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Title
**Transcriptomics analysis and identification of genes
involved in sex determination of date palm using RNA-
SEQ technique**

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Abstract

Flowering and fruiting in date trees was slow. At the end of the fifth year of growth, it is determined whether they are male or female. Therefore, it is necessary to determine the gender of seedlings produced from seeds or tissue culture for the design and cultivation of male and female plants in the field. Therefore In order to investigate and compare target genes involved in flowering and sex of date palm, the transcriptomes of male and female date palm cultivars (13 males and 12 females) were sequenced by Illumina Hiseq 2500 method. The beginning of flowering time in plants is a completely controlled phenomenon that depends on the environmental and internal parameters of the plant and it is controlled by the regulatory network of genes. Based on the results of this research, the identified genes had a role in three Photoperiodic pathways (with 15 genes), Autonomous (with 7 genes) and Gibberellin pathway (with 2 genes), While no gene was detected in the path of Vernalization. Photoperiodism. Gene ontology results were analyzed and it was found that from before flowering to the beginning of flowering and until the flower exits from the central part of the activity tree, nuclear genes have the highest increase in expression. So that during the reconstruction of the gene co-expression network, it was determined that 1500 genes had different expression compared to other genes, so that based on the analysis of the investigated regulatory networks, it was determined that two genes, SOQ and LOG3, were expressed in males and females, respectively. had a more and more key role in the studied gene networks compared to other studied genes. Therefore, considering that the present study is one of the first research projects to identify the genes involved in the flowering pathways of date palm, Perhaps by identifying and comparing the genes involved in different flowering pathways and identifying the genetic factor or factors affecting their control, it is possible to provide the ground for future applied research and the production of suitable cultivars in this valuable plant.

Keywords: Male and Female date palm cultivars, RNA-Seq, Comparative transcriptome, Differentially expressed genes, Regulatory network