



In silico identification of microRNAs and their target genes in watermelon (*Citrullus lanatus*)

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Highlights

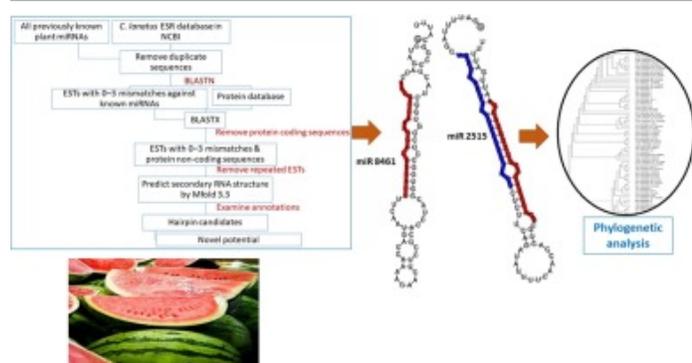
- *In silico* comparative genomics approach was used to identify miRNAs in [watermelon](#).
- Three potential miRNAs were predicted from 17,594 EST sequences in watermelon.
- These miRNAs demonstrated association with 19 different target proteins.
- The results warrants further analysis with a large number of EST sequences for appropriate picking of miRNAs.

Abstract

Watermelon (*Citrullus lanatus*) is an annual herbaceous crop, mainly grown for its fleshy fruit, which is an excellent source of vitamins and therefore fetches a huge market demand all over the world. Yield of watermelon can be improved by increasing the productivity that relies on plant growth, development and stress response. MicroRNAs (miRNAs), a group of short (~22 nt), noncoding, endogenous and evolutionary

conserved post-transcriptional regulatory RNAs, play a major role in various biological and metabolic processes associated with growth, development and stress response. In this study, we deployed a comparative genomics-based approach using expressed sequence tags (ESTs) to identify and characterize potential miRNAs and their target genes in watermelon. Three potential miRNAs (cla-miR-2515, cla-miR482d and cla-miR-8461) were predicted from 17,594 publicly available watermelon EST sequences, according to a series of filtering criteria used in the protocol. Moreover, 21 potential mRNA targets encoding for 19 different proteins linked to various metabolic processes such as inositol-3-phosphate synthase activity, metal ion binding and oxidoreductase activity were identified in watermelon genome, based on perfect or nearly perfect complementarity of miRNAs with their targeted mRNA sequences. Phylogenetic analysis of these miRNAs revealed that cla-miR8461 and cla-miR2515 are unique miRNAs closely related to *Schistosoma mansoni* and *Drosophila pseudoobscura*, respectively.

Graphical abstract



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Keywords

In silico identification; *Citrullus lanatus*; miRNA; Stress response; Expressed sequence tag (EST)

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