

**OCCURRENCE OF CASSAVA MOSAIC GEMINIVIRUSES AND
CASSAVA BROWN STREAK VIRUSES IN CASSAVA AND
WILD PLANT SPECIES IN UGANDA**

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ABSTRACT

Cassava (*Manihot esculenta crantz*) is an important food and cash crop worldwide. Currently cassava brown streak disease (CBSD) caused by Cassava brown streak ipomoviruses (CBSVs) and cassava mosaic disease (CMD) caused by Cassava mosaic geminiviruses (CMGs) are the major constraint to cassava production in East Africa. Occurrence of these viruses in alternative hosts is unknown and therefore potential risk posed to cassava cultivation. A survey was conducted in five agro ecological zones of Uganda, in 24 cassava growing districts to determine plant species that may be alternative hosts for these viral pathogens. Leaf samples plant species with virus-like symptoms found within or adjacent to cassava fields were picked and analyzed.

Overall CBSD mean incidence for the 24 districts was 38.4%. Kayunga district had the highest incidence (100%), while Soroti had the lowest incidence at 4.7% and two districts did not have CBSD. CMD mean incidence was 13.4%, with Busia having the highest incidence at 46% while Kamuli had the lowest incidence at 0.7% and five districts did not have CMD.

Nucleic acids were extracted from both cassava and suspected alternative plants, and tested for CMGs by conventional PCR and CBSVs by two-step RT-PCR and analyzed by agarose gel electrophoresis. Twelve (12) wild plant species were positive for CMGs with nine (9) plants positive with ACMV and three (3) plants positive for EACMV-UG. Ten (10) plants were positive for UCBSV and one (1) was detected with CBSV. PCR products were purified and quantification and Amplicons were sequenced in both directions. All nine ACMV sequences, three EACMV sequences and one CBSV sequence obtained from non-cassava host plants had significant similarities with sequences in the gene bank with sequence having 89–100% nucleotide sequence identity with cassava isolates from East and West Africa. Plant species identification was done for confirmed alternative host plants for CMGs and CBSVs, and plants were identified into seven species namely *Ageratum conyzoides*, *Asystasia gangetica*, *Solanum incanum*, *Leonotis nepetifolia*, *Hewettia sublobata*, *Erythrina abyssinica*, and *M. glaziovii*.

These results provide definitive evidence for the natural occurrence of cassava viruses in plant species besides cassava, acting as reservoirs for the viruses. This therefore demands appropriate measures to safeguard cassava production in Uganda.