.33
<i>L.S.D.</i>	<i>1.5</i>	<i>8.5</i>	<i>NS</i>
2002b			
Sweet potato	5.3	88.4	0.71
Sweet potato + maize	3.4	38.6	0.68
<i>L.S.D.</i>	<i>1.4</i>	<i>15.1</i>	<i>NS</i>

Intercropping has the disadvantage that the two crops interact agronomically and experiments also included the use of maize as a possible barrier to the whiteflies and also the use of the SPVD-resistant sweet potato variety, New Kawogo.

Barriers of both maize and New Kawogo diminished spread of SPVD, a result confirmed for maize in collaborative trials with farmers. Results of earlier researcher-led trials demonstrating control of SPVD achieved by roguing have also been confirmed in farmer-led trials in Uganda and Tanzania. These trials have demonstrated the benefits, including less infection both in rogued crops and in subsequent crops planted with cuttings obtained from them, and higher yields. These results now provide a range of control practices for

SPVD that can be used to supplement the use of resistant varieties. Inputs have also been provided to posters and a brochure designed to explain these benefits to farmers.

**Table 2.** The spread of SPVD to sweet potato surrounded by different possible barriers

Barrier crop	Mean SPVD incidence (%)		
	2002A	2002B	2003A
New Kawogo	10.3	9.3	8.8
Maize	9.2	-	11.5
No barrier	18.4*	11.6	13.0

\* Significantly more (P<0.05)

Casual observations suggested that cassava planted within typical small farmer plots, often close to or intercropped with sweet potato had fewer whiteflies than the frequently-damaging numbers found on isolated experimental plots. This limiting effect on whitefly numbers was then demonstrated when cassava was intercropped with sweet potato on-station but the sweet potato competed strongly with the cassava and reduced its growth. In a further on-station trial, a fourfold reduction in the numbers of whitefly nymphs present on cassava plants was achieved by draping them with old sweet potato foliage (compared to the numbers of nymphs on comparable cassava plants which had received no cassava foliage). This result is consistent with previous results in which reductions in whitefly adults or nymphs had been found on cassava plants intercropped with sweet potato but removes the confounding competitive effect of sweet potato plants on the growth of the cassava. Consequently, the most likely explanation for the reduction is that whitefly predators transferred with the old sweet potato foliage caused the reduction. This is a very exciting result as it offers the potential for reducing whitefly numbers sustainably using materials easily available to farmers.

*Augmenting the activity of whitefly parasitoids in cassava using sweet potato as a banker plant for parasitoids – Mr. R. Semaganda, Prof. E. Adipala, Makerere University, Kampala, Uganda*

## **Background**

Cassava production has been greatly hampered by the activity of the whitefly vector, *Bemisia tabaci*, the sole vector of cassava mosaic geminiviruses (CMGs) that cause CMD. Tremendous yield losses in the range of 15-24% have been attributed to CMD (Thresh et al., 1997). Interventions to control the CMD “pandemic” and the whitefly vector have been focused on the use of resistant varieties and phytosanitation. However, some of the resistant varieties support high whitefly populations (Sserubombwe *et al.*, 2001; Otim, 2002). Therefore, additional control strategies such as biological control are needed to manage *B. tabaci*. There are preliminary data supporting the occurrence of *B. tabaci* parasitoids on cassava in Uganda (Legg, 1995). In addition, Otim *et al.* (2001) in Uganda identified whitefly parasitoids of the family Aphelinidae [*Eretmocerus* sp. and *Encarsia sophia*] on cassava. However, to date, it is not clear to what extent these parasitoids reduce whitefly populations and hence reduce CMD damage. Under field conditions, it was found that parasitism of *B. tabaci* was low on cassava (Otim *et al.*, 2001) and on sweet potato (personal observation) and that parasitism only increased under low *B. tabaci* populations; a result that was attributed the limited fecundity and handling capacity of parasitoids under conditions of high whitefly abundance. However, the activity of parasitoids may be enhanced by using banker plants (Van Driesche and Bellows, 1996) to increase their timely arrival and abundance within cassava crops. Hence, experiments were carried out to investigate the possibility of using sweet potato as a banker crop for parasitoids to enhance colonization of *B. tabaci* in neighbouring cassava plants and thereby reduce CMD spread. This approach was supported by the fact that the cassava whitefly biotype is different from the biotype occurring on sweet potato and the fact that the two biotypes do not cross-colonize (Legg, 1994) whereas it was hypothesized that the parasitoids do not discriminate between the whitefly biotypes. The work reported as part of the Tropical Whitefly IPM Project of the System-wide Programme for Integrated Pest Management (SP-IPM) aimed:

1. To determine the distribution of sweet potato whitefly eggs, nymphs and parasitoid mummies on different sweet potato cultivars.
2. To identify and assess the occurrence and activity of the whitefly *Bemisia tabaci* and its parasitoids on sweet potato in contrasting agro-ecologies and seasons in Uganda.
3. To monitor the effect of intercropping sweet potato and cassava on parasitoid activity.
4. To monitor the effect of intercropping cassava and sweet potato on CMD incidence and severity and cassava whitefly population.

## **M.Sc. training at Makerere University, Kampala, Uganda**

*As part of the M.Sc training, the following courses were completed during 2001 and 2002*

1. *CC 601 Biometry /Applied Statistics*
2. *CC 603 Graduate Seminars*
3. *CS 601 Agronomy / Crop Production*
4. *CS 604 Disease Management*
5. *CS 608 Plant Tissue Culture*
6. *CS 609 Plant Breeding Technologies*
7. *CC 602 Research Methods*
8. *CS 612 Olericulture*
9. *CS 614 Physiology and Biochemistry of plant diseases*
10. *CS 603 Plant Breeding Methods*
11. *CS 605 Principles of Pest Management*
12. *CS 616 Crop Pest Ecology*
13. *CS 603 Crop Physiology*
14. *Cs 613 Epidemiology and Crop Loss Assessment*

### **Study of stratification of *B. tabaci* eggs, nymphs and parasitoid mummies on sweet potato**

Unlike for cassava, there is little published information on *B. tabaci* on sweet potato, its population dynamics and the behaviour of the different immature stages, parasitoids and the distribution of the different stages on the sweet potato plant. Therefore, two field studies were carried out to investigate the distribution of *B. tabaci* eggs, nymphs and parasitoid mummies on sweet potato vines. Results showed that sweet potato whitefly eggs were located on young leaves (first top 6 leaves) of the vine. The 1<sup>st</sup> and 2<sup>nd</sup> instar nymphs were located on leaves 5-6 but also occurred on young leaves while the 3<sup>rd</sup> and 4<sup>th</sup> instars (pupae) were located on leaves 9-16 which were relatively mature leaves. Parasitoid mummies were located on mature leaves of the sweet potato vine. This information provided the basis for the subsequent development of sampling protocols.

### **Occurrence and activity of sweet potato whitefly parasitoids in contrasting agro ecologies of Uganda**

The *B. tabaci* whitefly complex is attacked by many parasitoid species worldwide. However, there is scarce information published on the parasitoids attacking whiteflies especially on sweet potato in Africa. Two surveys were conducted during August/September 2002 and March/April 2003 at four sites with contrasting agro-ecologies in Uganda namely; Bulisa (low altitude, wet savannah), Kumi (eastern, mid-altitude, wet savannah), Rakai (western, mid-altitude, wet savannah) and Namulonge (central, mid-altitude, transition forest). The study indicated the presence of whitefly parasitoids in all survey sites. There were significant location differences in the occurrence of whitefly nymphs (3<sup>rd</sup> +4<sup>th</sup>) and parasitoid mummies. Both *Eretmocerus* species and *Encarsia sophia* parasitized nymphs were found at all the survey sites although the former were the most abundant. Percent parasitism was highest at Rakai where whiteflies were less abundant, and at Namulonge where whiteflies were most abundant compared to the other sites.

### **The activity of whitefly parasitoids in the cassava/sweetpotato intercrop system**

Field trials were conducted during 2002 and 2003 at Namulonge Agricultural and Animal Production Research Institute (NAARI) in Uganda to investigate the effect of intercropping cassava with sweet potato on whitefly parasitoids in cassava and the incidence and severity of cassava mosaic disease (CMD). Sweet potato was planted one month earlier than cassava to provide parasitoids for the whiteflies on cassava. Results from the two trials showed a significantly higher number of unparasitized *B. tabaci* nymphs in sole cassava compared to cassava intercropped with sweet potato. However, the adult *B. tabaci* population was only slightly higher in sole cassava but not significantly different from the population in cassava intercropped with sweet potato. Additionally, percent parasitism was higher in cassava intercropped with sweet potato but not significantly different with the sole cropping system. On the other hand, CMD incidence was significantly greater in sole cassava but there was no significant difference in symptom severity. These results suggest that there may be some benefits derived from the 'banker crop' approach of planting sweetpotato prior to cassava. However, further investigation will be required to clarify the reasons behind the differences demonstrated and to improve the approach through testing modifications to the single intercropping system tested.

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*Behavioural studies of whitefly parasitoids to enhance the management of Bemisia tabaci*  
– Prof. D. Gerling, Tel Aviv University, Israel

### **Background**

The Tropical Whitefly IPM Project has been exploring diverse opportunities for enhancing the activity of the natural enemies of *Bemisia tabaci*. In doing this, the Project has drawn on the expertise of Prof. Dan Gerling, a whitefly biocontrol specialist from Tel Aviv University, Israel. Prof. Gerling has supervised the MSc studies of Mr. Michael Otim (parasitoids of *B. tabaci* on cassava) and Mr. Richard Ssemaganda (parasitoids of sweetpotato, funded directly through this Project). In addition to guiding the research into the use of sweetpotato as a ‘banker crop’, Prof. Gerling has initiated studies on tritrophic interactions between natural enemies, their whiteflies hosts and the cassava and sweetpotato crop plants. Parasitoid species parasitizing *B. tabaci* on both cassava and sweetpotato have been identified, seasonal patterns of variation have been described, and differences in behaviour at different whitefly densities and on different varieties noted.

### **Tri-trophic studies**

More recent practical work for these studies has consisted of: constructing plant and insect cages, comparing different plant species for obtaining the best host for the studies of whitefly and parasitoid interactions, and studying the activities and biological cycles of *Eretmocerus mundus*, one of the two most abundant whitefly parasitoids occurring on both cassava and sweetpotato. Between 2002 and 2004, both cassava germplasm in tissue culture (varieties SS4 and Ebwanateraka) and parasitoids (all three species occurring in Uganda) were introduced from Uganda to Israel. The preliminary attempts at infesting cassava with the whitefly biotypes occurring in Israel were not successful, although this is not altogether surprising given what is known about the difficulty that non-cassava colonizing *B. tabaci* biotypes have in colonizing cassava. Several months were also spent in attempting to rear the introduced parasitoids on Israeli *B. tabaci*. These attempts were also unsuccessful although further studies are being undertaken to determine the reasons for this failure. Studies are being conducted concurrently in Uganda to examine the suitability of cassava and sweetpotato crops and the *B. tabaci* on them for parasitoids derived from each crop. Similarly, performance on a range of cassava varieties is being compared. These studies should provide important clues as to the factors that contribute to the relative success of parasitoid species in different situations, and the practical utility for the banker crop approach in which sweetpotato is intercropped with cassava. These are clearly key elements to be addressed in targeting the enhancement of whitefly control through the use of natural enemies.

*Effectiveness of Phytosanitation for the Control of Cassava Mosaic Disease and Sweetpotato Virus Disease in the Lake Zone of Tanzania – Mr. I. Ndyetabura and Prof. E. Adipala, Makerere University, Kampala, Uganda*

## **Background**

Cassava (*Manihot esculenta* Crantz) and sweetpotato (*Ipomoea batatas* L.) are two important root crops playing a great role as household food security crops in the Lake Zone of Tanzania. Cassava and sweetpotato are commonly grown both in intercropping and monocropping systems by many subsistence farmers. Other crops planted in intercrop with cassava and sweetpotato include maize, beans, cowpeas, and groundnuts. Both crops are also grown in intercrop with plantain/banana, young perennials such as pawpaw, coconut and trees such as mango.

The whitefly, *Bemisia tabaci*, is an important virus vector in both cassava and sweetpotato fields where cassava mosaic disease (CMD) and sweetpotato virus disease (SPVD) are prevalent. Viruses causing both CMD and SPVD are transmitted by *B. tabaci* and through vegetative propagation of infected cuttings taken from infected parent plants.

The most serious whitefly virus-vector problem in Africa is CMD caused by a group of cassava mosaic geminiviruses (CMGs). The yield losses due to CMD range from insignificant to 95% depending upon the cultivars used, environmental conditions and nature of the CMG infection. SPVD is caused by a combination of two viruses: *Sweetpotato chlorotic stunt virus* (SPCSV) (Family *Closteroviridae*: Genus *Crinivirus*) and *Sweetpotato feathery mottle virus* (SPFMV) (Family *Potyviridae*: Genus *Potyvirus*). Yield losses due to SPVD varied between 60 – 98% in 36 sweetpotato families (360 genotypes) in Uganda.

## **M.Sc. training at Makerere University, Kampala, Uganda**

*As part of the M.Sc training, the following courses were completed during 2002 and 2003:*

15. *CC 601 Biometry /Applied Statistics*
16. *CC 603 Graduate Seminars*
17. *CS 601 Agronomy / Crop Production*
18. *CS 604 Disease Management*
19. *CS 609 Plant Breeding Technologies*
20. *CC 602 Research Methods*
21. *CS 612 Olericulture*
22. *CS 614 Physiology and Biochemistry of Plant Diseases*
23. *CS 603 Plant Breeding Methods*
24. *CS 605 Principles of Pest Management*
25. *CS 603 Crop Physiology*
26. *Cs 613 Epidemiology and Crop Loss Assessment*

### **Effectiveness of phytosanitation in the control of cassava mosaic geminivirus under contrasting spread conditions.**

The experiment was planted in October 2002 at two sites in Bukoba district and one site in Muleba district in Kagera Region. The sites included Maruku Agricultural Research and Development Institute (MARDI), Kanoni Farmers' Extension Center (FEC) and Nsunga Farmers' Extension Center (FEC). Four varieties of known CMD resistance level were planted in a complete randomized block design, under four diseases management practices (roguing, selection, roguing + selection and nothing). The varieties included in this experiment were SS4 (very resistant), TMS 4(2)1425 (moderately resistant), Rushura (very susceptible) and Msitu Zanzibar (moderately susceptible). Data were collected on CMD incidence, severity and root yield at harvest.

### **Assessing the effectiveness of phytosanitation in controlling sweetpotato virus disease (SPVD)**

The trials were established at three sites in the same districts (Bukoba and Muleba). The sites included Kyaka and Maruku in Bukoba district and Ngenge in Muleba district. Five varieties differing in the level of resistance to SPVD infection were compared. These included Kigambilenyoko (susceptible), Sinia (susceptible), SPNO (moderately resistant), SP 93/2 (moderately resistant) and Polista (resistant). The experiments were planted in a complete randomized block design, with four disease management practices (roguing, selection, roguing + selection and nothing). Data were collected on SPVD incidence, severity and root yield at harvest.

### **Characterizing the CMD resistance of the main local and improved varieties of cassava common in Bukoba and Muleba districts**

One site (Ngenge) having high CMD inoculum pressure was used as the testing site. Seven varieties, both local and improved, were randomly planted in four replicates under natural disease inoculum conditions. The varieties included TMS 4(2)1425 (improved - moderately resistant), SS4 (improved - resistant), TMS 30572 (improved - moderately resistant), MM 96/8233 (improved - resistant), Rushura (local - very susceptible), Kaitampunu nyeupe (local - moderately susceptible) and Mukarukwatage (local - moderately susceptible). Planting was done in October 2002 and data were collected on CMD incidence and severity, plant growth parameters and root yield at harvest.

### **Characterizing the SPVD resistance of local and improved sweetpotato varieties common in Bukoba and Muleba district**

Planting was done in October 2002 in four farmers' fields at Kyaka. Each farmer was considered to be a replicate. Four improved varieties and four local varieties were included in this experiment. The improved varieties were: Polista, SPNO, SP 93/34 and SP 93/2. The local varieties comprised: Kigambilenyoko, Hidaya, Kombegi and Zerida. Data were collected on SPVD incidence and severity and root yield at harvest.

## **Results**

### *Covering comment*

Delays in reporting results of both the cassava and sweetpotato trials results for Tanzania have largely been due to the unfortunate January car accident in which the Tanzanian



MSc student doing these trials was involved. He sustained a broken leg and remains in hospital recovering, but should be discharged during April.

#### *Phytosanitation trials*

**Cassava phytosanitation trial:** At one month after planting, all plants sprouting with disease symptoms were uprooted in all experiments. Gap filling using the established nurseries was done in cassava trials at all sites. The sweetpotato phytosanitation trial at Kyaka was replanted due to the poor sprouting caused by a long dry spell that followed planting. Satisfactory sprouting was recorded at the other experimental sites. At two months after planting, the whitefly-infected plants in the roguing and roguing + selection plots were uprooted in both cassava and sweetpotato phytosanitation trials.

Although roguing at two months after planting in the cassava trial did have an immediate impact on CMD incidence, there was no clear distinction between rogued and un-rogued plots in terms of incidence at later stages of growth, indicating that much of the spread occurred after the initial roguing. Results for the second planting should provide a clearer indication as to whether selection has greater utility in reducing CMD and if there is any additional benefit to be gained from combining selection with roguing.

**Sweetpotato phytosanitation trial:** The sweetpotato phytosanitation trial was hindered firstly by poor initial sprouting at one of the sites, and secondly, by the difficulty in selecting disease-free planting material. As a result of this, differences in SPVD incidence were only demonstrated between varieties and sites. These deficiencies should be addressed in the second planting.

#### *Evaluation trials*

**Cassava evaluation trial:** All improved varieties had low average disease severity of 2.0. Local varieties, by contrast, had average disease severities that ranged from 2.6 - 3.6. Rushura had the highest disease severity of 3.6, followed by Kaitampunu nyeupe (2.8) and Mukarukwatage (2.6). Rushura had the highest disease incidence of 91.0%. This contrasted strongly with improved CMD resistant varieties, three of which were not diseased at all (Table 1). In the second season, a similar trend was observed. The trial results do suggest, however, that even under high CMD inoculum pressure conditions, the less susceptible local varieties, including Kaitampunu nyeupe and Mukarukwatage, might be sustained through selection of healthy stems at the end of the season. Significantly, farmers already seem to be pursuing such an approach, which in part explains the increasing frequency of cultivation of these two varieties in the post-epidemic situation in north-western Tanzania.

**Sweetpotato evaluation trial:** Very high incidences were recorded in the sweetpotato evaluation trial amongst local varieties, Kombegi and Zerida. The performance of improved varieties was mixed, ranging from > 40% (SP 93/34) to just over 5% (Polista). In common with previous trials here in elsewhere, however, the local varieties gave the greatest yields, providing further evidence for the apparent negative correlation between SPVD resistance and yield. As a consequence, control programmes should continue to assess the potential of Uganda-derived varieties (recently introduced to Tanzania) which

DO provide increased yields whilst having resistance to SPVD. Additionally, approaches to SPVD management that make use of existing farmer-preferred (and high yielding) varieties should continue to be promoted.

*Survey of SPVD and farmers perceptions in north-western Tanzania*

A survey was conducted during March 2003 in Bukoba and Muleba districts in north-western Tanzania both to characterize the spread of SPVD and to document farmers knowledge of and responses to the disease. Growers were interviewed and fields assessed at 32 locations in the main sweetpotato growing divisions of the two districts. SPVD was recorded throughout the study area and although most farms (50%) had low incidences from 5-19%, 22% of farms had potentially damaging incidences of 20-49%. 40% of growers recognized SPVD as a disease, many of them likening it to CMD, and 28% indicated that they do remove diseased plants, usually during weeding operations. None mentioned using resistance as a control approach, although some did recognize that certain varieties were less affected than others. These data highlight both the widespread importance of SPVD, in addition to the weakness of current understanding. Training initiatives clearly have an important role to play in future extension work.

Table 1. Sweetpotato and cassava variety evaluation trials Virus incidences (%) recorded in the first and second trials at the CMD and SPVD hot spots.

Crop	Variety	Season 1	Season 2
Cassava	TMS 4(2)1425	9.0	0.0
	Rushura	91.0	9.4
	SS4	0.0	0.0
	Kaitampunu	61.9	35.8
	MM 96/8233	0.0	0.0
	Migera	0.0	0.0
	Mukarukwatage	29.3	1.6
Sweet potato	Kigambilenyoko		35.3
	Hidaya		8.3
	Kombegi		58.9
	Zerida		60.2
	SP 93/34		42.9
	SP 93/2		15.7
	SPN/O		11.9
	Polista		5.8

**Note:**

- Data for the 1<sup>st</sup> season (sweetpotato) recorded at five months age and the second season recorded at four months age.
- Data for cassava, 1<sup>st</sup> season data recorded at eight months age and the second season data recorded at four months age.

Table 2. Mean and (maximum) CMD incidence (%) in cassava phytosanitation trial at Ngenge

<b>Variety</b>	<b>Roguing</b>	<b>Selection</b>	<b>Rog + Sel</b>	<b>Nothing</b>
Rushura	79.2 (100)	85.7 (100)	90.0 (0 (100))	83.8 (100)
SS4	0 (0)	0 (0)	0 (0)	0 (0)
TMS 4(2)1425	14.1 (56.5)	7.17 (16.7)	6.0 (24)	0.0 (0.0)
Msitu Zanzibar	6.9 (21.1)	17.8 (8)	28.15 (70)	10.0 (15)

Table 3. Mean and (maximum) CMD incidence (%) in cassava phytosanitation trial at Nsunga

<b>Variety</b>	<b>Roguing</b>	<b>Selection</b>	<b>Rog + Sel</b>	<b>Nothing</b>
Rushura	97.5 (100)	100.0 (100)	100 (100)	100 (0.0)
SS4	0 (0)	0 (0)	0 (0)	0 (0)
TMS 4(2)1425	28 (87)	13.7 (7.0)	26.9 (47.6)	40.6 (6)
Msitu Zanzibar	22.5 (34.8)	28.6 (65)	27.6 (45.5)	13.0 (19)

Table 4. Mean and (maximum) CMD incidence (%) in cassava phytosanitation trial at Maruku

<b>Variety</b>	<b>Roguing</b>	<b>Selection</b>	<b>Rog + Sel</b>	<b>Nothing</b>
Rushura	1.3 (5.3)	7.0 (22.7)	3.0 (11.8)	3.7 (5.9)
SS4	0 (0)	1.2 (4.8)	0 (0)	0 (0)
TMS 4(2)1425	1.1 (4.3)	0 (0)	0 (0)	0 (0)
Msitu Zanzibar	0 (0)	0 (0)	2.1 (4.3)	2.5 (8.0)

#### D4. Cassava host plant resistance for *Bemisia* spp. evaluated

*Host-plant resistance of South American cassava genotypes to African and Indian whitefly species – Dr J. Colvin and Dr. N. Maruthi, NRI, UK*

##### **Background**

The whitefly species, *Bemisia tabaci*, has a pantropical distribution and is the vector of cassava mosaic virus disease (CMD) in both Africa and India. This disease causes considerable yield losses and is a potentially devastating threat to cassava production in Asia and Latin America. In the recent past, high populations of *B. tabaci* were responsible for the rapid spread of the CMD pandemic in East Africa (Otim-Nape *et al.*, 2000). In addition to the yield losses caused by the transmission of cassava mosaic geminiviruses (CMGs), the high populations of *B. tabaci* on cassava have caused it to become a direct pest in its own right. Losses of more than 50%, for instance, were recorded in the worst affected varieties (Legg *et al.*, 2004; Omongo *et al.*, 2004), some of which have gained wide-spread acceptability amongst farmers due to their good tuber quality and resistance to CMD.

In Africa, another whitefly species, *Bemisia afer*, has been reported to cause losses to cassava in Africa and preliminary data suggests that it is the vector of cassava brown streak virus disease (Maruthi *et al.*, 2004). Cassava is primarily grown by subsistence farmers in Africa with few, if any, inputs. Differences in the acceptability of cassava varieties to whiteflies have been recognized for some time (Nair & Daniel, 1983; Maruthi *et al.*, 2001) and so host-plant resistance provides a potentially sustainable and environmentally friendly solution to this threat to the livelihoods of subsistence farmers in Africa and Asia.

High levels of resistance to the whitefly, *Aleurotrachelus socialis*, have been identified in neotropical cassava genotypes (Gomez & Bellotti, 2003; Arias *et al.*, 2004) and to biotype B of *B. tabaci* (Burbano, 2003). Research supported by this project aimed to allow whitefly-resistant germplasm from the neotropics to be evaluated for resistance to African and Indian cassava whiteflies. The research will potentially permit the combining of whitefly-vector resistance with resistance to CMD. Since whitefly resistance in cultivated crops is rare, this project offers a unique opportunity to eventually develop cassava cultivars with resistance to both the whitefly vector and CMD. This novel approach to reducing whitefly and virus-disease incidence in Africa has not been attempted for any other crop.

##### **Objectives**

- The shipment from CIAT and establishment of South American cassava genotypes at the Natural Resources Institute (NRI), UK.
- The collection and establishment of colonies of African cassava *B. tabaci* and *B. afer*, and Indian cassava *B. tabaci* at NRI.
- Screening cassava genotypes against African cassava *B. tabaci*.
- Screening cassava genotypes against African cassava *B. afer*.

- Screening cassava genotypes against Indian cassava *B. tabaci*.
- Assessing the effect of host-plant resistance on whitefly biology.
- Exchanging information on whitefly resistance with CIAT colleagues.

## Methodologies and Results

### *The shipment from CIAT and establishment of South American cassava genotypes at NRI*

Four cassava genotypes: Col 1468, MCol 2063, CG 489-34 and MEcu 72 with various degrees of resistance to South American whitefly species were sent by CIAT to NRI. The genotypes were received in glass tubes as tissue cultured plants (*in vitro* propagated). These were further sub-cultured and multiplied successfully by using the combined *in vitro* propagation and glasshouse protocols established at NRI.

### *The collection and establishment of colonies of African cassava B. tabaci and B. afer, and Indian cassava B. tabaci at NRI*

Three whitefly colonies, *B. tabaci* from Namulonge (Uganda), *B. afer* from Entebbe (Uganda) and *B. tabaci* from Trivandrum (India) were collected and established on cassava in the insectary at NRI. These populations were maintained throughout the project in order to supply the insects necessary for screening the cassava genotypes.

### *Screening cassava genotypes against African cassava B. tabaci*

Methodology. Cassava plantlets, with *c.* 5-8 expanded leaves, of each genotype were enclosed separately in individual, insect-proof containers. Ten male and ten female, 2-day-old, adult *B. tabaci* were released onto each plant. Eighteen days after release, the numbers of eggs, nymphs and adults per plant were recorded. After data collection, adults were released back onto the plants and the populations were left to increase for a further 18 days. At this point, the numbers of eggs, nymphs and adults per plant were recorded for a second time.

Results. Eighteen days after the release of the African cassava *B. tabaci* onto the cassava genotypes, there were no significant differences between the populations and it was evident that all of the genotypes could be colonized. The variety with the greatest level of resistance, however, was MEcu 72 (Table 1). Thirty-eight days after the African cassava *B. tabaci* were released, MEcu 72 still showed the highest level of resistance and the difference was now significant (Table 2).

### *Screening cassava genotypes against African cassava B. afer*

Methodology. The methodology followed for this experiment was the same as that used previously, except that only five male and five female insects per plant were used to begin the colonies. This change was considered appropriate in order to increase the chances of detecting any host-plant resistance effect.

Results. The level of *B. afer* resistance in the varieties MEcu 72, Col 1468 and CG 489-34 did not differ significantly, as the mean populations on these varieties were similar within the time periods of 18 and 38 days after colonization. MCol 2063, however, had a significantly higher mean number of eggs and nymphs in both generations and, by the second generation, it had over four times the mean population present on Col 1468. Development of *B. afer* was also significantly faster on MCol 2063, as the number of ‘pupae’ present was approximately five times higher on this variety (35.3 pupae) than on Col 1468 (6.2 pupae), 38 days after colony initiation.

#### *Screening cassava genotypes against Indian cassava B. tabaci*

Methodology. The methodology followed was the same as that used for *B. afer*.

Results. Eighteen days after the release of the adults, the varieties MEcu 72 and Col 1468 had the lowest populations of eggs and nymphs although these differences were not significant (Table 5). After a further 20 days, Col 1468 and MEcu 72 still had the lowest mean populations, although this difference was also not significant (Table 6).

#### *Effect of host-plant resistance on whitefly biology*

Methodology. Plants of the four South American cassava varieties were grown in the NRI glasshouse until they were three to four months old. It was decided to use older plants than in the previous experiments as any host-plant resistance effect may increase with plant age and therefore be detected more easily. The leaves of each plant were assigned numbers; the top leaf was given the number one, the second leaf number two, and so on.

Groups of five 2-day-old male and five 2-day-old female adult whiteflies were transferred to clip cages (10 adults per clip cage), which were attached to suitable leaves of the test plants. For the African *B. tabaci* and *B. afer* populations, the clip cages were situated so that they were either on leaves 1 or 2, 3 or 4, 5 or 6, 7 or 8, and 9 or 10. The Indian *B. tabaci* population was only positioned on leaves one to three. The whiteflies were then allowed to feed and oviposit on the leaves for 72 h. The clip cages were then removed and the surviving whiteflies collected and frozen.

After the removal of the whiteflies, the numbers of eggs per leaf were counted. For the African and Indian *B. tabaci* populations, the numbers of surviving insects per leaf was recorded 10, 20 and 30 days later. Due to its slower developmental time, an additional count was made for *B. afer*, 40 days after the removal of the clip cages.

Due to problems encountered with mites attacking the cassava test plants, the different whitefly populations were assessed at different times.

Results. The three whitefly populations all oviposited successfully on the four cassava varieties. For the African *B. tabaci*, there was a significant cassava genotype effect and the fewest eggs were produced on MEcu 72. For the other two populations, there was no

apparent cassava genotype effect. Overall, African *B. tabaci* oviposited the fewest eggs and Indian *B. tabaci* oviposited the greatest numbers of eggs (Table 7).

For all the whitefly populations on all the cassava genotypes, percentage survival decreased with time in a curvilinear fashion. For each whitefly population, survival to adulthood was broadly similar for each of the cassava genotypes. African *B. afer* populations had the lowest survival rates and Indian *B. tabaci* had the highest (Table 8).

For African *B. tabaci* and *B. afer*, mean numbers of eggs oviposited in the different leaf positions did not differ significantly (Table 8). This was also the case for Indian *B. tabaci*, which oviposited  $48.1 \pm 8.8$ ,  $44.7 \pm 9.1$ ,  $48.1 \pm 7.3$  eggs on the first, second and third leaves, respectively (ANOVA,  $P = 0.95$ ).

The percent survival to adulthood of the African *B. tabaci* and *B. afer*, on the leaf positions showed different trends. For African *B. tabaci*, survival was highest when eggs were laid on the first or second leaves and it decreased steadily thereafter to its lowest value of 36.9% at leaf category 9 or 10. The survival of *B. afer*, on the other hand, was highest when the eggs were oviposited on leaves five to eight (Table 10). For the Indian *B. tabaci*, survival remained high on the top three leaves. On leaves one to three, it was 63.4%, 54.1% and 71.2%, respectively.

#### *Exchanging information on whitefly resistance with CIAT colleagues*

A visit by Dr Colvin to CIAT took place from the 8-15<sup>th</sup> March, 2004. This visit was timed to coincide with the VI<sup>th</sup> Cassava Biotechnology Network meeting. Dr Colvin chaired the Plenary Session on Biotic Stresses affecting cassava. Many of the scientists working on aspects of cassava whiteflies attended the meeting and it afforded an opportunity to discuss how to get further funding to take this important work forward.

### **Discussion**

In the first set of experiments, where whitefly population growth was assessed on the different cassava genotypes, MEcu 72 was clearly the most resistant to African *B. tabaci* as it had the fewest eggs and nymphs present on it 18 days after colony initiation. After a further 20 days, this situation was maintained and the difference had become highly significant (Tables 1 & 2).

For *B. afer*, MEcu 72, CG489-34 and Col 1468 had similarly low numbers of nymphs and eggs present on them 18 days after colonization. MCol 2063, however, had three to four times as many eggs and nymphs present and was clearly the most susceptible to this species. Twenty days later, the resistance ranking, in terms of the relative numbers of *B. afer* present on each of the varieties, remained the same (Tables 3 & 4).

For Indian *B. tabaci*, the numbers of insects present on the different varieties did not differ significantly either on 18 or 38 days after colonization. Col 1468 and MEcu 72, however, had the lowest populations present (Tables 5 & 6).

When older plants were used to assess relative oviposition success and survival on the different varieties, a similar pattern was evident. For African *B. tabaci*, the numbers of eggs oviposited on MEcu 72 was significantly lower than on the other varieties. For *B. afer* and Indian *B. tabaci*, however, there were no significant differences apparent. In this set of experiments, the Indian *B. tabaci* oviposited greater numbers of eggs than either of the other two populations. It is not possible to attribute this effect to any definite factor, because the experiments were carried out at different times, and using different plants.

Within whitefly populations, the survival on the different genotypes was similar. African *B. afer* had the poorest survival followed by African *B. tabaci*. The Indian *B. tabaci* had the highest survival success.

For all of the whitefly populations, the leaf position that the females occupied did not significantly affect the numbers of eggs they oviposited. The percent survival of the eggs, however, varied depending on leaf position. For the African *B. tabaci*, survival decreased in a linear trend the lower down the plant the individuals were. For *B. afer*, the highest survival occurred on leaves five to eight. There may be a link between this observation and the different resting and oviposition site preferences of these two species in the field. Under field conditions, African *B. tabaci* is most commonly found on the top leaves of cassava plants, whereas *B. afer* has a different distribution on the plant (Fishpool & Burban, 1994) and is usually found on the lower leaves (Maruthi, 2004).

In a separate study, an African cassava genotype, Nase 9, which shows impressive resistance to *B. tabaci* in the field (Omongo, 2003), was screened in the under laboratory conditions using African *B. tabaci* and the methodology described above and was found to have a similar level of resistance to MEcu 72. The screening technique for detecting host-plant resistance to three Old World whitefly populations involved confining them on the cassava genotypes, where they were forced to feed. Although African *B. tabaci* could feed and reproduce successfully on Nase 9, populations on it in the field were very low and the whitefly population was probably choosing not to colonize it. In order to capture this element of host-plant resistance, we propose that further behavioural choice experiments need to be carried out to accurately assess these varieties.

From the results of this study, MEcu 72 clearly shows the most consistent pattern of resistance to whiteflies from Africa and India. We propose that future work to exploit this potential should involve further screening of genotypes at CIAT to identify additional sources of resistance, incorporation of a behavioural test to assess the African and Indian whitefly species' preferences for feeding on different cassava genotypes, identification of the genes involved in the resistance and plant breeding to cross whitefly resistant genotypes such as MEcu 72 with an African cassava genotype, such as Nase 9, which also has tolerance to cassava mosaic geminiviruses. Progeny from these crosses could then be tested both in the lab and field.



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Table 1. Mean numbers of African *B. tabaci* eggs and nymphs, 18 days after 10 male and 10 female adults were allowed to colonise each plant.

Cassava genotype	Number of plants	Mean eggs & nymphs ( $\pm$ SEM)
Col 1468	10	458.3 $\pm$ 40.7
Col 2063	15	439.8 $\pm$ 27.7
CG489-34	13	511.6 $\pm$ 30.4
MEcu 72	12	391.0 $\pm$ 22.3

ANOVA  $P = 0.053$

Table 2. Mean numbers of African *B. tabaci* eggs, nymphs and adults, 38 days after 10 male and 10 female adults were allowed to colonise each plant.

Cassava genotype	Number of plants	Mean eggs, nymphs & adults ( $\pm$ SEM)
Col 1468	10	2514.5 $\pm$ 257
Col 2063	15	2010.5 $\pm$ 129
CG489-34	13	2797.2 $\pm$ 285
MEcu 72	12	1639.3 $\pm$ 89.1

ANOVA  $P < 0.001$

Table 3. Mean numbers of African *B. afer* eggs and nymphs, 18 days after five male and five female adults were allowed to colonise each plant.

Cassava genotype	Number of plants	Mean eggs & nymphs ( $\pm$ SEM)
Col 1468	11	61.73 $\pm$ 17.4
Col 2063	8	228.12 $\pm$ 46.1
CG489-34	11	67.27 $\pm$ 19.7
MEcu 72	6	64.83 $\pm$ 10.9

ANOVA  $P < 0.001$

Table 4. Mean numbers of African *B. afer* eggs, nymphs and adults, 38 days after five male and five female adults were allowed to colonise each plant.

Cassava genotype	Number of plants	Mean eggs, nymphs & adults ( $\pm$ SEM)
Col 1468	11	92.2 $\pm$ 26.7
Col 2063	8	414.6 $\pm$ 89.1
CG489-34	11	151.6 $\pm$ 34.8
MEcu 72	6	118.2 $\pm$ 19.0

ANOVA  $P < 0.001$

Table 5. Mean numbers of Indian *B. tabaci* eggs and nymphs, 18 days after five male and five female adults were allowed to colonise each plant.

Cassava genotype	Number of plants	Mean eggs & nymphs ( $\pm$ SEM)
Col 1468	10	136.7 $\pm$ 29.8
Col 2063	11	245.5 $\pm$ 40.0
CG489-34	10	190.4 $\pm$ 26.4
MEcu 72	9	157.3 $\pm$ 23.9

ANOVA  $P = 0.088$

Table 6. Mean numbers of Indian *B. tabaci* eggs, nymphs and adults, 38 days after five male and five female adults were allowed to colonise each plant.

Cassava genotype	Number of plants	Mean eggs, nymphs & adults ( $\pm$ SEM)
Col 1468	10	247.6 $\pm$ 37.4
Col 2063	11	447.4 $\pm$ 92.5
CG489-34	10	456.4 $\pm$ 50.3
MEcu 72	9	396.1 $\pm$ 65.7

ANOVA  $P = 0.115$

Table 7. The mean numbers of eggs laid by the different whitefly populations on the four cassava varieties.

Cassava variety	Mean $\pm$ SE eggs laid by each whitefly population		
	<i>African B. tabaci</i>	<i>African B. afer</i>	<i>Indian B. tabaci</i>
MEcu 72	17.1 $\pm$ 1.94	37.0 $\pm$ 5.32	54.77 $\pm$ 6.46
Col 1468	24.96 $\pm$ 2.32	32.8 $\pm$ 3.31	40.11 $\pm$ 5.28
Col 2063	27.52 $\pm$ 1.62	32.6 $\pm$ 4.79	32.2 $\pm$ 4.75
CG489-34	32.72 $\pm$ 5.99	35.72 $\pm$ 4.54	60.66 $\pm$ 9.25
ANOVA	$P = 0.036$	$P = 0.871$	$P = 0.947$

Table 8. The percent survival to adulthood of the three whitefly populations on the four cassava varieties.

Cassava variety	Percent survival to adulthood of each whitefly population		
	<i>African B. tabaci</i>	<i>African B. afer</i>	<i>Indian B. tabaci</i>
MEcu 72	47.5	28.5	68.2
Col 1468	37.1	14.3	56.2
Col 2063	41.5	28.2	57.5
CG489-34	42.7	16.5	66.1

Table 9. The mean number of eggs laid per leaf position by the African *B. tabaci* and *B. afer* populations on the cassava genotypes. Data for the Indian *B. tabaci* population are included in the text.

Leaf position	Mean $\pm$ SE eggs laid by each whitefly population	
	African <i>B. tabaci</i>	African <i>B. afer</i>
1 or 2	27.5 $\pm$ 3.25	40.7 $\pm$ 4.03
3 or 4	23.1 $\pm$ 4.03	33.8 $\pm$ 4.24
5 or 6	31.1 $\pm$ 5.71	33.7 $\pm$ 6.33
7 or 8	25.9 $\pm$ 5.02	29.4 $\pm$ 3.86
9 or 10	21.1 $\pm$ 4.0	29.7 $\pm$ 4.86
ANOVA	$P = 0.58$	$P = 0.48$

Table 10. The percent survival to adulthood of the African *B. tabaci* and *B. afer* populations at the different leaf positions on the cassava plants. Data for the Indian *B. tabaci* population are included in the text.

Leaf position	Percent survival to adulthood by each whitefly population	
	African <i>B. tabaci</i>	African <i>B. afer</i>
1 or 2	48.4	20.8
3 or 4	44.0	21.5
5 or 6	40.7	30.4
7 or 8	38.6	27.6
9 or 10	36.9	19.5

## E1. Training manuals developed for NARS professionals

Phase 2 of the Tropical Whitefly IPM Project has focused on basic research and the development of IPM components. However, the project was set up such that its activities should complement the more 'downstream' and output promotion approach of allied projects also supported by DFID's CPP. Three of these projects have played an important complementary role in developing training materials both for use by NARS professionals, and for extension staff. R8167 (ZA0498) 'Promotion of sustainable sweetpotato production and post-harvest management through farmer field schools in East Africa' has developed a training manual covering the whole range of topics required for IPPM farmer field schools, including the management of virus diseases. This will be completed in 2004, and will provide an essential tool for both research and extension staff when involved with farmers in participatory learning or training programmes. The manual will be comprehensive, and will primarily serve as a source book for group leaders, trainers, extensionists and researchers. For the more practical farm-level work, project R8243 (ZA0545), entitled, 'Working with farmers to control sweet potato virus disease in East Africa', is approaching the completion of leaflets and posters in languages and using images appropriate for farmers in Uganda and Tanzania which incorporate training messages for the management of SPVD. Similar outputs are also being developed for CMD management through project R8303 (ZA0575), 'Maximizing, disseminating and promoting the benefits to farmers of cassava varieties resistant to cassava mosaic disease'. Both initiatives are based on the body of research information on these two whitefly-borne produced through diverse projects addressing these constraints, and including the Tropical Whitefly IPM Project.

Further information on these training outputs can be obtained from project reports and from the project leaders, Dr. R. Gibson (R8243 and R8303) and Dr. T. Stathers (R8167), both of NRI, UK.

## *Dissemination of results*

### **(i) Scientific papers and book chapters**

- Legg, J.P., Gerling, D., Neuenschwander, P.N. 2003. Biological control of whiteflies in sub-Saharan Africa. In: *Biological Control in IPM Systems in Africa*. Eds. Neuenschwander, P., Borgemeister, C. and Langewald, J. CABI International, Wallingford, UK. Pp 87-100.
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### **ii) Oral presentations in conferences, workshops and seminars**

- Legg, J.P., Mallowa, S., Sseruwagi, P. 2003. First report of physical damage to cassava caused by the whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Sternorrhyncha: Aleyrodidae). *3<sup>rd</sup> International Bemisia Workshop, 17-20 March, Barcelona, Spain*. Abstract. p41.
- Legg, J.P., Owor, B., Ntawuruhunga, P., Ndunguru, J., Sseruwagi, P. 2003. Cassava mosaic geminiviruses, *Bemisia* whiteflies, and the African pandemic of cassava mosaic disease. *3<sup>rd</sup> International Bemisia Workshop, 17-20 March, Barcelona, Spain*. Abstract. p50.

- Legg, J.P., Otim, M., Owor, B., Ntawuruhunga, P., Ndyetabura, I., Obiero, H., Kyamanywa, S., Colvin, J., Gerling, D. 2003. Managing cassava mosaic geminiviruses and their *Bemisia tabaci* vector in Africa: current practice and future opportunities. *3<sup>rd</sup> International Bemisia Workshop, 17-20 March, Barcelona, Spain*. Abstract. p131.
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### iii) Posters

Ndunguru, J., Taylor, N., Legg, J.P., Fauquet, C.M. 2004. FTA<sup>®</sup> cards greatly simplify sampling, archiving and recovery of viral and genomic DNA from cassava. Sixth International Scientific Meeting of the Cassava Biotechnology Network (CBN), Cali, Colombia, 8-14 March 2004.

### iv) MSc and PhD theses

#### *MSc completed – 2003*

Semaganda, R. 2003. Augmenting the activity of cassava whitefly parasitoids using sweetpotato as a banker plant for parasitoids. Makerere University, Kampala, Uganda.

Tumuboine, E. 2003. The effect of barriers and mixed cropping on the epidemiology of sweet potato virus disease in Uganda. Makerere University, Kampala, Uganda.

#### *MSc to be completed – 2004*

Ndyetabura, I. Phytosanitation for the management of cassava mosaic disease (CMD) and sweet potato virus disease (SPVD) in the Lake Zone of Tanzania

#### *PhD to be completed – 2004*

Ndunguru, J. Molecular characterization and dynamics of cassava mosaic geminiviruses in Tanzania

Sseruwagi, P. Molecular Variability of Cassava Bemisia tabaci and its Effect on the Epidemiology of Cassava Mosaic Geminiviruses in sub-Saharan Africa