ANALYSIS OF GENETIC HOMOGENEITY AND PROXIMATE COMPOSITION OF COCONUT DERIVED THROUGH MICROPROPAGATION

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Micropropagation of coconut (*Cocos nucifera* L.) plays an important role in mass propagation of homogenous plantlets. Occurrence of somaclonal variation is one of the major drawbacks related to *in vitro* culturing of plants. The objective of this study was to evaluate the micropropagated coconut plants for somaclonal variation and to determine suitability of the protocol developed for micropropagation of coconut. Genetic fidelity, proximate composition and fruit components were evaluated in this study. Sixteen Micropropagated coconut plants of three clones (clone 01, 02 and 03) of the same variety (CRIC 65) were selected for the extraction of genomic DNA. DNA was extracted from coconut spear leaves, using CTAB method and subjected to PCR based Simple Sequence Repeat (SSR) marker analysis using four microsatellite primer pairs (CNZ 04, CNZ 06, CNZ 10 and CNZ 12) and electrophoresed on polyacrylamide gels. The bands were visualized by silver staining. Thirty nine nuts from palms derived through micropropagation and 10 seed derived nuts of the same variety (CRIC 65) as control were subjected to proximate analysis. PCR and subsequent gel electrophoresis showed clear DNA bands and they were scored by visual observation. Clone 01 showed monomorphic banding pattern for CNZ 04 and CNZ 12, but different bands with CNZ 10 being problematic. Clones 02 and 03 established their genetic fidelity with all four primers. The results proved the genetic homogeneity among the plants of the clones with no incidence of somaclonal variation. In proximate analysis, there was no significant difference in the composition between coconut from micropropagated plants and seed derived plants. However, some fruit components significantly differed *($p<0.05$)* from seed derived coconuts due to mite damage. According to the results, the protocol used for the micropropagation of coconut, can be recommended as a safe method for the clonal mass propagation.

Keywords: Genetic homogeneity, Micropropagation, Molecular markers, Proximate composition, Somaclonal variation