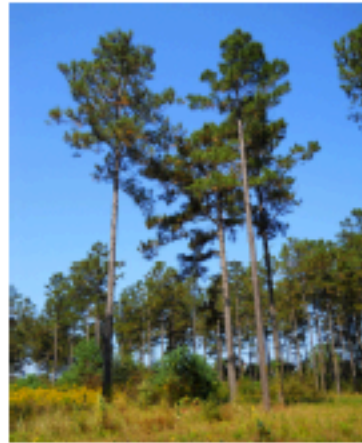


UNRAVELING MOLECULAR MECHANISMS OF COMPLEX TRAITS IN PINE WITH GENOME WIDE ASSOCIATIONS AND GENE COEXPRESSION NETWORKS

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INTRODUCTION



Loblolly pine (LP), a long-lived tree species, is the most productive and economically important wood species in the southern United States. Genetic improvement programs for pine trees in this region have focused on **survival**, early and rapid **growth**, **resistance** to diseases and pests and stem shape.

OBJECTIVES

In this study, we present the first comprehensive integrated analysis in LP of **genome-wide association study** (GWAS) and **gene co-expression networks** to provide an improved characterization of the gene space and to identify patterns of selection among orthologous gene families

MATERIAL AND METHODS



45 full sib-families (1999 individuals of *Pinus taeda*) phenotyped for **rust resistance**, **stem water potential** (SWP) and **volume** (VOL)



Genotyping with Illumina sequencing (**sequence capture** method) and FreeBayes (**31,589 filtered SNPs** with vcflib)



BLUP estimation (R package ASReml v.2), **population genetics** (R package adegenet), **GWAS** (FarmCPU method implemented in R package rMVP)



Gene coexpression networks (R software) based on RNA-Seq data from *Pinus taeda*

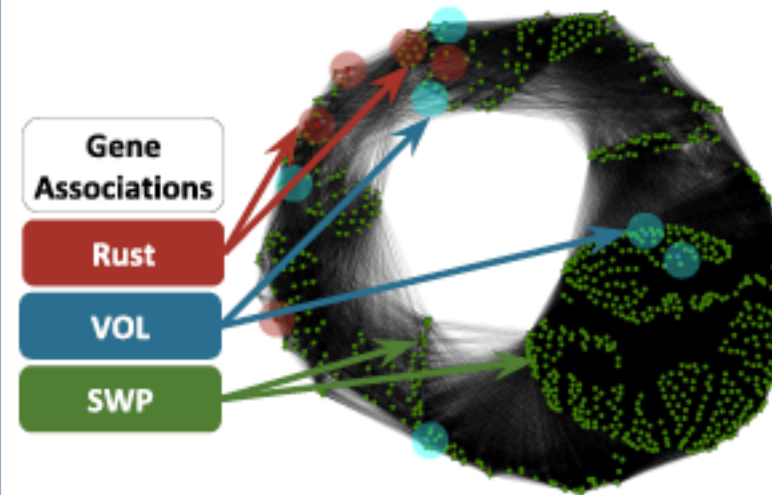
RESULTS

PHENOTYPIC ANALYSES

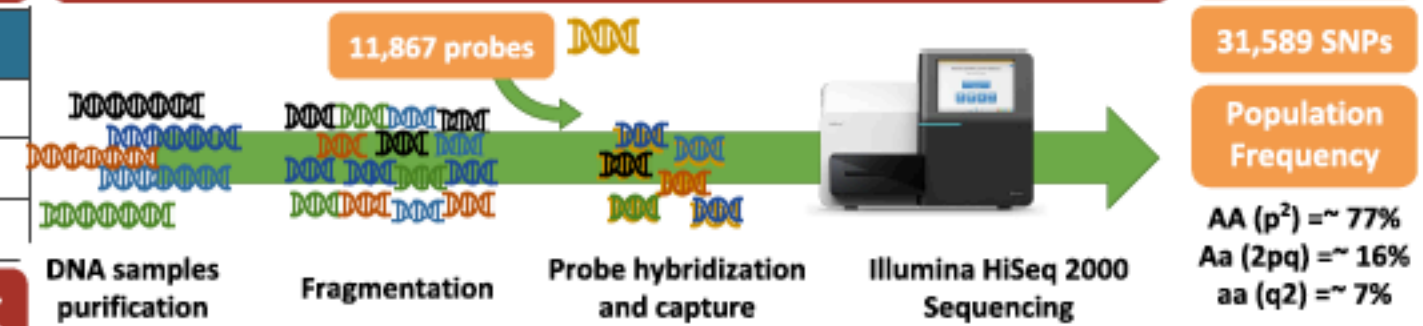
Narrow-Sense Heritability	
Rust	0.05 to 0.34
SWP	0.05 to 0.1
VOL	0.17 to 0.32

GENE COEXPRESSION NETWORK

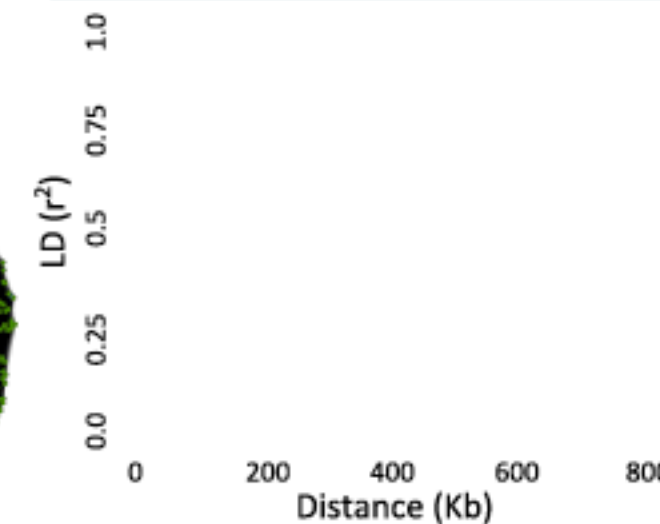
Network modelled with genes associated with the GWAS identified SNPs



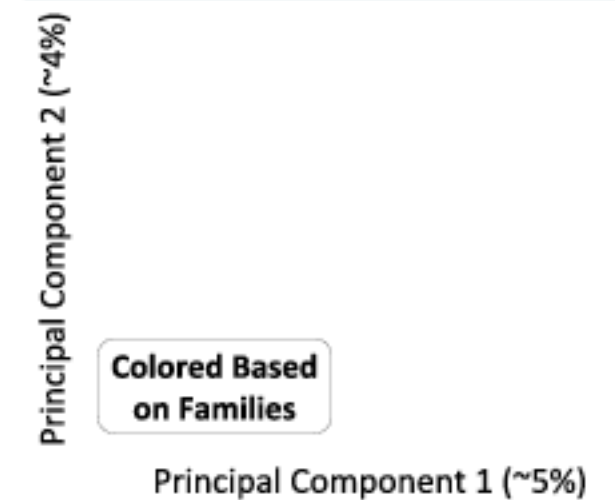
GENOTYPIC DATA



Linkage Disequilibrium Decay



Principal Component Analysis



GWAS RESULTS AND LINKAGE DISEQUILIBRIUM NETWORKS



ACKNOWLEDGMENTS AND FUNDING

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