EXTENSIVE CLONAL VARIATION IN DROUGHT-INDUCED GENE EXPRESSION CHANGES IN LOBLOLLY PINE

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In the next few decades, drought intensity is expected to dramatically increase in multiple areas along the range of the loblolly pine (*Pinus taeda* L.). Identifying and propagating loblolly varieties with high drought tolerance will be instrumental to maintain or increase productivity through large-scale replanting efforts. While phenotyping and breeding efforts have long recognized and tested varieties with increased resistance to aridity, determining the genetic basis of drought tolerance represents a more direct way to select loblolly varieties capable of sustaining a prolonged water deficit. Previous studies relying on population genomic or microarray-based gene expression data have begun to unveil the genetic underpinning of drought tolerance in loblolly pine. However, these analyses were based on a limited set of loblolly genes. Here, we applied for the first time an RNA-seq transcriptomic approach to specifically investigate the genetic response of two loblolly clones that were previously shown to exhibit either low or high drought tolerance. We analyzed 54,826 loblolly transcripts from 24 root samples and found significant variation in expression patterns between control and treatment (drought-simulated conditions) in both clones. More than 3,800 genes significantly changed their expression level in roots of water deficit stressed vs. control ramets. The two clones shared only 6-13% of upregulated and 10-11% downregulated differentially expressed (DE) genes. Although genes from some families known to be involved in drought responses, including dehydrins and LEAs, showed differential expression between control and treatment ramets in both clones, we found many gene families whose expression was affected only in one of the two clones. Notably, most DE genes were downregulated in the drought-sensitive clone and upregulated in the drought-tolerant clone. Our results unveiled thousands of genes involved in drought tolerance in loblolly and underscore the importance of investigating the genetic mechanisms of stress resistance across multiple varieties.