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**Many genomic positions in switchgrass contribute to flowering time, a major biomass yield determinant**

Genome-wide associations with flowering time in switchgrass using exome-capture sequencing data.

**The Science**

We performed genome-wide association studies to characterize the genetic architecture and genes underlying flowering time regulation in switchgrass. We then identified association with flowering time at multiple loci, including in a homolog of the gene FLOWERING LOCUS T and in a locus containing the gene TIMELESS, a homolog of a key circadian regulator in animals.

**The Impact**

Since late flowering allows for an extended period of vegetative growth and increased biomass production, flowering time is a major determinant of biomass yield in switchgrass (*Panicum virgatum*), a perennial bioenergy crop. A better understanding of the genetic regulation of flowering time in switchgrass will aid the development of switchgrass varieties with increased biomass yields, particularly at northern latitudes where late-flowering but southern-adapted varieties have high winter mortality.

**Summary**

Improving biomass yields in switchgrass, a North American perennial grass, is a key aspect of increasing its economic viability as a bioenergy feedstock. Since most biomass accumulates before flowering, flowering time is a major determinant of biomass yield. Many of the highest yielding switchgrasses are late-flowering varieties that originate from southern latitudes, but the yield advantages of these southern switchgrasses are often not realized at northern latitudes due to high winter mortality. A better understanding of the genetic regulation of flowering time will aid the development of switchgrass cultivars with a combination of desirable traits (e.g., flowering time, adaptation, feedstock quality) to increase biomass yields and bioenergy production, particularly at northern latitudes. Our results suggest that flowering time variation in switchgrass is due to variation at many positions across the genome and that genes in both the photoperiod and autonomous pathways likely generate switchgrass flowering time variation. Future work on expanded panels of southern-adapted and lowland samples, and of natural hybrids and bred crosses that break up population structure, will complement this study and expand our understanding of flowering time regulation in switchgrass.

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**Publications**

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