

Detection of QTLs for economically important traits in Loblolly Pine

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Abstract. Understanding the genetic basis of economic traits in forest trees has been a goal of tree breeders and forest geneticists. Genomic mapping using molecular markers is a powerful new tool that extends conventional quantitative approaches to genetic analysis. Phenotypic variation in height, volume, disease resistance, lignin etc. can be associated with segregating genetic markers if these traits are under the control of one or a few major genes (quantitative trait loci, QTLs). Our studies are directed toward detection of QTLs inherited from the common seed parent in a large half-sib family. The effects of these QTLs are representative of average effects across the population and thus can be interpreted as components of breeding value.

Cyclic shoot elongation was evaluated in an open-pollinated family from clone 9-1020. Yearly height measurements on 1,000 trees were taken over 3 years and QTLs have been identified. The heritability (additive genetic variation/phenotypic variation) for shoot elongation in young trees is approximately 1/2. The 2 QTLs found explain approximately 50% of the additive genetic variation expected to be transmitted by the seed parent in the half-sib family, which is about 14% of phenotypic variation. While these QTL effects are only a small portion of the total phenotypic variation in the family (3-4% each), they are the average effect of the alternative QTL alleles in the maternal with respect to a larger breeding population.

Yearly height measurements will continue to be taken to study QTLs over time. QTLs for volume, lignin content and rooting ability will also be evaluated.

Keywords: shoot elongation, QTLs. RAPDs. loblolly pine, half-sib family