

Abstract

Listed as vulnerable under Appendix II of CITES, populations of the commercially valuable African highland medicinal tree *Prunus africana* are threatened by over-exploitation in a number of countries. Here, random amplified polymorphic DNA (RAPD) analysis was used to assess patterns of genetic variation in the species in Cameroon and Kenya, two countries where exploitation has been particularly high and where information on genetic structure is a crucial input for developing the national management plans that are a requirement of CITES listing. Analysis of molecular variance (AMOVA), which employed 39 RAPD markers, indicated that a significantly greater proportion of total country variation partitioned among eight stands in Kenya than among nine stands in Cameroon (values of 55% and 24%, respectively), with important implications for conservation strategies. Kenyan stands appear to represent a particularly diverse resource for conservation, evaluation and domestication, although possible human movement of germplasm during cultivation raises integrity concerns. Data also shed light on the evolutionary history of *P. africana* stands. A genetic disjunction between western and central Kenyan populations was observed, with individuals from western Kenya more similar to geographically distant stands from Cameroon (> 2000 km) than to central Kenya (< 400 km). In the context of present-day floristic distributions and the historical data available, this disjunction appears more consistent with genetic exchange between east and west African highlands via migration (associated with climate change) than via long distance seed dispersal. Data suggested that conservation strategies for *P. africana* should place relatively more emphasis than currently on the status of surrounding phytochoria.