

Abstract

Moringa oleifera is an important multipurpose tree introduced to Africa from India at the turn of this century. Despite limited knowledge of the levels of genetic diversity and relatedness of introduced populations, their utilization as a source of seed for planting is widespread. In order to facilitate reasoned scientific decisions on its management and conservation and prepare for a selective breeding programme, genetic analysis of seven populations was performed using amplified fragment length polymorphism (AFLP) markers. The four pairs of AFLP primers (PstI/MseI) generated a total of 236 amplification products of which 157 (66.5%) were polymorphic between or within populations.

Analysis of molecular variance (AMOVA) revealed significant differences between regions and populations, even though outcrossing perennial plants are expected to maintain most variation within populations. A phenetic tree illustrating relationships between populations suggested at least two sources of germplasm introductions to Kenya. The high levels of population differentiation detected suggest that provenance source is an important factor in the conservation and exploitation of *M. oleifera* genetic resources.