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Identification and prediction of circular RNAs associated with cluster formation in Yaghooti grapes of Sistan and a methodology development to predict them

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Abstract

Circular RNA molecules (circRNA) are a relatively new group of RNA molecules that control several biological functions. Functionally, circRNAs can regulate the expression of their parent genes or act as microRNA (miRNA) sponges by preventing miRNAs from binding to their target genes. CircRNAs exhibit tissue-specific expression profiles depending on tissue type and developmental stage. Yaghooti grape from Sistan is a seedless species with small berries. The compact clusters are another striking feature of this grape variety that negatively affects its marketability. In this study, circRNAs involved in cluster formation were identified and the effects of gibberellin treatment on their expression levels were investigated. Of the 3,715 circRNAs identified, 900 cricRNAs are differentially expressed under gibberellin treatment at three stages of cluster development. Among the 503 miRNAs identified, 12 index miRNAs were selected. The results showed that miRNAs of vvi-miR156, vvi-miR164, and vvi-miR172 families control a gene network related to the flowering process of Yaghooti grape. The regulatory target of miR172 is a subfamily of APETALA2 (AP2) transcription factor genes. Two target genes, AP2 and RAP2.7, are required to initiate the flowering process, and miR172 regulates flowering timing by reducing their activity. In addition, miRNAs of the miR164 family affect lateral root production by controlling the expression of the NAC1 and NAC100 genes. Of the 29 circRNAs in the circRNAs-miRNAs-mRNAs interaction network, 12 circRNAs are highly conserved, indicating the accuracy of the predicted circRNA molecules. Data mining using ten different weighting methods identified 16 biomarker circRNAs in the stages of clustering. A decision tree classifier based on machine learning was developed with high performance to discriminate the input variable into the control or treatment group. Our results suggest that circRNAs may play a key role in the developmental and cluster formation processes of Yaghooti grape, as well as in the tolerance of the plant to drought stress.

Keywords: CircRNAs, Conservation, Data mining, Interaction network, miRNAs.