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Computational discovery of a miRNA and its putative target genes in *Ziziphus jujuba* using genome-wide expressed sequence tags

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Highlights

- A potential miRNA was identified in *Ziziphus jujuba* by a computational analysis of 2904 genome-wide expressed sequence tags.
- The novel miRNA showed putative down regulation of five target proteins that are involved in metabolic and developmental processes associated with plant growth and reproduction.
- The down regulation of these proteins appears to be helpful to the plant to overcome stress conditions.

Abstract

Ziziphus jujuba is an important fruit crop that is increasingly becoming popular among consumers due to its medicinal properties. Increasing worldwide demand for fruit poses new challenges to the industry, including the need for accelerated cultivar development of jujubes. To embark on cultivar development with improved traits such as high yield and disease resistance, molecular and conventional breeding, and genetic engineering become imperative. But

inadequate trait-enhancing alleles or gene pleiotropism limit the direct use of several identified genes. To overcome these issues, microRNAs (miRNAs) can be utilized in the breeding of jujubes as genetic modulators to fine-tune the regulation of gene expression, thus the discovery of miRNAs becomes important. In this study, using a computational approach, we identified one potential miRNA (zju-miR-215-3p) from 2904 expressed sequence tags. The miRNA showed downregulation of five target proteins (AP-2 complex subunit alpha, C2H2-type domain-containing protein, sentrin-specific protease 1, hydrolase_4 domain-containing protein and putative alpha-ketoglutarate-dependent dioxygenase), most of which are implicated in metabolic and developmental processes associated with plant growth and reproduction. The suppression of these proteins appears to be helpful for the plant to overcome stress conditions. Future studies are necessary to validate the miRNA by RNA sequencing and to confirm the molecular functions of the down regulations of target proteins.

Keywords

In silico analysis; Jujube; microRNA; Rhamnaceae; Post-transcriptional gene regulation; Stress tolerance