



Expression Pattern Analysis of Different Micro RNAs under Nitrogen Deprivation Condition in Root Tissues of Different Wheat Genotypes

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ABSTRACT: The regulatory roles of miRNAs in response to nitrate and N-deficiency have recently been explored in some of the crops. As far as wheat is concerned, number of miRNAs in general and nitrogen responsive in particular are very limited. In order to understand the possible role of miRNAs in nitrate sensing and deficiency in wheat, the expression pattern of micro RNAs, which are available in wheat miRBase (micro RNA database) depository, have been studied in a wheat genotypes such as HD-2967, Kalyan sona and NP-890 growing in optimum (4.0 mM NO₃⁻) and starved nitrate condition (0.04 mM NO₃⁻) in hydroponics. Differential expression of these micro RNAs have been studied in both chronic (15 days starvation) as well as transient (24 hrs.) nitrate starvation conditions in root tissues. The expression pattern of few differentially expressed miRNAs (under present study) under normal and starved nitrate conditions have been observed to be similar to other crop species while others are not reported in such condition. As far as HD-2967 is concerned, the differential expression in chronic and transient starved conditions have been observed in some of the conserved micro RNAs i.e. miR159b, miRNA160, miRNA399 and miRNA408 while others such as miRNA 159a, miRNA164, miRNA167 and miRNA444a have showed their presence under these conditions. Other miRNAs such as 1117, 1120, 1124, 1130, 1134 and 1139 also showed differential expression in root tissues under these conditions. The expression pattern of few miRNAs in case of Kalyansona and NP-890 has showed genotypic difference. The attempts of understanding expression pattern of nitrogen responsive miRNAs will help in unravelling the details of nitrate signal transduction and may provide new avenues in improving nitrogen use efficiency in wheat. © 2014 iGlobal Research and Publishing Foundation. All rights reserved.

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