

14. Populus Natural Variation Study, from Single Nucleotide Polymorphisms to Reduced Recalcitrance Biomass and Elucidation of New Function for an EPSP Gene

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Project Goals: The BioEnergy Science Center (BESC) is focused on the fundamental understanding and elimination of biomass recalcitrance. BESC's approach to improve accessibility to the sugars within biomass involves (1) designing plant cell walls for rapid deconstruction and (2) developing multi-talented microbes or converting plant biomass into biofuels in a single step (consolidated bioprocessing). BESC biomass formation and modification research involves working directly with two potential bioenergy crops (switchgrass and Populus) to develop varieties that are easier to break down into fermentable sugars. We are using both testing and generating of large numbers of natural and modified plant samples as well as developing genomics tools for detailed studies into poorly understood cell wall biosynthesis pathways.

Quantitative trait loci cloning for the discovery of genes underlying polygenic traits has historically been cumbersome in long-lived perennial plants like Populus. Linkage disequilibrium-based association mapping has been proposed as a cloning tool, and recent advances in high-throughput genotyping and whole-genome re-sequencing enable marker saturation to levels sufficient for association mapping with no a priori candidate gene selection. Here we illustrate the successful utilization of this technique to identify a novel isoform of a shikimate biosynthesis enzyme with hitherto unknown transcriptional regulatory activity. The 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase catalyzes the sixth step in the shikimate pathway and is functionally conserved across prokaryotes and eukaryotes. Despite observing protein sizes ranging from 317 to 675 amino acids in 41 sequenced plant genomes, no functional difference has been suggested for these various isoforms. Here, we report the identification of a Populus EPSP that functions as a transcriptional regulator of genes in the phenylpropanoid, flavonoid and tryptophan pathways. This isoform encoded a 518-residue protein with an N-terminus region showing structural similarities to the DNA-binding helix-turn-helix motif and it also exhibited nuclear-localization capability. Based on these observations, we propose a new model for transcriptional regulation of secondary cell wall and flavonoid biosynthesis in Populus.

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