CHARACTERIZATION AND SELECTION OF KENYAN SWEET POTATO (*Ipomoea batatas* L.) GENOTYPES FOR SWEET POTATO VIRUS DISEASE RESISTANCE AND HIGH DRY MATTER

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ABSTRACT

Sweet potato virus disease (SPVD) is a major constraint to sweet potato production in Kenya. In addition to SPVD, low production of sweet potato in Kenya is also due to lack of cultivars with consumer quality attributes such as high dry matter content. Use of resistant cultivars is the most effective means of controlling the disease. This study aimed at characterizing Kenyan sweet potato genotypes for SPVD resistance and high dry matter content using morphological and simple sequence repeat (SSR) markers. A total of 314 genotypes were collected, established in a screenhouse and evaluated for their reaction to SPVD using symptom severity. Severity of SPVD in each genotype was determined using a scale of 1-5; where 1= no symptoms and 5=very severe symptoms. Serological assays were done on 89 genotypes with a symptom severity score of between 1.00 and 1.50. Analysis of variance of the symptom severity scores showed that the genotypes responded differently ($P < 0.001$) to SPVD in the screenhouse. Twenty genotypes tested negative for both SPFMV and SPCSV and were considered resistant/tolerant to SPVD.

Three hundred and fourteen genotypes were planted in the field and characterized using 42 morphological traits based on the CIP Research Guide 36 followed by cluster analyses of the scored traits using unweighted pair group method with arithmetic means (UPGMA). Tuber dry matter content was determined 5 months after planting in the field. Phylogenetic analysis using morphological descriptors grouped the genotypes into two major clusters. None of the clusters clearly distinguished the 20 resistant genotypes from the 294 susceptible ones. The tuber dry matter content significantly ($P<0.001$) varied among the sweet potato genotypes. Genotypes with highest and lowest tuber dry matter content were not distinguished from each other using UPGMA phenogram generated. This indicates that morphological markers are not reliable in

identifying and classifying sweet potato genotypes into phenotypic groups based on their resistance to SPVD and high dry matter. Therefore, morphological markers supplemented with molecular markers need to be investigated for their potential application in identification of sweet potato genotypes with SPVD resistance and high dry matter content.

Eighty nine sweet potato genotypes were selected following graft inoculation with SPVD-infected scions and characterized using 6 SSR primer pairs. The amplified DNA fragments were screened by capillary electrophoresis on the ABI 3730 genetic analyzer and analysed using the Genemapper v3.7 software. Cluster and principal component analysis (PCA) were done using NTSYS-pc version 2.11T. Six primer pairs were highly polymorphic among the genotypes and polymorphic information content (PIC) varied from 0.33 to 0.81 with an average of 0.47. The number of alleles within the 89 genotypes across the 6 loci ranged from 10 to 17, with an average of 13.52. Cluster analyses showed Jaccard's coefficient from 0.5 to 1, with an average of 0.75 accounting for 50% variation among the 89 genotypes. The phylogenetic and PCA analysis clustered 89 genotypes into 2 main clusters and 5 subclusters. The dendrogram did not reveal any unique clustering of the sweet potato genotypes according to dry matter content or reaction to SPVD. The genetic differences among the SPVD resistant and high dry matter content genotypes revealed by the clustering into distinct groups suggest the presence of different sources of resistance to SPVD and high dry matter. This study therefore indicates that there is a high level of genetic diversity in sweet potato genotypes that are SPVD resistant and have high dry matter. These genotypes can be used as parents in breeding programmes aimed at improving the crop for the two traits.