

## Manipulation of Seasonal Dormancy as a Strategy to Improve Switchgrass Biomass Yield

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**Project Goals:** The Center for Bioenergy Innovation (CBI) vision is to *accelerate domestication of bioenergy-relevant, non-model plants and microbes to enable high-impact innovations at multiple points in the bioenergy supply chain*. CBI will address strategic approaches to increase the sustainability of biomass production to the current bioeconomy in the areas of: 1) high-yielding, robust feedstocks, 2) lower capital and processing costs via consolidated bioprocessing (CBP) to specialty biofuels, and 3) methods to create valuable byproducts from the lignin. CBI will identify and utilize key plant genes for growth, composition and sustainability phenotypes as a means of achieving lower feedstock costs, focusing on poplar and switchgrass. We will convert these feedstocks to specialty biofuels (C4 alcohols and C6 esters) using CBP at high rates, titers and yield in combination with cotreatment or pretreatment. CBI will maximize product value by *in planta* modifications and biological funneling of lignin to value-added chemicals.

To establish a sustainable biomass energy system, improving biomass yield and the seasonal distribution of production is crucial. The short growing cycle of switchgrass (*Panicum virgatum* L) cultivars limits not only the amount of biomass accumulated but also the seasonal distribution, which is restricted to one harvest per year at the end of summer. Like many warm season species, switchgrass evolved winter dormancy as an adaptation strategy to survive cold winters, especially in the most northern latitudes. Because of winter dormancy, switchgrass growth and biomass accumulation are repressed substantially during the short-photoperiod months even in southern environments where winter temperatures are mild. Reducing winter dormancy might be a viable strategy to increase yield in southern environments with mild winters. The overall objective of this research is to investigate the effects of manipulating winter dormancy in switchgrass, and to identify the genetic components (QTL and candidate genes) underlying winter dormancy and related traits such as flowering time and spring regrowth in a F1 pseudo-testcross from a non-dormant parent (B6) with a dormant parent (AP13). Genotyping-by-sequencing generated 2.5 million raw variants of which 3761 were single-dose (SDA) maternal alleles and 4133 were paternal SDAs. Linkage maps constructed with Mendelian segregating and distorted SDAs with a p-value  $\geq E^{-15}$  resulted in 18 linkage groups representing the nine K and nine N sub-genome chromosomes. A total of 3555 markers were mapped in the maternal map (2238 cM) and 3711 markers in the paternal map (1826 cM). QTL identification for one environment for fall regrowth height, NDVI, and spring emergence date showed several promising chromosome regions associated with the traits. Field data will continue to be collected and QTL analysis across years will be conducted. The substantial genetic variation in the onset and duration of dormancy shows potential for breeding of non-dormant or semi-dormant cultivars for the southern regions where winters are mild.

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