Systems biology and genomic approaches uncover distinct genes controlling switchgrass biomass and height

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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 addresses strategic barriers 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 biofuels using CBP with cotreatment at high rates, titers and yield in combination with catalytic upgrading into drop-in hydrocarbon fuel blendstocks.

Switchgrass (*Panicum virgatum*) is a perennial crop and is an important bioenergy feedstock for the future. As such, it is important to understand which genotypes confer increased yield of switchgrass which can lead to increased conversion of lignocellulose into biofuels. To this end, in this study we performed genome wide association studies from multiple common garden sites (Noble Research Institute and University of Georgia) across the United States to determine which genotypes were associated with increased switchgrass biomass. Furthermore, we leveraged a novel systems biology approach (Random Walk with Restart – Filter; RWR-Filter) using multiplex networks from multiple lines of biological experimental data in order to analyze genetic variants below standard thresholds of genome-wide significance. Using this approach, we attempted to glean mechanistic insight into the biological pathways underlying switchgrass biomass and height. RWR-Filter elucidated a number of genetic variants contributing to switchgrass height that were associated with genes known to be involved in abiotic stress signaling, and transcription factors known to modulate jasmonic acid and ethylene biosynthesis. Conversely, variants implicated in above-ground shoot biomass included genes related to cell wall biosynthesis, solute transport, maintenance of osmotic potential, and maintenance of cellular redox state. Our findings indicate that distinct genetic variants and biological pathways underlie two closely related phenotypes (above-ground shoot biomass and height) which are associated with increased switchgrass yield. By understanding which switchgrass genotypes confer optimal growth and biomass yield, we can better inform genomic selection efforts to increase feedstock productivity.