Evaluation of Morphological and Genetic Diversity of Some Peach Genotypes in Iran

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In this study, 24 peach genotypes were studied to determine the overall degree of polymorphism and to detect similarities among early, medium and late ripening peach genotypes by morphological and microsatellite markers. Morphological characters in three groups based on ripening time were considered according to peach descriptor. The variations were observed for traits related to morphology and fruit quality. Among the early ripening genotypes of peach, a crispy texture (called slow ripening) was detected. Factor analysis showed that the first four factors explained 86.74% of the total variation among the 24 genotypes. Cluster and principal component analysis showed a considerable phenotypically diversity in the peach germplasm. The cluster analysis by Wards method divided the genotypes into three main groups. In order to estimate their genetic diversity and to clarify their possible relationships, 20 SSR primer pairs, were used. A total of 112 alleles were produced with an average of 6.5 alleles per locus. The number of alleles (Na) varied from three for BPPCT036 to 10 for the UDP98-406. The effective number of allele (Ne) ranged from 2.08 in BPPCT036 to 06.06 for UDP98-414 with an average of 57.3 per locus. Expected heterozygosity ranged from 0.33 for BPPCT036 to 0.85 for UDP98-414 with an average of 0.70 per locus. The cluster analysis divided the genotypes into four groups. The Kosari peach was isolated in one subgroup. The second group consisted of two subgroups; most of them were late harvest genotypes.

Keywords: Early ripening peaches, Morphological Diversity, Microsatellite.

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