Assessment of Genetic Diversity Among Some Iranian Native Apple Genotypes and Commercial Cultivars Using SSR and SRAP Molecular Markers

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Most of the Iranian apple cultivars have been named based on their local names, therefore, their genetic relationships are not clearly specified. In order to determine genetic diversity of various Iranian apple genotypes and comparison between their genetic relations with commercial cultivars, we used microsatellite or simple sequence repeats (SSR) and sequence-related amplified polymorphism (SRAP) markers. Among 14 used microsatellite primer pairs, nine of them were polymorphic. The average number of alleles and observed heterozygosity (Ho) for all loci were 6.22 and 0.81, respectively, which confirmed the high genetic variability among genotypes due to self-incompatibility and cross pollination of apple. Among 56 SRAP primer combinations, 13 of them were polymorphic and produced 194 polymorphic bands (85.9%). The average of observed heterozygosity was computed as 0.34 that does not seem logicl, because apple is an self-incompatible plant. The results revealed that the microsatellite marker system is more reliable than SRAP marker system to indicate information of polymorphic and amount of heterozygosity in apple genotypes and despite nomenclature of apple cultivars based on local cultivation, the main origins of them do not match their geographical names. The genetic similarity of commercial apple trees indicates their common ancestory.

Keywords: Genetic polymorphism, Heterozygosity, Iranian apple، Molecular markers.

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