

International Conference

FROM SEED TO PASTA III A Sustainable Durum Wheat Chain for Food Security and Healthy Lives



Bologna - Italy, 19-21 September 2018

P.1.03

MICRO RNA RESPONSE TO CHRONIC AND SHORT-TERM NITROGEN DEPRIVATION IN DURUM WHEAT SEEDLINGS

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Nitrogen (N) is an important macronutrient for crop productivity; its availability is essential from the seedling stage since N is also a major component of chlorophyll. In durum wheat, phenotypic traits and yield are negatively influenced by N deficiency. MiRNAs are small non-coding RNA molecules that can regulate key genes in response to stress, thus contributing to environmental adaptation of plants.

In the present work, durum wheat cultivars Ciccio e Svevo were grown in standard and in N starvation conditions, and leaves and roots were collected at the seedling stage (Z14). Eight small RNA libraries were obtained and sequenced. After bioinformatics analyses, 294 miRNAs were detected, including 7 newly identified. Using quantitative qPCR, expression levels of selected miRNAs and corresponding target genes were evaluated in durum wheat seedlings subjected to chronic or short-term (6-48 hours) N stress conditions.

Some miRNAs showed an immediate response to N stress, others exhibited a gradual up- or downregulation during the short-term stress, which was either maintained or not during a longer (chronic) stress period. One of the newly identified miRNAs, ttu-novel-106, showed to be immediately downregulated after nitrogen starvation conditions, while MYB-A, its putative target gene, was straightaway upregulated. These results were validated using 5^[2] RACE assay that allowed the identification of the ttu-novel-106 putative cleavage site in the *MYB-A* gene sequence. Additionally, the *PHOSPHATE 2* (*PHO2*) gene showed an opposite expression trend compared to its regulatory miRNA ttu-miR399b. Identification of putative ttu-miR399 binding sites at the 5^[2] UTR region of *TtPHO2* and cleavage validation were carried out for this gene.

This work provides novel insights into the activation mode of durum wheat miRNAs in response to N deprivation, confirming the importance of miRNAs in the adaptation of seedlings to N stress, and opens new perspectives for the use of miRNAs in breeding programs.

ABSTRACT