

Accelerated Domestication of *Populus* for Bioenergy Production and Enhanced C Sequestration

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The carbon sequestration potential of poplar (*Populus* sp.) can be enhanced by increasing 1) aboveground productivity, 2) carbon allocation belowground to root production, and 3) carbon partitioning into chemical constituents that are more recalcitrant to microbial degradation. The availability of the poplar gene sequence and the concurrent development of genomic resources and tools, including advanced-generation structured pedigrees, high density genetic linkage marker maps, whole-genome microarrays and high throughput, short-read sequencing platforms for global transcript profiling, and broad spectrum metabolic profiling, make the identification of quantitative trait loci (QTL) associated with these traits relatively facile. Furthermore, the identification and validation of candidate genes associated with high value traits can also be addressed by these modern genomic tools, but they remain the key challenges given the large number of gene targets in an identified QTL interval and the paucity of information for the majority of genes. The current status of our research in poplar on enhancing drought tolerance, increasing fine root production, and increasing the production of secondary metabolites (m) will be highlighted. Particular attention will be given to the use of metabolomics to validate the function of candidate genes, and the coupling of metabolite profiling and QTL analysis for the identification of mQTL that can be exploited to increase the production of secondary metabolites belowground for increased carbon sequestration.

Acknowledgements: This research was supported by the Office of Biological and Environmental Research of the U.S. Department of Energy. Oak Ridge National Laboratory is managed by UT-Battelle, LLC, for the U.S. Department of Energy under contract DE-AC05-00OR22725.

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