

Genome-wide dynamic spatial gene expression and alternative polyadenylation in red clover.

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Red clover (*Trifolium pratense* L.) is a cool season forage legume, grown throughout the Northeastern USA. Red clover provides high value feed to the livestock because of high protein content and easy digestibility. To date, genomic resources for red clover are scarce. We have constructed a *de novo* transcriptome assembly of red clover representing different tissue types. The draft assembly consists of 37,565 contigs, genes, with N50 and average contig length of 1,707 and 1,262 bp, respectively. A comparative study with three other legume species, *Medicago truncatula*, *Glycine max* and *Phaseolus vulgaris*, showed a high degree of sequence conservation between red clover and other legumes. The assembled transcriptome was annotated to allow identification of putative function. A comparative gene expression analysis between different tissue types was performed using the assembled transcriptome as the reference, which revealed dynamic gene expression patterns across different tissue types and also identified spatially dynamic gene co-expression clusters. Additionally, our genome-wide survey of mRNA polyadenylation in the different tissues revealed evidence of alternative polyadenylation (APA) in different tissues. Alternative polyadenylation can result in differential stability of mRNA's and production of alternate proteins. A major difference in poly(A) site usage between root and flower tissues was observed. Genes representing tissue-enriched clusters, and those that were observed to be alternatively polyadenylated in different tissues, were subjected to Gene Ontology enrichment analysis to identify over-represented functional groups. Identification of these tissue-enriched gene co-expression clusters can help in future research focusing on developmental studies across tissues or in biotechnological improvement of red clover. Comparison of genes displaying APA and differentially expressed genes between tissue types has allowed us to identify set of genes where APA might play a role in regulation of tissue-specific gene expression. Altogether, we provide an analysis of tissue-enriched gene expression and alternative polyadenylation in red clover tissues.