

Abstract

The genus *Warburgia* (Canellaceae) contains four tree species that are of valuable medicinal importance and are all found in Africa. Genetic diversity present in wild populations of these species is under great threat due to unsustainable harvesting for medicines and indiscriminate felling for timber and agricultural expansion. There is therefore an urgent need for conservation of these species. Some authors disagree about the taxonomy of the genus and list different species as synonyms. Amplified fragment length polymorphism (AFLP) technique was used to determine the genetic relationships between three species to resolve the taxonomic confusion. The amount of genetic variation within and among populations was assessed to guide strategies for their conservation and sustainable utilization. Four AFLP primer pairs (*EcoRI/MseI*) generated a total of 185 amplification products. Analysis of molecular variance revealed most variation among individuals within populations (63%, $P < 0.0001$), but variation among populations (37%, $P < 0.0001$) was highly significant as well. Constrained analysis of principal coordinates based on the Jaccard distance confirmed the separation among populations (38.2%, $P < 0.0001$). A phenetic tree and ordination graphs showed a clear distinction of *W. ugandensis* from *W. salutaris* and *W. stuhlmannii*. *W. ugandensis* populations from Uganda and western Kenya formed a subgroup that clustered away from the rest of the *W. ugandensis* populations. *W. salutaris* and *W. stuhlmannii* populations showed little genetic differentiation. An implication of the data to genetic management and taxonomic clarification is discussed.