SASHA
Sweetpotato Action for Security and Health in Africa

Yield impact of Sweetpotato Begomoviruses: Are They Significant?

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We established the occurrence and distribution of begomoviruses in Kenya. Field survey was conducted in major sweetpotato growing regions (i.e., Western, Nyanza, Coast, and Eastern). A total of 896 samples were collected and tested by PCR to confirm begomoviruses. One hundred and sixty-seven (167) tested positive from the different regions. Rift Valley had the highest level of infection at 47%, Western – 16 %, Nyanza – 19 %, Coast – 11 %, Eastern – 10 % and Central – 12 %. Two seasons of a field trial using virus tested and virus infected plants of varieties 'Kakamega' and 'Ejumula' were conducted to establish effect of begomoviruses by themselves or in combination with common viruses on yield.

Fig. 1 Sweetpotato field symptom expression on the variety Ejumula. From the top left: 1) rugosity - associated with begomovirus; 2) leaf deformation, reduction, chlorosis, vein clearing associated with SPVD; 3) chlorotic spots – SPCSV and 4) purpling associated with SPFMV (Credit B. Wanjala)

What is the problem?

Virus infections are among the most important constraints of sweetpotato production in Sub-Saharan Africa (SSA). Among the more than 30 described viruses infecting sweetpotato Sweet potato chlorotic stunt virus (SPCSV) and Sweet potato feathery mottle virus (SPFMV) are considered the most wide-spread and devastating. In combination, they cause the sweetpotato virus disease (SPVD), which has been reported throughout SSA. However, begomoviruses have increasingly been recognized as common in sweetpotato worldwide, but there are only limited studies on the yield impacts they may have. Previous studies in the USA have shown that begomoviruses by themselves can cause up to 40% yield loss depending on sweetpotato variety. Other studies have shown co-infections of begomoviruses and SPCSV led to increased begomovirus titers. Nevertheless, begomoviruses often cause no or show only mild symptoms. Thus, there is a necessity to determine the prevalence of begomovirus infections in Africa and their potential yield affects on local sweetpotato cultivars.

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Kenya Plant Health Inspectorate Service

KALRO
Kenya Agricultural & Livestock Research Organization

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Fig. 2 Marketable (top) and Non-marketable (bottom) roots of var. Ejumula infected with SPCSV + begomoviruses (Credit B. Wanjala)

What do we want to achieve?

We would like to establish the genetic diversity of begomoviruses in Kenya. Understanding the occurrence of begomoviruses will contribute towards phytosanitary processes in preventing spread of viruses to new areas. On the other hand, we want to determine the potential impact of begomoviruses on sweetpotato yields in Africa.

Where are we working?

Surveys for detection of begomoviruses and next generation sequencing were performed in sweetpotato growing regions of Kenya and will complement those performed previously in other African countries. Begomovirus yield trials were conducted at the Kiboko station of the Kenya Agricultural and Livestock Research Organization (KALRO) for two seasons to evaluate the impact on yield.

How are we making it happen?

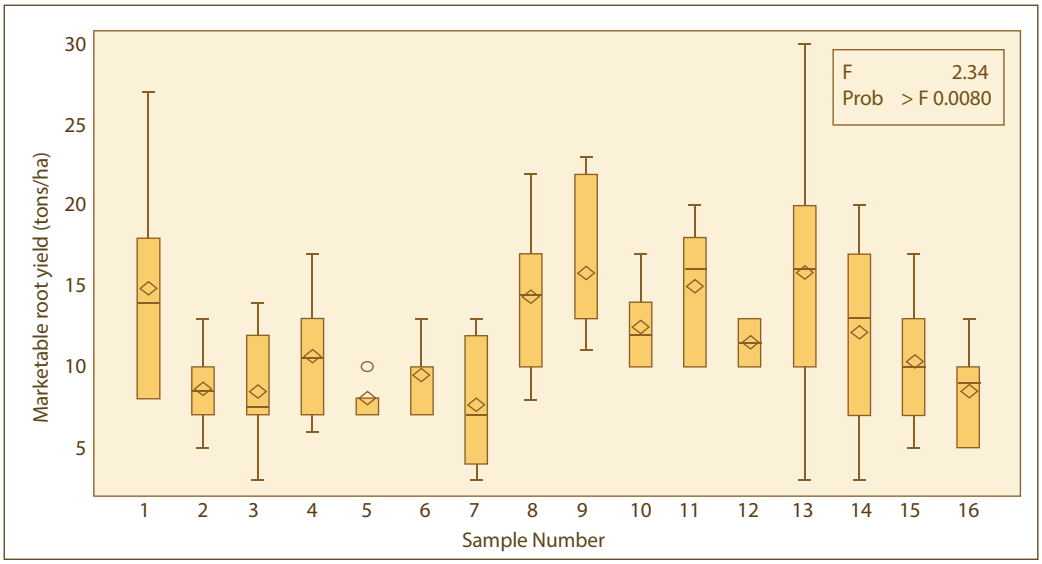
We conducted a survey in Kenya and all samples that tested positive for begomovirus will be sequenced using a generic virus detection method developed at CIP called small RNA sequencing and assembly (sRSA) to determine diversity of begomoviruses in Kenya.

What have we achieved so far?

Leaf samples were collected in sweetpotato growing counties in Kenya. Eight hundred and ninety-six samples were collected and analyzed by PCR. One hundred and sixty-seven samples were identified to be positive (18.6%). On the other hand, two seasons of a field trial using virus-tested and virus-infected (with Begomovirus, sweetpotato feathery mottle virus (SPFMV), and sweetpotato chlorotic stunt virus (SPCSV), alone and in all possible dual combinations) plants of varieties 'Kakamega' (considered moderately virus resistant) and 'Ejumula' (considered virus susceptible) were installed and concluded at Kenya Agricultural and Livestock Research Organization (KALRO)–Kiboko.

Large variations in the trial rendered most of the differences statistically non-significant. However, a trend for reduction in yield was observable in 'Kakamega' when begomoviruses were infecting it which was not evident for 'Ejumula'. Ejumula was much more affected by SPFMV and SPCSV infections (Fig. 3). Infection with SPFMV/SPCSV/begomo had a high number of non-marketable roots. In addition, high above ground biomass did not translate to high root yield.

Fig. 3 Root yield (tons/ha) for the average of two seasons of plants with grafted virus status as indicated for each entry: 1- Negative Control-Ejumula, 2 – SPCSV infected- Ejumula, 3 – SPFMV- Ejumula, 4 - Begomo+SPCSV infected-_Ejumula, 5 - Begomo+SPFMV infected-_Ejumula, 6 - SPVD_Ejumula 7- Begomo+SPVD infected_Ejumula, 8- Begomo infected_Ejumula, 9 Negative Control_Kakamega, 10 - SPCSV_Kakamega, 11- SPFMV_Kakamega, 12 - SPFMV_Kakamega, 13 - Begomo+SPFMV_Kakamega, 14 - SPVD_Kakamega, 15 - Begomo+SPVD_Kakamega and 16 - Begomo_Kakamega



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