The current status of cassava infecting viruses in Kenya: first national survey

ELIJAH ATEKA and FRANCIS MWATUNI

[1]Department of Horticulture, Jomo Kenyatta University of Agriculture and Technology P.O. Box 62000-00200, Nairobi Kenya.
[3]Kenya Plant Health Inspectorate Services, P.O. Box 49592 (0200), Nairobi Kenya.
Email:**eateka@agr.jkuat.ac.ke**

Introduction

Cassava (*Manihot esculenta* Crantz) is a major staple food for many communities in sub-Saharan Africa. In Kenya, cassava is cultivated on over 90,000 ha of land, with an annual production of about 540,000 t. The crop is grown by resource poor farmers for subsistence, and is an important food security crop. While cultivation is concentrated in Nyanza and Western Provinces (60%), cassava is also grown in the Eastern (10%) and Coast Provinces (30%). Despite potential yields of up to 32 t/ ha., production is constrained by cassava mosaic disease (CMD) which reduce cassava yields to between 5 and-10 t/ ha: (Munga, 2000; Were et al., 2004). Cassava mosaic disease (CMD) and Cassava brown streak disease (CBSD) are are endemic in Africa and Asia and often result in yield losses of up to 50%. No detailed information is available about the occurrence and distribution of CBSD in Kenya while information about the strains and distribution of CMD is limited (Were et al., 2004). The objective of this study was to determine the incidence, prevalence and severity of CMD and CBSD in Kenya

Materials and Methods

Survey

A country wide survey was conducted through Eastern, Nyanza, Western and Coast Provinces of Kenya. Fields with pure or intercropped cassava were selected and randomly surveyed at 5 to 10 km intervals along selected routes. In each field, geographic coordinates were recorded using a global positioning system (GPS; Magellan GPS 315, San Dimas, CA).

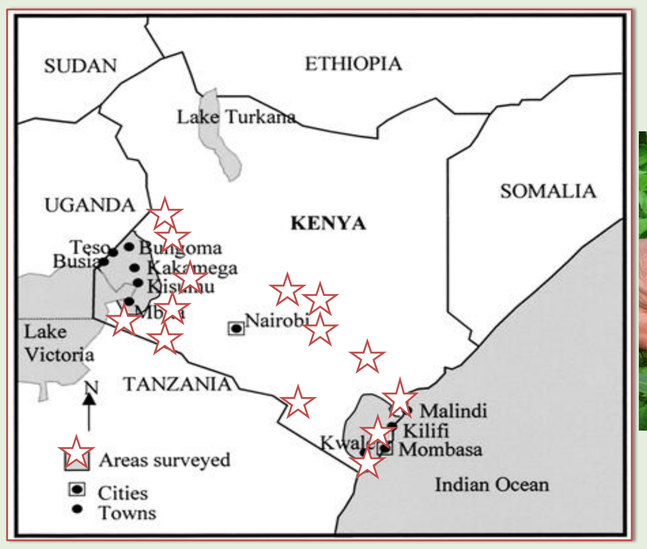

Figure 1. Sites surveyed during the study

Disease and whitefly assessments

Representative plants were sampled along X-shaped transects in each field for determination of disease incidence, severity and whitefly counts (Sseruwagi et al. 2003). Symptoms severity for both diseases was visually scored on a disease severity scale of 1 to 5. Young and tender leaves from plants infected with CMD were picked and preserved in falcon tubes containing silica gel granules.

Nucleic acid extraction and detection of CMV and CBSV

Total nucleic acid (TNA) was extracted from dry leaf samples using CTAB method (Lodhi et al., 1994). Universal primers JSP 001/JSP 002 were used to detect African cassava mosaic virus (ACMV). Polymerase chain reaction (PCR) detection of EACMV was conducted using the primers EAB555/F (5'-TACATCGGCCTTTGAGTCGCATGG-3') and EAB555/R (5'-CTTATTAACGCCTATATAA-ACACC-3').

Detection of CBSV was carried out by reverse transcription (cDNA synthesis) prior to amplification using the primer pair CBCP-F/R (Ndunguru *et al.* 2005), to amplify the coat protein of CBSV.

In all cases, the PCR products were visualized following electrophoresis in 1.5% agarose gels. Representative PCR products of ACMV, EACMV, DNA Satellites and CBSD were sequenced to confirm their identity.

Results

Province	*No.of fields*	*CMD incidence*	*CMD prevalence (%)*	*Whitefly counts*	*CMD severity*
Eastern	23	57.4±0. 3b	78.0±2.0d	1.86±0.16b	3.1±0.3a
Nyanza	26	51.0±0.4d	96.0±2.0a	3.18±0.17a	3.2±0.2a
Western	25	47.0±0.3c	82.0±3.0c	1.16±0.07c	2.7±0.2b
Coast	20	74.0±2.0a	93.0±2.0b	2.99±0.21a	3.4±0.1a
Mean	**94**	**57.35**	**87.25**	**2.2975**	**3.1**

Table 2. CMD incidence, prevalence severity and whitefly population counts

Province	*No.of fields*	*CBSD Incidence (%)*	*CBSD prevalence (%)*	*CBSD severity*	*Whitefly counts*
Eastern	23	0.0 ± 0	0.00	1.0±0b	1.86±0.16b
Nyanza	26	1.54± 1.13b	7.692	1.03±0.01b	3.18±0.17a
Western	25	0.71±0.38b	8.00	1.01±0.01b	1.16±0.07c
Coast	20	33.99±6.56a	80.00	1.64±0.04a	2.99±0.21a
Total/Mean	**94**	**9.06**	**23.923**	**1.17**	**2.2975**

Table 3. CBSD incidence, prevalence severity and whitefly population counts

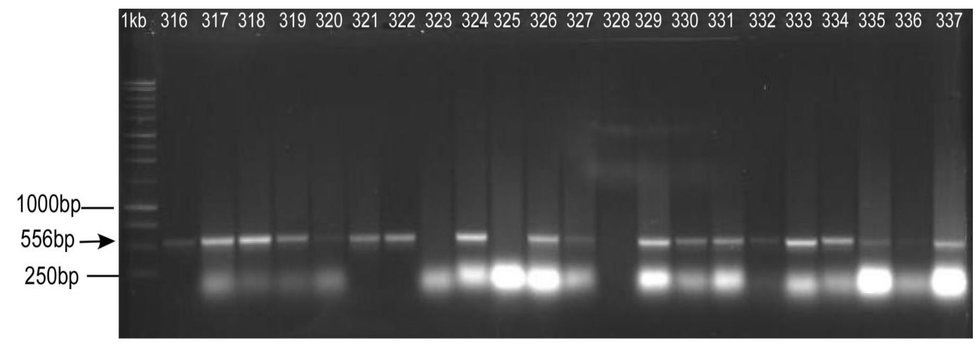

Plate: Amplification of EACMV DNA B component

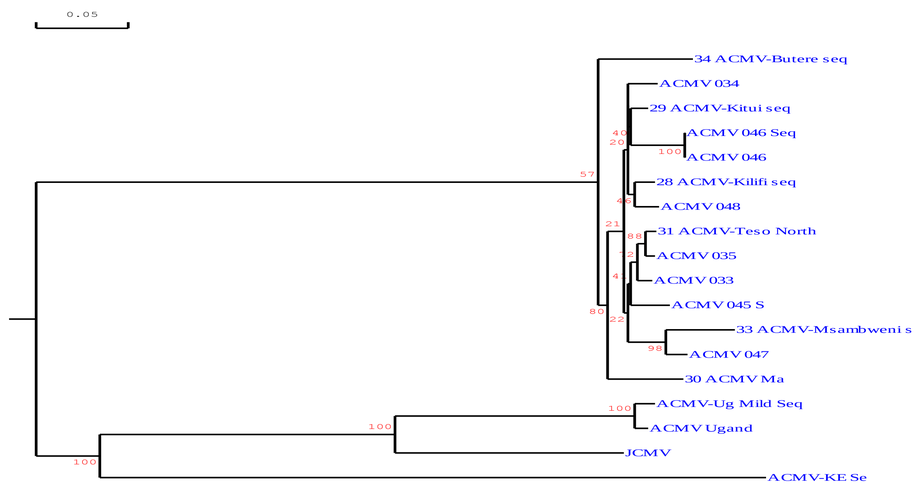

Fig. Phylogenetic tree of ACMV isolate sequences under study

Results and Discussion

This survey of viruses infecting cassava in Kenya was the first national comprehensive study covering all areas where cassava is grown. Cassava Mosaic Disease incidence was observed to be highest in Coast Province. East Africa cassava Mosaic Virus was more widespread than ACMV in the country. EACMV was detected in samples collected from all the provinces and was distributed across the country. Coast Province was, for the first time, confirmed to have the virus. Detection of ACMV in Eastern Province and Coast Province presents a new challenge in the management of CMD in these regions and the county at large. Dual infections of EACMV and ACMV point to the possibility of more severe forms of CMD due to synergism between EACMV an ACMV). CBSV was also observed to be spreading rapidly in the highlands, contradicting the old believe that it is confined to the coastal areas. The characterization of the viruses as well as the identification of varieties resistant or tolerant to these viruses at a national and regional scale is recommended.

Acknowledgements

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