

Genomic Selection and Genome-wide Association Analyses for Bioenergy Traits in Switchgrass

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Project goals: 1. Employ exome capture to assess SNP marker diversity across the entire range of switchgrass. 2. Initiate genomic selection and phenotypic selection (as a control) on two switchgrass populations. 3. Identify genes involved in flowering time regulation in switchgrass. 4. Conduct candidate gene and QTL analyses of genes related to recalcitrance in switchgrass. 5. Develop bioinformatic tools to support switchgrass research within and outside of GLBRC.

Abstract: Switchgrass, a relatively high-yielding and environmentally sustainable biomass crop, has been chosen by the USDA and the USDOE as one of the main sources of bioenergy in the US. However, further genetic gains in biomass yield and quality must be achieved to make it an economically viable bioenergy feedstock. Genomics-assisted selection methods are particularly promising for generating rapid genetic gains in switchgrass and meeting the goals of a substantial displacement of petroleum use with biofuels in the near future. Here, we report on two types of analyses supporting the use of genomics-assisted selection for switchgrass breeding: genomic selection (GS), i.e., the use of genome-wide marker information to directly predict performance in breeding programs, and genome-wide association studies (GWAS), i.e., the search for regions in the genome showing significant associations with the traits of interest. We assessed GS prediction procedures for biomass yield, plant height and heading date in breeding populations and achieved prediction accuracies which, we believe, should motivate the implementation of GS in switchgrass breeding programs. We are currently performing GWAS for morphological and quality traits in a diversity panel and, according to preliminary results, we should be able to identify several candidate genomic regions involved in the elaboration of important bioenergy traits. The results in GS and GWAS that we are presenting here will pave the way for upcoming breeding experiments which will compare genomics-assisted selection to traditional types of selection and generate new cultivars for sustainable bioenergy production.

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