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**Transcriptional analysis of flowering time in switchgrass**

Known flowering time orthologs display differential expression patterns between early- and late-flowering switchgrass genotypes.

**The Science**

In this study, we identified flowering time gene candidates that could be employed to manipulate flowering time in upland, cold-tolerant switchgrass cultivars, with the goal of increasing total biomass yield for these northern accessions.

**The Impact**

The candidate genes presented here may be used to guide switchgrass improvement through marker-assisted breeding and/or transgenic or gene editing approaches.

**Summary**

Over the past two decades, switchgrass (*Panicum virgatum*) has emerged as a priority biofuel feedstock. Since the bulk of switchgrass biomass is in the vegetative portion of the plant, increasing the length of vegetative growth will lead to an increase in overall biomass yield. The goal of this study was to gain insight into the control of flowering time in switchgrass that would assist in developing cultivars with longer vegetative phases through delayed flowering. We used RNA sequencing to assess genome-wide expression profiles across a developmental series between switchgrass genotypes belonging to the two main ecotypes: upland, typically early flowering, and lowland, typically late flowering. Leaf blades and tissues enriched for the shoot apical meristem (SAM) were collected in a developmental series from emergence through anthesis for RNA extraction. We then sequenced RNA from samples that flanked the SAM transition stage for expression analyses. The analyses revealed differential expression patterns between early- and late-flowering genotypes for known flowering time orthologs. Namely, we identified genes shown to play roles in photoperiod response and the circadian clock in other species as potential candidates for regulating flowering time in the switchgrass genotypes analyzed. Based on their expression patterns, many of the differentially expressed genes could also be classified as putative promoters or repressors of flowering. The candidate genes presented here may be used to guide switchgrass improvement through marker-assisted breeding and/or transgenic or gene editing approaches.

**Contacts (BER PM)**

N. Kent Peters
Program Manager, Office of Biological and Environmental Research
kent.peters@science.doe.gov, 301-903-5549

**(PI Contact)**

Shawn M. Kaeppler
University of Wisconsin - Madison
smkaeppl@wisc.edu

Michael D. Casler
USDA-ARS & University of Wisconsin - Madison
mdcasler@wisc.edu

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**Publications**

Tornqvist, C.-E. *et al.* “Transcriptional analysis of flowering time in switchgrass**.”** *BioEnergy Research* **10**, 700-713 (2017) [DOI: 10.1007/s12155-017-9832-9].

**Related Links**

<https://link.springer.com/article/10.1007/s12155-017-9832-9>

**PM Recommendation for SC Web Publication**