

*Melia volkensii* (Gurke.) is a popular fast growing agroforestry tree species in the East Africa's arid and semi arid lands (ASALs). The species is valued for its high quality termite resistant timber. In addition, its fruits are eaten by livestock thus making it the species of choice by small-scale farmers. However, the species has been overexploited and information on its existing gene pool is currently lacking. The present work was therefore carried out using random amplified polymorphic DNA (RAPD) markers to assess genetic diversity within and between populations in order to suggest appropriate conservation and management strategies. Eight RAPD primers generated 38 scorable polymorphic bands which were used to estimate genetic distances between populations and for construction of neighbour-joining phenograms. Analysis of Molecular Variance (AMOVA) indicated significant genetic differentiation between populations in the eastern and the coastal regions with 21.1%, ( $P < 0.0002$ ) of the total variation attributed to differences between these regions. There was a clear split between populations from Eastern and Coastal populations of Kenya. These differences may be due to ecogeographical association with genetic variation and should be conserved to retain the full breadth of genetic variation of the species.

Key words: *Melia volkensii*, random amplified polymorphic DNA, genetic variation, agroforestry species.