192. Abiotic stress induced Poplar transcriptome analyses.

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Project Goals:
1) To identify a whole genome-wide functional gene network (an interaction network of genes) for poplar using gene orthology based projections and identify subnetworks associated to abiotic stress tolerance and bioenergy related traits, 2) To identify a set of candidate genes which interact to produce abiotic stress resistant phenotypes, and to identify diagnostic genetic markers associated with the sub-networks, 3) To create an interactive online resource of regulatory and metabolic network of abiotic stress associated candidate genes and genetic markers for the poplar tree improvement community.

Abstract:
Improving abiotic stress of poplar clones used in plantation forestry is of significant economic importance. To better investigate the complex physiological, cellular, and molecular processes that underlie abiotic stress response in poplar we are investigating drought, heat, salt and cold stress induced transcriptomes from the reference Populus trichocarpa Nisqually-1 genotype. The mRNA was isolated from leaf, xylem and root tissue types at three time points including the control untreated and after early and prolonged stress time points. The RNA-Seq based transcriptome data is currently being analyzed for (1) identifying genes in the weighted co-expressed gene network, (2) compare the expressed gene network with the baseline poplar functional gene network constructed by orthology driven projection from the Arabidopsis probabilistic gene network, (3) reference genome guided and de-novo assembly of transcripts, (4) identifying gene loci and transcripts showing stress induced alternative splicing patterns with intron retention events (5) improving reference genome annotation by identifying novel gene loci and transcript isoforms. To validate key gene interactions and identify novel protein-protein interactions in an Y2H screening, cDNA libraries are being constructed from salt and drought stress treated poplar tissues. Following baseline experiments on reference Nisqually-1 genotype, we are in the process of conducting similar coexpression analyses studies of drought and salt resistant genotypes of poplar hybrids.

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