Abstract/Description

Cassava is a crucial food crop in the western region of Kenya, producing 60% of the country's production. It is mainly grown by small-scale farmers for subsistence use, with any surplus being sold. Many cassava landraces from the western region have been seriously affected by two viral diseases, cassava mosaic disease (CMD) and cassava brown streak disease (CBSD) but have not been conserved, together with associated farmer knowledge, in national or international germplasm repositories. This study aimed at collecting landraces and associated farmers' knowledge, identifying collected cultivars and determining their genetic diversity. In addition, the incidence and distribution of CMD and CBSD was determined. A collection mission was undertaken covering five counties of western Kenya; Kakamega, Bungoma, Busia, Migori and Homabay. A total of 256 cassava samples were collected from 203 households. In addition, leaf samples were taken from 210 perceived improved varieties and genotyped with the landraces using DArTSeq to confirm whether any of the landraces were infact improved varieties. Stakes from the collected landraces were established in the glasshouse for sprouting and subsequent virus indexing. Molecular diagnostics revealed that 60.5% of collected samples were CMD positive with 33.2% of these being East African Cassava Mosaic Virus and 27.3% being African Cassava Mosaic Virus, and 22.7% were CBSD positive with 12.1% being Cassava Brown Streak Virus and 10.6% being Ugandan Cassava Brown Streak Virus. Interestingly CMD causing viruses were found in all the counties but CBSD-associated viruses were not detected in Kakamega or Bungoma counties. Dual infection of the CMD and CBSD-causing viruses were also found on collected cassava landraces from Busia, Homabay and Migori. These results confirm the urgent need for deployment of varieties with dual resistance to CMD and CBSD. Key informant interviews highlight the importance of cooking as well as eating properties of cassava and yield and time to maturity amongst other characteristics. A total of 57 unique genotypes (39 landraces and 18 improved varieties) were identified. Cassava germplasm from western Kenya was found to have low genetic variability, and this, coupled with the incidences of CMD and CBSD emphasizes the urgent development and deployment of varieties with dual virus resistance. Farmer and consumer preferences should be used to inform priority traits in cassava breeding programmes for the region.