

Genetic Diversity Among Iranian Cantaloupe Landraces (*Cucumis melo* L.) Using Microsatellite Markers

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Abstract

The genetic diversity among 43 accessions of melon (*C. melo* L.), 41 from Cantaloupensis group alongside two from Indorus group, was assessed by variation at simple sequence repeats marker bands using 18 pair primers. The extracted genomic DNA was amplified with 12 pair primers and PCR products were separated on a DNA sequencing gels. A total of 98 alleles were identified with an average of 4.90 alleles per primer combination. Genetic distances among the accessions ranged from 0.0 for the most similar to 0.76 for the most-diverged ones. The mean GD (Nei's coefficient) among accessions was 0.219. The average of polymorphic information contents (PIC) for the 12 melon SSR markers was 0.542. CMCT134b, CMTC168, CMBR43 and CMAT141 loci had respectively the highest PICs, which could be used for further analysis. Genetic relationships among accessions were represented by a dendrogram based on similarity coefficient matrix with UPGMA method. Cluster analysis classified the accessions into 11 major groups. Cluster analysis indicated wide range of diversity across the Iranian and foreign accessions. The most distance was detected between Mahali e Darab and Amrikaie (76%). In general, poor relation was found between geographical and genetic diversity, whereas some relations was observed in cluster 2. The tetraploid accessions were mainly placed in the group 1. Principle component analysis had a very good co-ordination with dendrogram of genetic diversity. These results suggest that the SSR markers are valuable tools for identification and diversity analysis in cantaloupensis.

Keywords: Melon, Molecular markers, Genetic diversity, Microsatellites, Primer

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