

193. Genetic Control of Flowering in Switchgrass

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Project Goals: The goal of this project is to identify the genes involved in flowering time and to elucidate genetic mechanisms controlling the flowering responses of switchgrass. The specific objectives are to: 1) Conduct a genome-wide association study (GWAS) of flowering time in both lowland and upland panels; 2) Validate genes associated with flowering time in segregating populations; and 3) Examine transcriptome profiling with extreme genotypes using RNA sequencing.

The timing of phase change from juvenile (vegetative) to adult with reproductive competence is a key factor influencing biomass yield of switchgrass. A decline in biomass yield is typically observed in switchgrass immediately following completion of flowering. In temperate regions of the USA, if flowering time can be delayed about 4-5 weeks, biomass yield can potentially increase 30-50%. The use of late-flowering switchgrass genotypes has proven an effective mechanism to increase biomass production in the northern USA. Southern populations (lowland ecotypes) of switchgrass can be 4–6 weeks later in flowering time than upland types, and selection of late flowering genotypes with southern origin, but adapted to northern conditions, can extend vegetative growth. To develop a rational strategy for creating improved switchgrass with late flowering, it would be beneficial to have a better understanding of the genes that control flowering time in switchgrass. Through GWAS of 1.3 million single nucleotide polymorphisms with 510 diverse individuals from both lowland and upland panels, we have identified 10 genes significantly associated with flowering time. One candidate gene is a homolog of Flowering Locus T (FT). We have developed 3 mapping populations derived from upland (early flowering) and lowland (late flowering) materials and established the populations in the field [in DeKalb, IL and West Lafayette, IN](#). Flowering time will be evaluated in two locations over multiple years. We will genotype the mapping populations using exome capture and genotyping-by-sequencing, and further detect and verify genetic associations in the mapping populations of switchgrass. Knowledge generated from the project will aid breeding programs in developing late flowering varieties of switchgrass that fully utilize the growing season and achieve high biomass yield.

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