

GENETIC VARIATION IN THE THREATENED MEDICINAL TREE PRUNUS AFRICANA IN CAMEROON AND KENYA: IMPLICATIONS FOR CURRENT MANAGEMENT AND EVOLUTIONARY HISTORY

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Summary

Prunus africana is important medicinal tree threatened by over-exploitation in a number of African countries and therefore, development of national management strategies for conservation and sustainable use are important. A RAPD analysis used to assess patterns of genetic variation in Cameroon and Kenya revealed that significantly more variation partitioned among Kenyan populations than in Cameroon, with a clear genetic disjunction showing between Kenyan stands. Data suggest both particular opportunities and concerns for genetic management in the countries especially in the context of domestication in agroforestry systems.

Key words

Conservation, floral history, genetic management, *Prunus africana*, random amplified polymorphic DNA (RAPD)

Introduction

Prunus africana (Hook. f.) Kalkman (Rosaceae) is a geographically widespread Afromontane tree, commercially important for its bark, which in high demand in the treatment of benign prostatic hyperplasia. This has led to notable destruction of the species in natural forests, leading to concerns on the long-term sustainability of harvesting and the conservation of the species. As a result, *P. africana* is listed under Appendix II of the CITES. Despite these concerns, planting programmes in Cameroon and Kenya have enjoyed some success indicating potential for *circa situ* conservation if coupled with sustainable managed harvesting. A prerequisite for the efficient use of genetic resources in any planting program is a detailed understanding of the extent and distribution of genetic variation available within the species. In this study, random amplified polymorphic DNA (RAPD) analysis to assess genetic structure among *P. africana* stands in Cameroon and Kenya, with a primary objective of determining more efficient management strategies for both countries.

Materials and Methods

Leaf material was taken from a total of 161 individuals from 18 stands of *P. africana*, in Cameroon and Kenya as well as a single stand from Uganda. Collection focused on Cameroon and Kenya mainly because destructive exploitation in both countries has recently been high, but opportunities exist in both cases for *circa situ* conservation through smallholder cultivation or plantations (Cunningham *et al.*, 1997; Simons *et al.*, 1998). Secondly, earlier research by Dawson and Powell (1999) on a smaller number of stands suggested more

detailed analysis of these areas that could provide information on the evolutionary history of the species. Total genomic DNA was extracted from the sampled leaf material and RAPD-PCR undertaken according to Dawson *et al.* (1995)

Data analysis

A principal coordinate analysis of individual RAPD phenotypes was undertaken with the PAST 0.82 software package (Hammer *et al.*, 2002). Analysis of molecular variance (AMOVA) based on Euclidean distances between individuals was undertaken with the ARLEQUIN 1.1 software package (Schneider *et al.*, 1997). Genetic diversity (*H*) levels were calculated for each stand.

Results and Discussion

Analysis of molecular variance (AMOVA) employed 39 RAPD markers and at a country level indicated significantly more variation among eight Kenyan than nine Cameroonian stands of *P. africana* (values of 55% and 24%, respectively). Data suggested both particular opportunities and concerns for genetic management in Kenya, particularly in the context of domestication in agroforestry systems. A genetic disjunction between western and central Kenyan stands of *P. africana* was also evidence in a principal coordinate analysis, which grouped western Kenya individuals with geographically distant material from Cameroon (> 2,000 km) rather than proximate central Kenya (< 400 km). In the context of historical data available on African highland flora, data were more consistent with genetic exchange between West and East African stands via repeated migrations associated with climate change cycles, rather than a long distance dispersal model.

Proposed areas of interest on *P. africana* in Biotechnology

- Green labelling to control destructive felling and bark smuggling
- Genome mapping to identify key regions of interest
- Improve bark/leaf BPH control phytochemical yield
- Improve tree growth rate

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