

Abstract

Scattered populations of the same tree species in montane forests through Africa have led to speculations on the origins of distributions. Here, we inferred the colonization history of the Afromontane tree *Prunus africana* using seven chloroplast DNA loci to study 582 individuals from 32 populations sampled in a range-wide survey from across Africa, revealing 22 haplotypes. The predominant haplotype, HT1a, occurred in 13 populations of eastern and southern Africa, while a second common haplotype, HT1m, occurred in populations of western Uganda and western Africa. The high differentiation observed between populations in East Africa was unexpected, with stands in western Uganda belonging with the western African lineage. High genetic differentiation among populations revealed using ordered alleles ($N(ST) = 0.840$) compared with unordered alleles ($G(ST) = 0.735$), indicated a clear phylogeographic pattern. Bayesian coalescence modelling suggested that 'east' and 'west' African types likely split early during southward migration of the species, while further more recent splitting events occurred among populations in the East of the continent. The high genetic similarity found between western Uganda and west African populations indicates that a former Afromontane migration corridor may have existed through Equatorial Africa.