

Abstract

Cassava brown streak disease (CBSD) is caused by two cassava brown streak viruses (CBSVs) transmitted by whiteflies (*Bemisia tabaci*). CBSD significantly inhibits cassava production in Kenya through losses of up to 100% in farmer-preferred but susceptible varieties. As a management strategy, the present study evaluated the effect of CBSD on two local varieties (Thika-5 & Serere) and 15 improved genotypes in lower Eastern Kenya. Between October 2016 and June 2017, the genotypes were infected with CBSVs through whitefly transmission under field experiment at SEKU research farm (1.31°S, 37.75°E) and chip-bud grafting at KALRO-Katumani (1.35°S, 37.14°S) greenhouse conditions. RCBD and CRD experimental designs were respectively applied in field and greenhouse assays. CBSD symptoms were quantified through disease incidence (DIC) and severity (DSY) every 3 months for the field experiment and weekly for greenhouse assay. At harvest, storage root necrosis (SRN) was scored and non-necrotic roots weighed as marketable root yield (MRY). Molecular diagnostics was accomplished through duplex RT-PCR. Results revealed significantly ($P \leq 0.01$) higher foliar field DIC (81- 100%) and SRN (2.3 – 5.0) recorded in Thika-5 and Serere compared to all the improved genotypes that were foliarly asymptomatic (0% DIC and mean SRN of 1.0). Concomitantly and substantially lower ($P \leq 0.01$) MRY (1.99 – 2.16 t/ha) were bulked by Thika-5 and Serere compared to 10 improved genotypes that bulked 5.81 – 9.21 t/ha MRY. Upon chip-bud graft infection, Thika-5 and Serere showed higher DIC of 81 – 90% compared to four improved genotypes with 20 - 35% DIC. Correlations between MRY, DIC and SRN were inverse and significant ($P \leq 0.01$). RT-PCR detected pre-dominantly CBSV. In conclusion, the natural whitefly-based transmission of CBSVs was ineffective compared to chip-bud grafting. The inverse correlations between CBSD symptoms and yield corroborated the deleterious impact of CBSD on cassava production. The ten improved, high yielding and asymptomatic genotypes identified in the current study could potentially be used to confer resistance against CBSD into farmer-preferred but often sensitive varieties.