MULTIPLICATION, CONSERVATION AND GENETIC CHARACTERIZATION OF SELECTED MACADAMIA GERMPLASM IN KENYA

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ABSTRACT

Macadamia tree is a low-input crop with high returns per unit area and hence has high potential in poverty reduction and wealth creation. However, the genetic diversity of Macadamia germplasm in Kenya is not yet known. Multiplication rates are low and existing information on ecological adaptation is limited. Hence, the rate of breeding and expansion is not commensurate with existing potential and demand.

Four main studies were carried out. The first study tested the response of 39 accessions to cuttings, grafting and tissue culture propagation methods, for multiplication and subsequent ex situ conservation of Macadamia germplasm. Shoot regeneration from M. integrifolia was achieved at a rate of eight shoots per explant, using single nodal explants cultured on half strength MS medium supplemented with 2.0 mg/L BAP, 1 mg/L IBA and 30 g/L sucrose and gelled will 9 g/L Biotec_ agar (pH 5.7). With the development of rooting procedures, a complete protocol will be available for multiplication and in vitro ex situ conservation of Macadamia germplasm in Kenya.

In the second study, analysis of 39 GPS data points using ArcView GIS 3.3 mapped the accessions on to six major agro-ecological zones; UM1, UM2, UM3, UM4, LH1 and UHO. All accessions except five were mapped on Nitosols.

Distribution of Macadamia in relation to soils was established, and coupled with the information on agro-ecological zoning, breeders have the opportunity for selection and breeding to expand Macadamia acreages.

In the third study, the accessions were assessed for morphological diversity based on a set of standard qualitative and quantitative characters of leaf, fruit and flower. Phylogenetic analysis based on UPGMA for leaf traits using XLSTAT (2009) grouped the accessions into three major

clusters corresponding to M. tetraphylla, M. integrilfolia, and their hybrids. The highest morphological diversity, 81.57, was between M. tetraphylla and M. integrilfolia. After principle component analysis, PC1 was effective in grouping the accessions in to three clusters consistent with phylogenetic analysis. This indicates that leaf traits in Macadamia can be used fro quick classification by breeders in the field.

The fourth study analyzed the genetic diversity of 26 out of the 39 accessions using six AFLP primer combinations. The 26 accessions were from five populations Bob Harries, Thika, Kirinyaga, Embu, and Meru. Genetic diversity analysis using GenAlEx version 6.2 revealed that Bob Harries was the most genetically diverse with the highest percentage of polymorphic loci of 80% and highest mean heterozygosity, He of 0.295 while Thika population had the least diversity of 67.3 % of polymorphic loci and He of 0.224. The Embu population was distantly related to all the population and it contained a private allele, making it unique and worth for breedingand conservation. Phylogenetic analysis using TFPGA distributed the 26 accessions in to four clusters and exhibited a highly hybridized germplasm. The AFLP markers were found to be very effective in genetic characterization of Macadamia and provided sufficient information that can immediately be used by breeders for effective sampling for selection, hybrid variety development and conservation. This study reveals existence of high genetic diversity in Macadamia germplasm in Kenya that is widely adapted. The germplasm should be vegetatively propagated by grafting for ex situ conservation before finalization of a tissue culture protocol, for breeding purposes.