

Abstract

Germplasm collection the first step for plant breeding. As primitive culturing of variant cultivars of melon, there is probably valuable water melon gene pool in Iran. The genetic diversity of fifteen Sistan water melon landraces and forty five native water melon cultivars, were analyzed using simple sequence repeat (SSR) markers. Collectively 9 primers which contained different simple sequence repeat (microsatellite) were used as single primer, and tested for PCR amplification. 41 polymorphic bands of 40 loci were scored. They were then used to estimate the genetic similarity among accessions using cluster analysis based on similarity coefficient matrix using Unweighted Pair Group Method with Arithmetic mean method (UPGMA). The results showed that among accessions mean genetic distances (Jaccard's coefficient) and mean polymorphism information content (PIC) were 0.74 and 0.78, respectively. The primer (AC)₈ G had the highest PIC (0.93). Cluster analysis indicated wide range of diversity across the genotypes used. The least of genetic distance was observed between Sephidak deh kohneh and Sephidake adimi accessions revealing closer genetic relationship of two accessions with each other than with others. The highest genetic distance was observed between Keshideh khatdar and Ghandak milak. According to the results and indicating the efficiency of this marker in separation of cultivars, collection and molecular evaluation of genotypes from different distribution regions of this genus can afford complementary information about its diversity and taxonomy.

Key words: water Melon, Genetic diversity, SSR marker



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