

Abstract

The economic importance and role of plants, especially led researchers do a lot of research on genetic diversity. Retrotransposons are main transposable elements in the plant genome where they move in genome via an intermediate RNA. In this study REMP marker was applied to identify the retrotransposon markers and genetic diversity in eight varieties of cucumber (*Cucumis sativus* L.) F1 hybrid, which are cultivated in greenhouses Sistan region. After DNA extraction by the CTAB method. PCR was performed using designed primers collected data were analyzed using the software Genealex. Most retrotransposons were active in the genome and produced 56 polymorphic bands using 8 REMP primers. The percentage of polymorphic (PPL) for the REMP primers was 45.09. Results show expected average of heterozygosity (H_e) 0.18, Shannon index (I) 0.27, effective number of alleles (N_e) 1.3 Cluster analysis based on the obtained data from REMP, Das similarity coefficient algorithm and complete linkage, put the 8 genotypes in four main groups and different people of the groups could be applied as crossing parents in breeding programs and hybrid seed production program.

Keywords: Cucumber (*Cucumis sativus* L.), Retrotransposons, genetic diversity, REMP



دانشگاه زابل

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**Investigation on genetic variation of Cucumber (*Cucumis sativus* L.)
by *REMAP* marker**

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