**Abstract**

Cassava mosaic begomoviruses (CMBs) are a major threat to cassava production in Kenya. Management of these viruses is constrained by rapid spread by their insect vector, *Bemisia tabaci*, and by movement of infected planting materials. From June through September of 2015, a survey was carried out in major cassava growing areas of Kenya to investigate the diversity and distribution of CMBs. A total of 250 samples were collected from symptomatic plants and tested for the presence of known begomoviruses in Africa using CMB species-specific primers. Results revealed exceptional diversity among the begomoviruses. We report the first detection of *East African cassava mosaic Cameroon virus* (EACMCV) in 7.6% of the samples tested. The other begomoviruses detected were *African cassava mosaic virus* (ACMV*)*, *East African cassava mosaic virus* (EACMV), *East African cassava mosaic virus-Uganda variant* (EACMV-Ug), *East African cassava mosaic Kenya virus* (EACMKV), and *East African cassava mosaic Zanzibar virus* (EACMZV). Mixed infection was a common occurrence, with up to six begomoviruses detected in a single plant. We also found that viruses previously detected in specific geographical locations have since spread to new locations: EACMZV, which was initially found only in the coastal region, was found in all the major cassava growing areas in Kenya and was the most prevalent begomovirus there, with infections in 66.8% of the samples tested. The geographical overlap of CMB species, the emergence of EACMCV and the high level of co-infection of CMBs increase the size and diversity of the viral gene pool and raise concerns of recombination and synergism. Our findings highlight the importance of screening and controlling the movement of planting materials. We recommend further work aimed at understanding the biological and epidemiological implications of the increased begomovirus diversity and the high level of co-infection in Kenya.

**Keywords**: Geminivirus, Co-infection, CMBs, EACMC

**Introduction**

Cassava mosaic disease is a viral disease affecting cassava production in Sub-Saharan Africa (SSA), where cassava is the staple root crop (Patil & Fauquet, 2009). This disease is caused by a group of viruses referred to as cassava mosaic begomoviruses (CMBs) in family *Geminiviridae*, genus *Begomovirus* (Legg & Fauquet, 2004; Patil & Fauquet, 2009). In Africa alone, nine CMB species have been identified: *African cassava mosaic virus* (ACMV)*, East African cassava mosaic virus* (EACMV)*, East African cassava mosaic Zanzibar virus* (EACMZV)*, East African cassava mosaic Kenya virus* (EACMKV)*, East African cassava mosaic Malawi virus* (EACMMV)*, East African cassava mosaic virus Cameroon virus* (EACMCV) *, South African cassava mosaic virus* (SACMV)*, cassava mosaic Madagascar virus* (CMMGV)*,* and *African cassava mosaic Burkina Faso virus* (ACMBFV) (Legg et al., 2014).

In Kenya, previous surveys have identified four CMB species: ACMV, EACMZV, EACMKV and EACMV (Bull et al., 2006; Were et al., 2007). Based on those studies, these viruses appeared to be geographically localized, which was attributed to a large expanse of non-cassava cultivated land separating the cassava growing regions (Bull et al., 2006). Previous studies in Kenya have reported mixed infection only of ACMV and EACMV. Mixed infection with multiple CMBs occurs where there is geographical overlap of the species (Pita et al., 2001; Harimalala et al., 2015).

Begomoviruses have a high rate of recombination resulting in new species and new variants; therefore, diversity and mixed infection are of great concern (Fondong et al., 2000; Pita et al., 2001; García-Andrés et al., 2007). Current information on virus diversity, geographical distribution and co-infection is vital in keeping track of emerging CMBs. This study involved a survey carried out in major cassava growing areas in 2015 to determine the status of CMBs in Kenya. One begomovirus previously unreported in Kenya is documented, as is the delocalized distribution of CMBs. This information will provide a baseline for recombination studies and for deployment of CMD resistant cassava and other management strategies.

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**Discussion**

We conducted a countrywide survey in 2015 to determine the status of CMBs in the major cassava growing areas in Kenya. The study revealed the presence of *East African cassava mosaic Cameroon virus* (EACMCV), a CMB species previously unreported in the country, in three regions (***Figure 3***) (Bull et al., 2006; Obiero et al., 2007; Mwatuni et al., 2015). The study also revealed geographical overlap of CMB species in all four major cassava growing areas in Kenya. We observed the highest percentage (72.4%) of co-infection with multiple CMBs ever reported in the country or, to our knowledge, in other parts of Africa (Harimalala et al., 2015; Mwatuni et al., 2015).

 In addition to EACMCV, this study also confirmed the presence of ACMV, EACMV, EACMKV, EACMZV and EACMV-Ug, which have all previously been reported in Kenya. But unlike other studies where they reported distinct geographical localization of the various CMB species, the study found that all the CMB species were found in the major cassava growing areas with the exception of EACMKV and EACMCV **Figure 3** (Were et al., 2003; Bull et al., 2006; Mwatuni et al., 2015;). The geographical overlap of these viruses in this survey is likely associated with the unchecked movement of infected planting materials.