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Genetics and plant breeding in Agriculture

**Identify and compare LncRNAs in male and female date
cultivars using RNA-SEQ
technique**

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Abstract

The Date palm is a monocotyledonous, dicotyledonous and perennial plant belonging to the palm family and one of the native plants of the country, which has been in the country's export basket for a long time. Flower development is one of the main stages in the emergence of an organ focused on sexual reproduction in flowering plants, and flowering processes are regulated by a very complex set of pathways controlled by floral meristem identity genes, flower cycle and some evolutionarily conserved lncRNAs. In order to identify the pathways and lncRNAs involved in date palm flowering using the RNA-Seq technique, flower bud samples were collected from date palms of the date palms and tropical fruits of Minab Research Station, and total RNA was extracted from the samples collected from the flower buds of different male and female cultivars and compared equals were mixed with each other and at the end two replicates were obtained from each pooled sample and sent for sequencing. After receiving the sequencing results, the necessary analyzes were performed using appropriate software. The results of the present research showed that many lncRNAs were involved in the flowering pathways of date palm in three pathways: light cycle (thirteen cases), self-stimulation (one case) and gibberellin pathway (four cases), while no lncRNAs were detected in the vernalization pathway. Next, lncRNAs identified based on sequence were compared with lncRNAs reported in other plants and their similarity and relationship with candidate genes were determined. Ontology analysis was investigated in the category of biological processes, molecular functions and cellular components. After examining the relative expression profile of FLC, CO, FT, LFY and AP1 genes with the help of Real Time-PCR technique, the results showed that except FLC gene, CO, FT, LFY and AP1 genes have relatively high relative expression in date palm. Also, based on the results, eight lncRNAs in male cultivars and seven lncRNAs in female cultivars related to gender determination were identified in this study. It is hoped that by identifying and comparing the lncRNAs involved in different flowering pathways and identifying the genes related to them, it will be possible to provide the ground for future applied research in this valuable plant.

Keywords: flowering, lncRNAs, date palm, sequencing, RNA extraction