

A panel of cultivate specific marker based on polymorphisms at microsatellite markers for Iranian cultivated Almonds (*Prunus dulcis*).

ABSTRACT

Molecular markers developed for *Prunus* also offer a powerful tool to study the evolution of the genome, and for understanding of genome structure and determinants of genetic diversity. Two hundred eighty almond genotypes/cultivars from different origins distributed throughout Iran besides some foreign cultivars and their hybrids with Iranian ones were collected. Microsatellite analysis was carried out using 9 pair flanking SSR sequences previously cloned and sequenced specifically in almond. The total number of detected alleles was 152 (9 to 20 alleles per locus with an average of 16.87). The mean PIC value of the polymorphic loci was relatively high (0.81) and the mean value for H_e was 0.83, so that we were able to distinguish 98% of the genotypes using 5 loci. In cluster analysis, the genotypes were divided into 2 major groups, foreign cultivars and Iranian almond genotypes. Principal coordinate analysis based on Shared Allele method indicated proper distribution of the studied markers through the genome. Some specific markers were recorded among the germ plasm which can be used efficiently in rapid and precise identification of the related genotypes and also in breeding programs through MAS. Genotypes were coded using our suggested coding method for genotype molecular identification.

Keyword: Almond; DNA barcoding; Genetic identification; Molecular marker; Microsatellite; *Prunus dulcis*.