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miRNome analysis of Einkorn Turkish Wheat Cultivar (Siyez) under drought stress

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Viticum monococcum is the domesticated form of Einkorn wheat which is a staple food of early farmers for many thousand 🗘 years. Siyez is one of the most famous einkorn wheat cultivar and domesticated in Kastamonu, Turkey. MicroRNAs (miRNAs) are known as short non-coding RNAs that regulate gene expression at post-transcriptional level. In this study, miRNAs and their target genes were determined after drought stress in leaf and root samples of Siyez. Four small RNA libraries were constructed. Sequencing was performed on the Illumina HiSeq 2500. All bioinformatics analysis was carried out using CLC Genomics Workbench v.10. Although there are many studies related with transcriptome analyses in wheat, microRNA deep sequencing under drought stress in einkorn wheat has been firstly performed. After drought treatment, expression level of 30 and 69 miRNAs were increased and decreased, respectively. Expression level of tae-miR9672a-3p, tae-miR9666a-3p, tae-miR9773, tae-miR5048-5p and tae-miR167c-5p were significantly raised, whereas tae-miR395a/b, tae-miR9674a-5p, taemiR9662b-3p, tae-miR159a/b and tae-miR5200 expressions were remarkably reduced after drought stress application in Siyez. To identify potential regulatory effects of miRNAs on mRNAs, target genes were also predicted for all libraries. A detailed bioinformatics analysis showed that miRNAs up-regulated in response to drought stress, such as tae-miR9661-5p, tae-miR156 primarily targeted transcripts associated with activation of immune regulator SRFR1 and SBP-box genes. In the current study, a temporal miRNA-guided post-transcriptional regulation responded to drought was observed in leaf and root tissues of einkorn wheat. This kind of stress induced miRNA identification studies open new perspectives for designing novel wheat breeding strategies. This work was financially supported by The Scientific and Technological Research Council of Turkey (TUBITAK) with Grant Number 215Z354.

Biography

Mehmet Cengiz Baloglu is an Associate Professor of Department of Genetic and Bioengineering at Kastamonu University. He has received his PhD from Middle East Technical University and has established molecular biology, transcriptomics and bioinformatics research laboratories at the Kastamonu University. He has published over 50 peer-reviewed manuscripts on topics concerning with gene identification in plants, transcriptome and miRNA analysis using NGS and abiotic stress in plants. He is serving as an Associate editor and Editorial Board member for International journals with high impact factors.

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