Abstract

Melia volkensii is a popular multipurpose tree species in Kenya's arid and semi arid lands (ASALs). The species has been overexploited in the recent past leading to erosion of genetic diversity. The aim of this study therefore was to assess the levels and distribution of genetic diversity of selected Kenyan populations. Nine populations were analyzed using random amplified polymorphic DNA (RAPD) markers. The levels of genetic diversity were low (H = 0.0663 to 0.1372). The populations were differentiated into two groups, eastern and coastal regions, which are also distinguished by eco-climatic conditions. The groups were also subdivided into farmland and natural populations. Higher genetic diversity was found within farmland (H = 0.1075) than in natural populations (H = 0.0690). The analysis also revealed that more variation (75.4%) existed within populations. The genetic differences observed between the regions and at sub-regional level (farmland versus natural populations) constitute important units, which should be considered for conservation, improvement and sustainable utilization of the species.