

Transcriptional Analysis of Flowering Time in Switchgrass

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Project Goals: The project is intended to develop tools to streamline and improve efficiency for development of switchgrass as a sustainable biofuel crop. We use genomic information from maize and other species to identify genes responsible for traits that make switchgrass a more sustainable biofuel crop and to develop DNA-based selection methods to speed up the process of developing improved switchgrass cultivars. One of the project's objectives is to identify genes involved in the control of flowering time, a trait correlated with biomass yield. The work described below details one of the approaches we used to investigate flowering time in switchgrass.

Over the past two decades, switchgrass (*Panicum virgatum*) has emerged as a priority biofuel feedstock. The bulk of switchgrass biomass is in the vegetative portion of the plant, therefore, increasing the length of vegetative growth will lead to increase in overall biomass yield. The goal of this study was to gain insight into the control of flowering time in switchgrass, to assist in developing cultivars that have extended vegetative phases through delayed flowering. RNA-sequencing was used to assess genome-wide profiles of transcription across time, between switchgrass genotypes belonging to the two main ecotypes: upland, typically early flowering, and lowland, typically late flowering. Leaves and tissues enriched for the shoot apical meristem (SAM) were collected in a developmental series from emergence through anthesis for RNA extraction. The morphology of the SAM was also tracked to determine the stage of meristem transition and to choose samples that flanked the SAM transition for sequencing and expression analyses. The analyses revealed differential expression patterns between early- and late-flowering genotypes for known flowering time orthologs. In addition, based on expression patterns, many of the identified genes could be classified as putative promoters or repressors of flowering. The candidate genes presented here will be further supported by functional confirmation in switchgrass or the model grass, *Brachypodium*, and may be used to guide switchgrass improvement through marker assisted breeding and/or transgenic or gene editing approaches.

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