

ABSTRACT

Genetic diversity of blackberry (*Rubus* subgenus *Rubus* Watson) is essential for efficient breeding and improvement of its pomological traits and yield. In this research, simple sequence repeats (SSRs) were used to determine the genetic diversity of 90 blackberry accessions collected from six different counties in Kenya. From 11 SSR markers used to genotype the blackberry accessions, a total of 127 alleles were generated. The average number of alleles (A) per locus was 4.00 while the expected heterozygosity (HE) of the SSR loci varied between 0.34 and 0.50, with a mean of 0.467. Polymorphism information content (PIC) values ranged from 0.357 to 0.753 with a mean of 0.520. HE of the blackberry accessions were higher than the observed heterozygosities (H_O), having 0.75 and 0.64, respectively. Analysis of molecular variance (AMOVA) revealed 95% variability within accessions and 5% ($P < 0.01$) among accessions. Cluster analysis using the Jaccard's similarity coefficient grouped the accessions into three classes: I, II and III, consisting of 31, 52 and 7 accessions, respectively. The clustering was random and did not group the accessions according to their geographical origin, indicating that accessions found in Kenya are closely related. This study detected considerable levels of genetic diversity within the analyzed accessions, which could be exploited in a blackberry breeding program.

Key words: Simple sequence repeats (SSRs), *Rubus* subgenus *Rubus* Watson, genetic diversity.