

Abstract

Warburgia ugandensis is an important medicinal tree species in Eastern Africa used to treat several ailments. Wild populations are under great threat due to unsustainable harvesting for medicines and indiscriminate felling of trees for timber and firewood. There is an urgent need for developing and implementing conservation strategies of this species and information on genetic structure is a crucial input. Analysis of molecular variance (AMOVA), which employed 141 AFLP markers revealed most genetic variation to be among individuals within populations (59%, $P < 0.0001$), but variation among populations (41%, $P < 0.0001$) was highly significant as well. Constrained ordination analysis illustrating the relationship among populations showed a clear distinction between *W. ugandensis* from Uganda and western Kenya and other *W. ugandensis* populations. No correspondence was shown in some cases on pair-wise genetic distances and geographic distances among populations. These findings suggested that conservation strategies for the species in Kenya should place relatively more emphasis on the revealed genetic structuring within the country.