

عنوان مقاله:

Genetic Diversity in Iranian Melon Populations and Hybrids Assessed by IRAP and REMAP Markers

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نویسندگان:

S. Gholamzadeh khoei - *Department of Plant Breeding and Biotechnology, Faculty of Agriculture, Urmia University, Urmia, Islamic Republic of Iran*

B. Abdollahi Mandoulakani - *Department of Plant Breeding and Biotechnology, Faculty of Agriculture, Urmia University, Urmia, Islamic Republic of Iran*

I. Bernousi - *Department of Plant Breeding and Biotechnology, Faculty of Agriculture, Urmia University, Urmia, Islamic Republic of Iran*

خلاصه مقاله:

Retrotransposons (RTNs) constitute informative molecular markers for plant species because of their ability to integrate into a multitude of loci throughout the genome and thereby generate insertional polymorphisms between individuals. In the present study, RTN-based molecular markers, IRAP (inter-retrotransposon amplified polymorphism) and REMAP (retrotransposon-microsatellite amplified polymorphism), were applied to study RTN integration events and genetic diversity in 100 melon genotypes (88 genotypes from 11 populations, three inbred lines, and 9 hybrids). A total of 94 and 262 loci were amplified using 5 IRAP and 15 REMAP primers, respectively. The percentage of polymorphic loci (PPL) in populations ranged from 39% (Zivari Shahrood) to 48% (Shadegani E). The Mantel test between IRAP and REMAP cophenetic matrices evidenced no significant correlation ($r = 0.29$). IRAP+REMAP-based cluster analysis using UPGMA algorithm and Dice similarity coefficient depicted 6 groups among 100 melon genotypes. AMOVA revealed the higher level of genetic variation within populations (67%) compared to among populations (33%). The mean F_{st} values of all groups, except for group VI, were more than 0.20, demonstrating differentiation among the populations and genetic structure of the studied melon collection.

کلمات کلیدی:

Cucumis melo, Genetic variability, Remel, Retrotransposon

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