Abstract

Using databases of previously published primers, we optimised six nuclear microsatellite markers for Prunus africana for the purposes of studying spatial genetic structure and gene flow. To assess variability, these and three previously transferred loci were screened in populations from Kenya and South Africa. Across both populations most loci were polymorphic, with the exception of a single locus which failed to amplify in the South African samples, exhibiting between 2 and 22 alleles and levels of expected heterozygosity (He) ranged from 0.059 to 0.932. Departures from Hardy–Weinberg equilibrium were detected for all loci but not for all populations. The estimated null allele frequency was very low to moderate and no evidence for linkage disequilibrium was detected.