

عنوان مقاله:

Experimental Validation and Characterization of Sugarcane Genome-Encoded MicroRNAs and Their Targets Using PCR-Based Expressional Methodology

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خلاصه مقاله:

MicroRNAs (miRNAs) are typically small, endogenous, non-coding RNAs molecules that regulate gene expression at post-transcriptional level by mRNA degradation or translational repression. They are composed of ۱۸-۲۶ nucleotides and are conserved during evolution for the development of new miRNAs in a variety of plants. Sugarcane (*Saccharum officinarum*) is generally a valuable food and forage crop grown all over the world. Until now, different sugarcane miRNAs have been characterized for plant development and stress responses. In this research, ۵۰ unique conserved sugarcane miRNAs from ۴۴ different miRNA families have been predicted using a variety of genomics-based tools. The predicted sugarcane miRNAs were validated using a set of ۱۵ randomly chosen primers and RT-PCR. Stem loop secondary structures are created using MFOLD tool. The psRNA-Target algorithm identified ۷,۹۷۶ various protein targets of sof-miRNAs including ۵۵ specific GO terms. They have significant targets in biological, cellular, and molecular functions. Moreover, the sof-miR۵۲۰۵a regulates sulfur compound biosynthetic process and ۹۶۵۳a directs ubiquitin-dependent protein catabolic process. Consequently, the RNA binding and thylakoid membrane are controlled by sof-miR۹۶۵۷b and ۲۰۹۱, respectively. As a result, the outcomes of the novel sugarcane miRNAs target a variety of substantial genes that aid in controlling the environment for sugarcane to produce a higher quality crop

کلمات کلیدی:

.Biological process, miRNA, RT-PCR amplification, *Saccharum officinarum*, Web logo

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