

## ABSTRACT

This study was undertaken as a preliminary step in determining genetic diversity of naturalized pumpkins in Kenya. It entailed allelic patterns, frequency, inbreeding coefficient, molecular variance, cluster and inter-population genetic analyses. It utilized 96 pumpkin accessions and five fluorescent SSR markers in capillary electrophoresis. Data were captured using ABI 3730 software, and analyzed using GeneMapper V 4.1 software. Measures of genetic variability were determined using GenAlEx 6.5, genetic diversity within and among accessions using Power Marker V 3.25 and data contained in the electrophenograms by GeneMapper V 4.1 software. XLstat 2014 was used for cluster and GenAlEx 6.5 software for principal coordinates analyses. DNA quantity ranged from 62.7 to 2992 ng/ $\mu$ l and quality from 0.56 to 2.1 of 260/280 absorbance ratio. Fluorescent SSR markers detected 23 alleles with an average of 4.6 alleles per marker, with size ranging from 181 to 326 bp. A total of 934 distinct DNA fragments were identified. Mean PIC was 0.49, observed heterozygosity 0.5048, genotype number 6.8, gene diversity 0.5491, and polymorphism 98.5% across the markers. Mean allelic patterns showed great variation among the accessions. Cluster and principal coordinate analysis revealed distinct accession groups independent of their geographic origin. AMOVA indicated that genetic differentiation was significant ( $P=0.02$ ). Total molecular diversity of 3% was attributed to regional differences, 9% to accession differences within regions, while 88% to differences within accessions. The  $F_{ST}$  of 0.026 indicated very little genetic differentiation due to continuous selection of pumpkin seeds by farmers. The present study proved that fluorescent SSR markers and capillary electrophoresis are effective in estimating genetic diversity and detecting polymorphisms present in pumpkin accessions in Kenya. The genetic diversity should be related with desirable quantitative and qualitative traits and used in improving pumpkin into commercial cultivars. The KK-3 and KK-56 accessions with unique, private and locally common alleles should be prioritised during conservation efforts.