

Abstract

Cassava mosaic Begomoviruses (CMBs) and cassava brown streak viruses (CBSVs) respectively cause cassava mosaic disease (CMD) and cassava brown streak disease (CBSD). Transmitted by whitefly vector (*Bemisia tabaci*), both diseases significantly inhibit cassava production in Kenya. This study examined the prevalence and distribution of CMD and CBSD in different agroecological zones (AEZ) of lower Eastern Kenya through a multi-stage sampling survey. Sampling involved stopping at regular pre-determined intervals of about 15 to 20km between farmers' fields along transect in each zone. Thirty plants were randomly sampled along diagonals of each field to determine both disease incidences. General results revealed 73% CMD and 53% CBSD prevalence in lower Eastern Kenya. Specifically, both disease incidences were high in LM4 (68% CMD and 26% CBSD), followed by UM4 (55% CMD and 19% CBSD) and least in LM5 (30% CMD and 8% CBSD). Whitefly (*Bemisia tabaci*) infestation significantly and positively correlated with CMD and CBSD incidences further indicating considerable contribution of the vector in spreading both diseases. Molecular diagnostics performed on leaves of randomly selected plants detected ACMV that cause CMD and CBSV that causes CBSD. High distribution of CBSD and CMD in lower Eastern Kenya as assessed in this study could potentially be integrated in future CMD and CBSD resistance breeding or virus management programs within the region.