

Genome-Wide identification of different dormant *Medicago sativa* L. microRNAs in response to fall dormancy

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Background: MicroRNAs (miRNAs) play a critical role in post-transcriptional gene regulation that down-regulate target genes by mRNA degradation or translational repression. Evidence is increasing for their crucial roles during plant development. Identification of miRNAs at the global genome-level by high-throughput sequencing is essential to functionally characterize miRNAs in plants. Alfalfa (*Medicago sativa* L.) is one of the most widely cultivated perennial forage legumes worldwide. Fall dormancy is an adaptive character related to the biomass production and winter survival in alfalfa. However, little is known about miRNA-mediated developmental regulation of fall dormancy in alfalfa. Here, we applied high-throughput sRNA sequencing and genome-wide mining to identify miRNAs that were responsive to fall dormancy.

Results: Four sRNA libraries were generated and sequenced from alfalfa leaves in two standard varieties, at two time points. Through integrative analysis, we identified 51 novel miRNAs of 206 families. We also identified 28 miRNAs associated with fall dormancy, including 20 known miRNAs and 8 novel miRNAs. Both high-throughput sequencing and RT-qPCR confirmed that 8 known miRNA members were up-regulated and 6 known miRNA members were down-regulated in response to fall dormancy. Among the 51 novel miRNAs, 5 miRNAs were up-regulated and 3 miRNAs were down-regulated in response to fall dormancy, respectively. In addition, 566 and 583 candidate potential miRNAs were identified at the genome level of *Medicago truncatula* and transcriptome of *Medicago sativa*.

Conclusion: We identified 20 known miRNAs 8 new miRNAs that were responsive to fall dormancy by high-throughput sequencing of small RNAs from *Medicago sativa*. Our data provides a useful resource for investigating miRNA-mediated regulatory mechanisms of fall dormancy in alfalfa, these findings are of importance for our understanding of the roles played by miRNAs in response of plants to abiotic stress in general and fall dormancy in alfalfa.