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The spatiotemporal expression patterns of microRNA in response to high temperature stress in rice

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Global warming coupled with climate change is one of the important limiting factors that affect crop yields throughout the world. MicroRNAs (miRNAs) are a novel class of endogenous, non-coding small RNAs that have been established as ubiquitous regulators of post-transcriptional gene regulation via degradation or translational repression of the cognate mRNA targets. Thus, understanding the miRNAs mediated regulatory schemas for heat stress tolerance is necessary to raise novel crop varieties that can withstand or avoid stresses imposed by a changing environment. In the present study, Analysis of NGS datasets (Illumina , GA) of control and heat stressed c-DNA libraries generated from Flag leaf and Spikelet's of heat tolerant and sensitive indica rice cultivars identified several known and novel miRNAs that displayed a spectrum of response ranging from stable to very variable in nature between tissues and across cultivars. In depth profiling of miRNA expression patterns across tissues under various heat stress treatments also identified specific miRNAs that are highly de-regulated by high-temperatures. To understand the functional implications of miRNAs, their targets were identified. The predicted targets include transcription factors, protein kinases, ATP-binding proteins, HSPs, HSFs, Growth-regulating Factors, oxidoreductases, antioxidants etc. that are linked with various metabolic & cellular processes thereby regulating the stress responses. Future studies of these miRNAs may provide better understanding of the molecular links, behind these regulatory networks and may deliver fresh application routes for rice improvement during heat stress.

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