

## COMPUTATIONAL IDENTIFICATION OF CITRUS RETICULATA L. microRNAs AND THE CIS-ACTING REGULATORY ELEMENTS TO PREDICT THE EXPRESSION PROBABILITY OF THEIR RESPECTIVE MIR GENES

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*MicroRNA(miRNA), a small non-coding class of RNA that regulates the gene expression, is conserved among several plant species. In the present study, an in-silico approach was adopted to identify miRNA from the known expressed sequences tags (ESTs) of Citrus reticulata L. A total of 17 miRNAs from 23 different ESTs along with their secondary structures and targets were predicted. The identified 63 targets include several transcription factors, proteins that regulate plant growth, development, flowering, and seed development together with stress response. The cis-regulatory element present at the promoter region of the MIR genes of C. reticulata showed relevance towards light responsiveness, auxin, gibberellins, abscisic acid (ABA), anthocyanin responsiveness, salicylic acid responsiveness, anaerobic induction, circadian control, nitrate dependent regulation of the cell cycle and DNA replication, defense, and stress responsiveness. The present study identifies the miRNAs along with their regulatory elements in C. reticulata. The study will also support the research on miRNAs identification from the genomic data of different plants and prediction of the possibilities of expression of identified MIR genes based on the presence of upstream promoter and other regulatory elements.*

**Key words:** miRNA, Citrus reticulata, Expressed Sequence Tag, Cis-regulatory element, psRNATarget.

ОБЧИСЛЮВАЛЬНА ІДЕНТИФІКАЦІЯ мікроРНК І ЦИС-ДІЮЧИХ РЕГУЛЯТОРНИХ ЕЛЕМЕНТІВ CITRUS RETICULATA L. ДЛЯ ПЕРЕДБАЧЕННЯ ВІРОГІДНОСТІ ЕКСПРЕСІЇ ЇХНІХ ВІДПОВІДНИХ ГЕНІВ MIR

МікроРНК (miRNA), невеликий клас некодуючих РНК, який регулює експресію генів, обмежені декількома видами рослин. У цьому дослідженні було застосовано підхід in-silico з метою визначення

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мікроРНК у відомих маркерних експресованих послідовностях (EST) *Citrus reticulata* L. Загалом було передбачено 17 мікроРНК із 23 різних EST, а також їхні вторинні структури та цілі. До ідентифікованих 63 цілей входять декілька транскрипційних факторів, білки, що регулюють ріст, розвиток, цвітіння рослин та розвиток насіння, а також реакцію на стрес. Цис-регуляторний елемент, присутній у промотерній ділянці MIR генів *C. reticulata*, продемонстрував свою актуальність щодо реакції на світло, ауксин, гібберелліни, абсцизову кислоту (ABA), антоціанін, саліцилову кислоту, щодо анаеробної індукції, контролю циркадного ритму, нітратозалежного регулювання клітинного циклу та реплікації ДНК, захисту та реакції на стрес. У цьому дослідженні було встановлено мікроРНК та їхні регуляторні елементи в *C. reticulata*. Наше дослідження також буде корисним для вивчення можливості ідентифікації мікроРНК на основі геномних даних різних рослин та передбачення можливості експресії ідентифікованих генів мікроРНК на основі наявності висхідного промотера та інших регуляторних елементів.

**Ключові слова:** мікроРНК, Citrus reticulata, маркерна експресована послідовність, цис-регуляторний елемент, psRNATarget.

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Received June 27, 2022  
Received October 03, 2022  
Accepted September 18, 2023