

## **Abstract**

Nowadays cultivation of greenhouse hybrid cucumber (*Cucumis sativus* L.) has been widely spread. Out of season cucumbers cultivation causes its economic importance. Genetic diversity estimation of important crop plants has an importance in breeding of cultivars with desirable traits. Retrotransposons are main transposable elements in the plant genome where they move in genome via an intermediate RNA. In this study, IRAP 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 of Sistan region. After DNA extraction by CTAB method, PCR was performed using designed primers. Collected data were analyzed using the Genealex software. The findings showed that most retrotransposons were active in the genome and produced 72 polymorphic bands using eight IRAP primers. The percentage of polymorphic (PPL) for the IRAP primers was 35.05. Results showed expected average heterozygosity ( $H_e$ ) of 0.13, Shannon index ( $I$ ) of 0.18 and effective number of alleles ( $N_e$ ) equal to 1.8. Cluster analysis based on the obtained data from IRAP, Das similarity coefficient algorithm and complete linkage, put the 8 genotypes in four main groups and different members of the groups could be applied as crossing parents in breeding programs and hybrid seed production strategies.

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



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

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