Associations Genetics of the Loblolly Pine Metabolome

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Stress tolerance phenotypes in forest trees have been primarily examined at large morphological and anatomical scales. Here, we examine 214 primary and secondary metabolites in loblolly pine (*Pinus taeda L.*) in an effort to dissect these micro-scale phenotypes into their genetic components. A preliminary analysis of six clones revealed that metabolomic profiles could be reliably characterized using GC/TOF mass spectrophotometry. This technology has been applied to a set of ~400 clones collected across the range of loblolly pine. Each clone has two biological replicates, with each biological replicate having two technical replicates. Genetic associations between ~4,000 single nucleotide polymorphisms (SNPs) and each metabolite will be examined using standard general and mixed linear models. Only 40% of the targeted compounds are known fully, thus establishing this as a novel look into the spectrum of biologically important and putatively adapted metabolites within forest trees.

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