

**Analysis of the interaction between cassava brown streak ipomoviruses and selected cassava varieties in Tanzania**

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Cassava (*Manihot esculenta* Crantz) is an important staple food crop in sub-Saharan Africa, but its production is adversely hampered by viral diseases. The most important is cassava brown streak disease (CBSD) caused by cassava brown streak ipomoviruses (CBSIs) {Genus *Ipomovirus*, family, *Potyviridae*; cassava brown streak virus (CBSV) and Ugandan cassava brown streak virus (UCBSV). CBSD causes significant yield losses in East and Central Africa. This study aimed at analysing the interaction between CBSIs and their cassava host under diverse agro-ecological conditions and CBSD pressure in Tanzania to contribute to CBSD management strategies. In this study, (1) a protocol for absolute quantification of CBSIs was optimized and validated (2) The genetic diversity of CBSIs and virus titre were determined in selected cassava varieties (3) cassava degeneration due to recycling of planting material was assessed under high CBSIs inoculum condition in Bagamoyo, Tanzania during the short (vuli) and long (masika) rainy season (4) The response of elite cassava varieties to CBSIs under diverse agro-ecological environments in Tanzania was evaluated. Varieties differed significantly in virus titre whereas higher virus titres were observed in root than in leaves. Younger crops (2MAP) had higher virus titre in leaves than old crops (12MAP). CBSIs were equally distributed across agro-ecological sites. Significantly higher, *B. tabaci* abundance, CBSD incidences and reduction in root yield were observed in Vuli than in Masika suggesting higher degeneration rates in the vuli. Cassava varieties responded significantly different across agro-ecological zones with the greatest impacts of CBSD in north-western Tanzania. Results of this study will be useful in informing breeding strategies. Evaluating cassava for release and in commercial seed production in designing new cassava.