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## ***De novo* assembly for the identification of novel and conserved heat-responsive microRNAs in wheat (*Triticum aestivum* L.)**

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MicroRNAs (miRNAs) are small endogenous RNAs of ~22 nucleotide that have been shown to play regulatory role by negatively affecting the expression of genes at the post-transcriptional level. Information of miRNAs on some important crops like soybean, *Arabidopsis* and rice etc. are available, but no study on heat-responsive novel miRNAs has yet been reported in wheat (*Triticum aestivum* L.). In the present investigation, a popular wheat cultivar HD2985 was used in small RNA library construction and Illumina HiSeq 2000 was used to perform high throughput sequencing of the library after cluster generation; 110,896,604 and 87,743,861 reads were generated in the control (22°C) and heat-treated (42°C for 2 h) samples respectively. Forty four precursor and mature miRNAs were found in *T. aestivum* from miRBase v 19. The frequencies of the miRNA families varied from 2 (tae-miR1117) to 60672 (tae-miR159b). We identify 1052 and 902 mature miRNA sequences in HD2985 control and HS treated samples by mapping on reference draft genome of *T. aestivum*. Maximum identified miRNAs were located on IWGSC\_CSS\_3B\_scaff (chromosome 3B). We could identify 53 and 46 mature miRNA in the control and HS samples and more than 516 target genes by mapping on the reference genome of *Oryza sativa*, *Zea mays* and *Sorghum bicolor*. Using different pipelines and plant specific criteria, 37 novel miRNAs were identified in the control and treated samples. Six novel miRNA were validated using qRT-PCR to be heat-responsive. A negative correlation was, however, observed between the expression of novel miRNAs and their targets. Target prediction and pathway analysis revealed their involvement in the heat stress-tolerance. These novel miRNAs are new additions to miRNA database of wheat and the regulatory network will be made use of in deciphering the mechanism of thermotolerance in wheat.

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