



Bioinformatic Study of miRNAs Involved in Wheat (*Triticum aestivum*) Vernalization

Nooshin Ashoori*, Reza Fotovat, Maryam Mortezaefar, Nastarn Mehri

Department of Agronomy and Plant Breeding, Faculty of Agriculture, University of Zanjan, Zanjan, Iran

*n_aashoori@znu.ac.ir

Abstract: Vernalization is one of the most important adaptations of winter cereals to environmental conditions that makes the plants able to control their growth according to seasonal variations [1]. miRNAs are non-encoding, single-stranded and small molecules that have a role in gene expression regulation and plant growth and development. Moreover, it has been demonstrated that miRNAs play an important role in many biological and metabolic processes. Due to the nature of strong conservation of miRNAs in plant species, the use of bioinformatics studies can help to identify new miRNAs in different species [2]. Previously recorded miRNAs involved in vernalization were obtained from miRBase and their homologies were searched in the EST database by Blastn, then secondary structures of them were evaluated by mfold website, online RNA secondary structure prediction software [3]. In this study, three miRNAs, miR172, miR319, miR156, are involved in vernalization of. AP2, TCP, SPL and ARF are regulated as the most important target genes, respectively, by miR172, miR319, miR156 and miR167. These genes play an important role in flowering and transferring from the vegetative phase to reproduction in plants.

Keywords: miRNA; vernalization; target gene; EST.

References

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