

AN ANNOTATED CONSENSUS GENETIC MAP FOR *PINUS TAEDA* AND EXTENT OF LINKAGE DISEQUILIBRIUM IN THREE GENOTYPE-PHENOTYPE DISCOVERY POPULATIONS

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A consensus genetic map for loblolly pine was constructed by merging three previously published maps with a map from a pseudo-backcross between loblolly pine and slash pine. The consensus map positioned 3700 markers via genotyping of over 1200 individuals from four pedigrees. Functional predictions for nearly 3500 mapped EST markers were improved by alignment to full-length loblolly pine transcripts. Alignments to the loblolly pine genome mapped over 3000 scaffold sequences onto the 12 linkage groups. The consensus genetic map was used to compare the extent of genome-wide linkage disequilibrium in an association population of distantly related individuals (ADEPT2), a multiple-family pedigree used for genomic selection studies (CCLONES), and a full-sib quantitative trait locus mapping population (BC1). Weak linkage disequilibrium was observed in CCLONES and ADEPT2. Average squared correlations, R^2 , between genotypes at SNPs less than 1 cM apart was less than 0.05 in both populations, and R^2 did not decay substantially with genetic distance. By contrast, strong and extended linkage disequilibrium was observed among BC1 full-sibs where average R^2 decayed from 0.8 to less than 0.1 over 53 cM. The consensus map and analysis of linkage disequilibrium establish a foundation for comparative association and QTL mapping between genotype-phenotype discovery populations.

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