Molecular tagging of agronomic traits using simple sequence repeats : informative markers for almond (Prunus dulcis) molecular breeding.

ABSTRACT

Informative markers are most applicable in breeding purposes, so that can be considered as an initial point to search the genome for the related traits and hold promise for speeding up the fine mapping and identification of genes responsible for variation in agronomic traits. Association mapping as a combination of molecular and morphological data is the best choice to find informative markers, particularly in crops that are limited to no more than one generation per year. A total of 39 (Seventeen quantitative and 22 qualitative) traits were recorded during two years among 53 almond genotypes/cultivars. Extracted almond genomic DNA was PCRamplified using 9 pair flanking SSR sequences previously cloned and sequenced specifically in almond. For correlation analysis between molecular markers and morphological traits and identification of possible informative markers, a stepwise regression analysis in both levels of significance 0.05> and 0.01> was employed. The results of stepwise regression analysis revealed a significant correlation between the morphological traits and some of the studied microsatellite loci. A total of 141 positive markers out of 556 polymorphic bands (135 alleles obtained from 9 SSR loci) were identified for different traits. For some of the morphological traits more than one informative markers were detected, which consequently their additive effects, degree of dominance and sum of the positive and negative effects needs to be further analysis. These informative markers can be considered as candidate markers for scanning the genome for related morphological (particularly agronomical) traits, mapping and finally breeding programs.