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ABSTRACT

Genetic diversity of 89 sweet potato genotypes was evaluated using morphological and molecular markers. Eighteen aerial and sixteen storage root characters were used in the morphological characterization. Analysis of variance showed that all the characters evaluated were significantly different ($P<0.01$) between the genotypes. The dendrogram obtained using phenotypic characters separated the genotypes into two major clusters with a Euclidean distance ranging from 0.0 to 6.98. Twenty three unique alleles, ranging from 3 to 6 per locus were detected using six simple sequence repeats (SSR) markers. Cluster analysis showed a Jaccard co-efficient ranging from 0.5 to 1.0 indicating high genetic diversity. Comparison between morphological and molecular data using the mantel test revealed a low correlation ($r = -0.05$) between the two data sets. Despite the poor correlation both techniques showed a high degree of variation among the genotypes suggesting great genetic diversity in Kenyan sweet potato genotypes that can be utilized in breeding programs.

Key Words: Genetic diversity; SSR markers; Morphological characters; Sweet potato; Cluster analysis