ABSTRACT

Climate change (CC) is widely regarded as a threat to food security in Sub-Saharan Africa (SSA), with some studies linking its impact on African agriculture with the specificities of small scale livelihoods that require robust crops for different agro-ecologies in the region. Cassava (*Manihot esculenta* Crantz) is a clonally propagated crop in the tropics cultivated for its adaptability to diverse climate conditions. It serves as a staple food and livelihood for more than 800 million people worldwide. In spite of its importance as a food security crop in SSA, cassava production has long been faced with major constraints: the spread of cassava brown streak disease (CBSD) which is manifested as a corky necrosis in the storage root caused by either of two virus species, cassava brown streak virus (CBSV) and Ugandan cassava brown streak virus (UCBSV). It is also threatened by severe incidences of cassava mosaic disease (CMD) caused by six virus of genus begomovirus. The combined effect of these viruses leads to 100% yield loss in susceptible varieties. The lack of clean planting materials, slow rate of multiplication of cultivars and slow adoption rate of introduced improved cassava varieties that are considered to be low in genetic variability compared to the local FPVs hence limiting its expansion and utilization on large scale. Generation of genetic diversity in FPVs is fundamentally important in enhancing the potential of cassava in meeting the demands of end user and the changing climate. The management of this cassava economic diseases is currently only by phytosanitary improvement of the local preferred varieties through resistance breeding. This study however, proposes to screen for CBSVs and CMD, determine efficacy of different *in vitro* technologies for virus cleaning and determine the combined viruses' tolerance introgression and identity of Filial 1 (F1's) progeny generated from cassava parental crosses.

These will be achieved through field agronomic assessment, virus screening by conventional PCR and RT-PCR; meristem tip excision thermo- and chemotherapy technologies for virus cleaning and authentication of the F1 progeny obtained from cassava parental crosses will be confirmed by simple sequence repeats (SSRs) markers from cassava and capillary electrophoresis. The outcome will be development of cleaned, improved FPVs and increased adoption hence increased cassava productivity in Kenya, and beyond.

Key words: cassava, CC, diseases, SSRs, RT-PCR