

## Abstract

Indigenous fruit trees are widely used by humans in southern Africa. Little information is however available on regional genetic variation in these species, knowledge essential for their proper use and conservation. Here, we begin to address this gap by assessing RAPD and chloroplast variation in *Sclerocarya birrea*, a fruit tree that has been important to humans in the region for millennia. A strong overall positive correlation between genetic (RAPD) and geographic distances was observed for 12 populations of *S. birrea* subsp. *caffra* sampled from seven countries (standardised Mantel statistic,  $r_M = 0.857$ ,  $P < 0.001$ ), supporting a ‘structuring-by-distance’ model in devising genetic management strategies. Cluster analysis indicated, however, that genetic distances between geographically proximate stands were high on occasions, suggesting that inclusion of multiple stands nationally can sometimes be useful in rangewide management. Overall, an analysis of molecular variance (AMOVA) indicated that 19% of RAPD (assumed nuclear) variation partitioned among *S. birrea* subsp. *caffra* stands. Consistent with other nuclear–organellar comparisons for tree species, a much greater proportion of chloroplast variation (70%) partitioned among stands, suggesting a rather limited role for seed compared to pollen in mediating gene flow. Further analysis of *S. birrea* involved additional sampling from Tanzania of two other recognised subspecies (subsp. *birrea* and subsp. *multifoliolata*) that are not otherwise found in the southern Africa region. AMOVA indicated that more RAPD (29%) and chloroplast (75%) variation partitioned among relatively proximate subspecies stands (4 populations, 1 subsp. *caffra*, 2 subsp. *birrea* and 1 subsp. *multifoliolata*) in Tanzania than among subsp. *caffra* stands sampled extensively across southern Africa, suggesting Tanzania should be a focus for genetic management activities.