

Abstract

Due to the production of dates in the country, identification of new cultivars, correction of available varieties and the study of diversity among different varieties are necessary. To do this research, the leaves of 15 different varieties of dates were collected from Saravan city and was evaluated through the evaluation of the intergenic regions of trnH-psbA. DNA extraction was done by Dolaport method after young leaves were sampled. After PCR was performed using TrnH-psbA gene primers (IGS), PCR products were electrophoresed on 2% agarose gel and stained. Observation and shooting of amplified bands were done using duct gel. Duplicate products for sequencing and after sequencing, the sequences for each of the cultivars studied were recorded in the NCBI database. The quality of the sequences was investigated using Chromas software, and then, using the ClustalW method, MegAlign software was mapped and a dendrogram of phylogenic relationships and sequence similarity matrix was drawn to determine genetic relationships and genetic distances between genotypes. Sequence analysis showed that 787 positions were identified in the trnH-psbA bronchial region. There were 174 positions with removal and addition, among which 538 single-position and 30 polymorphic positions were recognized. There were also 613 positions without removal and addition. In the population studied, 23 Singletones were detected and 4 haplotypes were detected. Haplotype diversity index was 0.371. The homology of the sequence of the mango samples examined together represented a total sequence of 116 pairs of games among them. The highest rate of transfer was of purine (0.05%) and the least amount of pyrimidine (15.41%). In this study, the ratio of dN/dS was 0.25. The genetic distance was from 0.002 to 0.049 and the most intra-regional variation was related to the Gozloo cultivar.

Key words: dates, Intra-species genetic variation, DNA barcoding, TrnH-psbA intergenic region



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**Thesis for obtaining a Master's degree in Agricultural Engineering-Biotechnology in
Agriculture**

**Molecular analysis of trnH-psbA (IGS) genes of some palm cultivars in Sistan and
Baluchestan province**

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Summer 2017