

INCIDENCE AND SEVERITY OF CASSAVA VIRUS DISEASES IN MALAWI

¹Benesi, I.R.M., ¹Theu, M.P.K.J., ¹Mazuma, E.D.L., ²Tairo, F.D, and ²Ndunguru, J

¹ Chitedze Agricultural Research Station, P.O. Box 158, Lilongwe, Malawi,

² Mikocheni Agricultural Research Institute, P.O. Box 6226, Dares Salaam, Tanzania



Introduction

Cassava is the most important root crop, and the second most important staple crop after maize in Malawi. It is grown across the country and is a staple food crop for more that 30% of the people along the central and northern shore areas of Lake Malawi.





Figure 1. Left cassava farmers shares constraints of cassava with experts, right preparation of sima from cassava flour

Its production is greatly constrained by abiotic and biotic constraints. Cassava mosaic disease (CMD) and Cassava brown streak disease (CBSD) are the most damaging biotic constraints of cassava in Malawi.

Comprehensive surveys and subsequently diagnosis of viruses in Malawi have been hindered by inadequate capacity in infrastructure and human resource, which poses a serious threat to production of cassava in Malawi.

This study conducted a countrywide survey and determine the incidence and severity of cassava virus diseases infecting cassava in Malawi.

Materials and Methods

Field surveys

Sixty eight cassava fields were surveyed in 3 regions for incidence and severity of CMD and CBSD between March 2009 and April 2010. Fields were selected at an interval of 10-15-km. In each field, 15 cassava plants along a diagonal were inspected for symptoms of CMD and CBSD, and were scored for severity (2). Adult whitefly (*Bemisia tabacii*) abundance was counted on the 5 youngest apical leaves. CMBs were detected by PCR using degenerate primers EBB556F/R for EACMV, JSP001/002 for ACMV, CP5'/CP3' for SACMV (2) and species specific primers for EACMMV, EACMV and EACMZV

designed from DNA A components of the respective virus species in this study. CBSV and UCBSV were detected by RT-PCR using primer pair (1). Representative PCR products of each virus species were confirmed by direct sequencing.

Results and Discussion

Incidence of CMD and CBSD in Malawi

The most common viral disease observed on cassava in frequency prevalence order was CMD followed by CBSD. CMD was observed in 19(36.6%) of the 52 cassava fields surveyed with mean symptom severity of 3.2, while CBSD was observed in 22 (42%) of the 52 fields in 2 regions with mean symptoms severity of 3.4 (Table 1). However, no CBSD symptoms were observed in the fields surveyed in southern region. Fields in the central region had the highest CMD incidence of 45.3% followed by southern (40.8%) and northern region had the least CMD (23.8%) (Table 1 and Figure 2 A&B).



| Region | No. of Fields | CN | /ID | CBS | D | No. of adult | |
|----------|------------------|------------|------------|------------|--------------|----------------------|--|
| | | Incid. (%) | Sev. (1-5) | Incid. (%) | Sev (1-5) | whiteflies/ plant | |
| Northern | 17 | 23.8 | 3.2 | 54.8 | 3.0 | 1.7 | |
| Central | 23 | 45.3 | 3.3 | 29.2 | 3.9 | 3.1 | |
| Southern | 12 | 40.8 | 3.1 | 0 | 1 | 1.6 | |
| Mean | | 36.6 | 3.2 | 42.0 | 3.4 | 2.2 | |

PCR and RT-PCR analysis for CMD and CBSD

Of the 240 leaf samples collected, 150 (62.5%) tested positive at least to one of the 4 specific primers used for CMBs detection. Ninety (37.5%) samples tested negative to all 4 primers. Twenty five (16.7%) of the 150 positive samples were co-infected with more than one virus species, EACMMV+EACMCV, EACMCV+EACMZV, EACMMV+EACMZV and EACMMV+EACMZV (Table 2). RT-PCR showed 24(75%) of the 32 samples had single infection of UCBSV while 4 (12.5%) samples had dual infection of CBSV and UCBSV (Table 2). No PCR product was produced on 4 (12.5%) samples, which were apparent healthy symptomless plants. Sequence comparison of the representatives virus species for CMBs and CBSV were similar to the corresponding *spp* in the databank (EMBL)

| | PCR/RT-PCR | | | | | | | | | | |
|---------|------------|--------|--------|--------|---------------------------|------------|---------------------------|-------|------|-------------|------------------------|
| REG-ONS | EACMV | EACMS> | EACMCV | EACMZV | EACM MV +EACM CV | V +EACM | EACMM V +EACM ZV | +EACM | CBSV | C B S | CBS V +UC BSV |
| North | 7/46 | 1/46 | 18/46 | 3/46 | 2/46 | 2/46 | 0/46 | 1/46 | 0/20 | 14/20 | 4/20 |
| Central | 31/119 | 22/119 | 10/119 | 2/119 | 8/119 | 5/119 | 4/119 | 3/119 | 0/12 | 10/12 | 0/12 |
| South | 10/75 | 21/75 | 0/75 | 0/75 | 0/75 | 0/75 | 0/75 | 0/75 | - | - | - |
| Total | 48/240 | 44/240 | 28/240 | 5/240 | 10/240 | 7/240 | 4/240 | 4/240 | 0/32 | 24/32 | 4/32 |



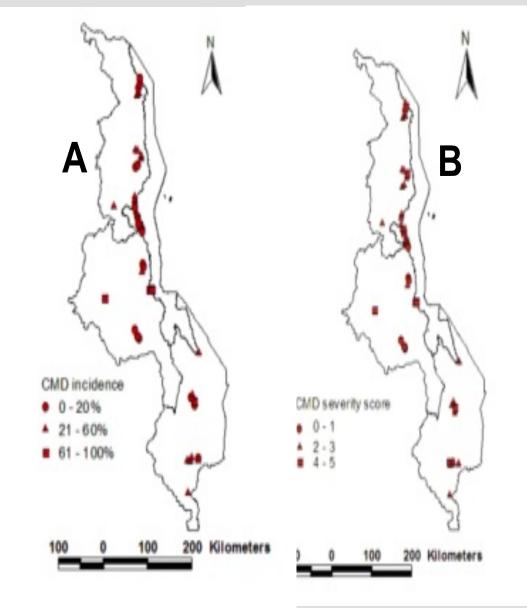


Figure 2. Maps of Malawi showing: A) Incidence and B. Severity for CMD

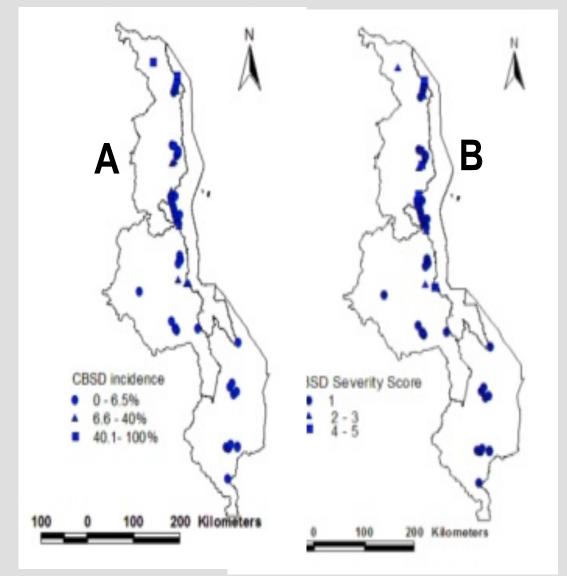


Figure 3. Maps of Malawi showing: A) Incidence and B. Severity for CBSD

Whitefly abundance

Abundance of whitefly/ plant/ region ranged from 1.7 to 3.1, with an overall average of 2.2 (Table 1). The highest number recorded per plant was in Central region. No correlation was observed between whitefly abundance and CMD and CBSD incidence.

Discussion

Incidence and severity for CMD and CBSD varied with northern and central regions having higher incidences than southern region. Six viruses EACMV, EACMMV, EACMCV, EACMZV and UCBSV were the most prevalent in cassava fields in Malawi. The prevalence of CMD and CBSD in Malawi is mostly due to recycling of virus-infected planting materials.

This report provides comprehensive information on the status of incidence, disease symptom severity and occurrence of viruses infecting cassava in Malawi. This information is important for the formulation of disease management strategies. With the generated viruses and disease prevalence maps, one can determine the areas to concentrate in distributing clean planting materials and intensify preventive measures to halt further spread of CMD and CBSD.

References

- 1. Mbanzibwa, D. R., Tian Y. P., Tugume, A. K., Mukasa, S. B., Tairo, F., Kyamanywa, S., Kullaya, A and Valkonen, J. P. T. (2010). Simultaneous virus-specific detection of the two cassava brown streak-associated viruses by RT-PCR reveals wide distribution in East Africa; mixed infections; and infections in *Manihot glaziovii*. J Virol Methods.171: 394-400
- 2. Ogbe, F., Dixon, A.G.O, Hughes, J. d'A., Alabi, O.J., and Okechukwu, R (2006). Status of Cassava Begomoviruses and their new natural hosts in Nigeria. Plant Dis 90:548-553
- 3. Zhou, X., Y. Liu, L. Calvert, C. Munoz, G.W. Otim-Nape, D.J. Robinson, and B.D. Harrison. (1997). Evidence that DNA-A of a geminivirus associated with severe cassava mosaic disease in Uganda has arisen by interspecific recombination. J Gen Virol 78: 2101–2111.

ACKNOWLEDGEMENT: This study was supported by the regional cassava diagnostic project funded by the Bill and Melinda Gates Foundation through Mikocheni Agricultural Research Institute (MARI)