

## **DEEP SEQUENCING-BASED CHARACTERIZATION OF WHEAT miRNome UNDER STRESS CONDITIONS**

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The molecular response of plants to stress is a complex process based both on the modulation of transcriptional activity of several stress-related genes and on post-transcriptional regulation. MicroRNAs are endogenous small non-coding RNAs of about 20-24 nt that are known to play key regulatory roles in plant response to stress, besides being involved in development and morphogenesis. Most of the reports that link a specific microRNA to stress response are based on its down/up-regulation when plants are exposed to stress. Usually stress-induced miRNAs target negative regulators of the stress responsive genes, while the targets of stress down-regulated microRNAs are positive regulators or stress up-regulated genes.

In this work the wheat miRNome in drought-stressed plants has been characterized by a deep sequencing approach on Illumina GAII-X and candidate stress-induced microRNAs have been identified. Besides, an *in silico* analysis of gene expression for the identification of putative stress-related microRNAs has been developed.