Abstract

Allanblackia, a dioecious fruit tree native to sub-Saharan Africa, is the subject of increased international interest for oil production for the global food market. Until recently, however, *Allanblackia* has been an overlooked wild tree, with very little known about its biology that could guide domestication. Here, we applied amplified fragment length polymorphisms (AFLPs) to assess the genetic composition of populations of five important *Allanblackia* species. Data indicated significant differentiation between certain species and occasional misidentification of taxa during collection. Misclassification suggested that care is required when sampling germplasm, especially when domesticating single species in areas where related taxa are sympatric. Genetic relatedness between species and the geographic proximity of distributions sometimes but did not always correspond. This likely reflects complex evolutionary processes related to migration and dispersal in the genus and indicated that a simple 'sampling-by-distance' model for assessing variation is not always appropriate. High AFLP variation suggested that Cameroon presents particular opportunities for domestication. In a comparison with AFLPs, we tested the value of *de novo* simple sequence repeats (SSRs) for detecting genetic variation in the same populations of *Allanblackia*, with a view to later applying these markers to determine optimal tree-planting ratios (female to male trees) and configurations during on-farm planting. Four primer pairs from a genomic library of one member of the genus—*Allanblackia stuhlmannii*—appeared suitable for research in this taxon (revealing 4.75 alleles per locus on average). However, cross-species application appeared limited (occurrence of null alleles?), suggesting either generic expressed sequence tag SSRs or specific suites of primers for each taxon are required.