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**GENOMIC CHARACTERIZATION OF MOUNT KENYA
LOCAL BANANA (*Musa spp.*) GERMPLASM**

BY

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ABSTRACT

East African Highland banana is believed to be unique from any other banana elsewhere in the world and its diversity has increased with time due to somatic mutation. Traditionally, morphological and agronomic traits have been used in bananas as a measure of genetic diversity. Banana is a heterogeneous plant with many overlapping morphological, biochemical and physiological attributes which are influenced by environmental factors and show a continuous variation. In Kenya, the farming communities complicate the matter even further by conferring many local names for the same cultivar making it harder to collect, identify and classify banana cultivars while avoiding duplication.

To overcome many of these phenotypic constraints, there was need to come up with a better and a more reliable method of genotypic banana classification. AFLP markers were chosen for this study because of their robustness, reliability and reproducibility, and because no knowledge of DNA sequence was required before it could be used. The aim of the study was to characterize popular Kenyan banana accessions collected from Mount Kenya region using amplified fragment length polymorphism (AFLP) markers and determine their genetic relationships with the reference cultivars.

Suckers of thirty-four popular local banana cultivars were collected and planted at Kenya Agricultural Research Institute (KARI) Katumani. The reference cultivars were obtained from INIBAP Belgium. The DNA was extracted using CTAB method and amplified by a PCR. The fragments were analysed by denaturing polyacrylamide gel electrophoresis using an automated 377XL DNA sequencer (Applied Biosystems). Data was collected and analyzed using GeneScan version 3.0 and Genotyper version 2.1, respectively, and genetic relatedness calculated using the Analysis of Molecular Variance (AMOVA).

Ten fluorescently labeled primers were combined in 12 different combinations. Out of these, 16.7% failed to produce scorable bands. The Neighbour Joining and Unrooted Tree dendrograms produced, grouped local cultivars together but separate from the reference cultivars. Reference cultivar *poyo* (AAA genome) was grouped together with 94% of the local cultivars implying that these cultivars had a 'AAA' genome. This confirmed results of other earlier studies, which report that most of East African Highland bananas have 'AAA' genome. The remaining 6% were grouped with *kelong mekintu* an 'AAB' genome, suggesting they might have this genome. The 34 local cultivars were separated according to their geographical and ecological distribution as well as genomic constitution.

The many sub-clusters exhibited by the dendrograms could be due to genetic variability within the local germplasm arising from mutation over time since bananas are clonally propagated. This technique can be used to determine the banana diversity not only in Kenya but to all the East African highland bananas and the germplasm can be conserved without duplication. It can also be used in fingerprinting to detect somaclonal variation during *in vitro* propagation.