

## ANALYSIS OF THE SMALL RNAOME FROM AN APULIAN LANDRACE OF WHEAT UNDER WATER DEPRIVATION

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Wheat is an important and highly valued staple food, that own features suitable for production of bread and pasta making. Its production cycle depends on rainfall, so yields are strongly affected by water availability. Therefore, the level of drought stress tolerance in wheat is one of the most important traits to cope with the impact of expected climate changes.

Different classes of endogenous small RNAs (sRNAs) have been identified as fundamental to the response to biotic/abiotic stress, acting as important gene regulatory factors. There are two main categories of sRNAs: microRNAs (miRNAs) and short interfering RNAs (siRNAs). In addition, there are other sRNA types in plants, such as the heterochromatic siRNAs (hc-siRNAs), natural antisense transcript siRNAs (nat-siRNAs), and phased secondary small interfering RNAs (phasRNAs). The latter class originates from a phasRNA-producing genomic region and has been identified in several plants. It plays a role in disease resistance, but few studies have examined its role during drought stress. Another level of regulation is modulated by peptides encoded by plant primary miRNA transcripts (miPEPs), that are able to specifically increase transcription of their associated miRNA.

Local varieties or landraces are important genetic resources with a high potential for adaptation to environmental conditions and represent a major source of genetic variability for breeding. In the last fifteen years, landraces have been actively conserved ex situ and in situ under the political commitments of various global and regional conventions and

treaties implemented by the European Union (EU). In the framework of the Italian PSR 2013-2020, a durum wheat landraces named "Grano Buono di Rutigliano" (GBR) was collected in central Apulia.

In the present study, we investigated the potential of GBR to cope with water deficit. In addition, we profiled miRNAs, miRNA isoforms (isomiRs), and phasiRNAs that respond to drought stress, to gain insights into molecular strategies for stress acclimation. We predicted the target genes of differentially expressed miRNAs, and inferred their ontological functions. Finally, analysis of miRNA primary transcripts was performed to determine the presence of related miPEPs.

Data analyses showed a group of 24 predicted miRNAs associated to 17 miRBase sequences from *Arabidopsis*, *Triticum* and *Hordeum*. Furthermore, 41 predicted new miRNAs were associated to 34 sequences from the Wheat microRNA Portal. Finally, psRNATarget was used to identify the putative miRNAs targets. About 43,300 putative target transcripts (out of the 299,067 annotated transcripts) were associated to a total of 405 miRNAs. The regulatory molecules identified likely underpin the performance of the Apulian landrace GBR under water restriction indicating possible involvement in further breeding efforts.