

Abstract

Cassava (*Manihot esculenta* Crantz) is one of the most cultivated tuberous crops as a sustainable source of food security and family income among the poor in the developing world. Despite this economic significance, cassava's tuber yield is significantly reduced by viral diseases and pests among them cassava mosaic disease (CMD), cassava brown streak disease (CBSD) and cassava green mites (CGM). CMD and CBSD are respectively caused by cassava mosaic begomoviruses (CMBs) and cassava brown streak viruses (CBSVs) which often result in 100% yield losses in susceptible cultivars. Through a field-based randomized complete block designed experiment, the present study screened fifteen cassava genotypes sourced from different breeding programs and local landraces in Kenya for resistance against CMD, CBSD and CGM. Genotypic differences for either diseases incidence (INC) or severity (SVY) and marketable root yield (MRY) was significant ($P \leq 0.05$). Both disease and pest incidences were generally low (0-15%) indicating potential suppression. Genotypes were grouped into disease tolerant (DT) and disease susceptible (DS) classes with significantly higher MRY of 23.8 t/ha bulked by a DT genotype TME-419 and least MRY of 2.1 t/ha recorded in a DS cultivar Thika2. The negative correlation observed between MRY and both disease incidence and severity indicated the inhibitory role of CMD and CBSD on cassava production. Molecular diagnostics two CMB species, African cassava mosaic virus (ACMV) and East Africa cassava mosaic virus (EACMV) and CBSVs in some tolerant and all susceptible genotypes. Four (990005, TC4, TC14 & TME419) high yielding and DT cassava genotypes identified in the current study could potentially be used as parents in future breeding programs for introgression of tolerance traits in farmer preferred but susceptible local landraces.