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In silico identification and functional annotation of miRNAs and their targets from EST and GSS of onion (*Allium cepa* L.)

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Abstract

MicroRNAs are a class of approximately 20-24 nucleotides (nt) endogenous small RNAs that negatively regulate gene expression and play vital roles in multiple biological processes, including plant growth, development and responses to environmental stresses. Onion (*Allium cepa* L.), also called as "queen of kitchen" is a bulbous vegetable crop cultivated in almost all parts of the world. However, the miRNA repertoire of onion is highly ambiguous. In the present study, we report the computational identification of miRNAs and their targets from expressed sequence tags (ESTs) and genome survey sequences (GSSs) of *Allium cepa* L as well as functionally annotated the target genes. By following a stringent pipeline, we used 20225 ESTs and 10725 GSS from onion to identify 9 new potential miRNA belonging to 8 different miRNA families (miR172, miR1134, miR1223, miR6219, miR7725, miR8570, miR8703 and miR8752). Under a stringent condition, 26 potential targets were identified for the 8 miRNAs with distinct functions related to growth and development, signal transduction, metabolism, defense and stress responses. Overall, the present finding will make the pathway for understanding of molecular mechanisms of miRNA in onion and understanding their involvement in post-transcriptional gene silencing mechanism towards regulation of stress responses in this economically important plant.

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