MAPPING QUANTITATIVE TRAITS FOR WOOD DENSITY IN LOBLOLLY PINE

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EXTENDED ABSTRACT

We have been focusing on identifying the quantitative trait loci (QTLs) which control wood property traits in loblolly pine *(Pinus taeda L.).* Previously GROOVER *et al.* (1994) mapped QTLs for wood specific gravity (WSG) using data from 177 progeny of a three-generation pedigree. This pedigree was constructed from two grandparental pairs which both displayed divergent values for WSG (scored as an average value of WSG for the first 8 years 0f growth). A conservative single-factor ANOVA approach (EDWARDS *et al.,* 1987) was used to detect five QTLs on five different linkage groups at p 0.05 (GROOVER *et al.* 1994).

More recently KNOTT *et al.* (in press) extended the methods of HALEY *et al.* (1994) and VISSCHER and HALEY (1996) to fit an outbred model. These methods were used to re-analyze the WSG data by fully utilizing the three-generation structure of this outbred pedigree. These analyses combine information from a number of linked markers to provide the most powerful test for the presence of genetic variation. At regular genomic intervals the probability of an offspring being each of the four possible genotypes is calculated (HALEY *et al.* 1994). These genotypic probabilities were combined to consider the difference in effect of the alleles inherited from the maternal parent (ie, the difference in effect between the allele that originated in the high-WSG grandparent and that for the low-WSG grandparent), the paternal parent and an interaction term (which provides information about the deviation from additivity of the four alleles). The phenotypes are then regressed onto these probabilities using least squares analyses (HALEY and KNOTT 1992; HALEY *et al.* 1994). These regression methods are relatively simple and compare favorably to maximum likeliehood methods, thereby allowing the analysis of more complex (and potentially more realistic) genetic models (HALEY and KNOTT 1992; HALEY *et al.* 1994). Therefore, in addition to identifying regions that harbor a single QTL, we can now estimate the effects of whole linkage groups, test for the presence of polygenic variation and also test for the action of several linked QTLs (VISSCHER and HALEY 1996; KNOTT *et al.* in press).

In the re-analysis of WSG in KNOTT *et al.* (in press), a sex-average map consisting of 12 linkage groups was constructed from 171 progeny and a subset of 119 genetic markers (selected from 316 available makers based on informativeness and even spacing). Analyses

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were performed for one and two QTLs per linkage group. Two levels of significance were reported for each analysis (Lander and Kruglyak 1995). A "suggestive level" is where 0ne significant result is expected by chance in a genome-wide analysis. A "significant level" is where a significant result is expected to occur 0.05 times in a genome-wide analysis. The genome-wide analysis includes 12 independent tests (one for each linkage group). Therefore, $p < 0.083$ and $p < 0.0043$ (using Bonferoni's correction) would be required for each linkage group to obtain a suggestive and significant genome-wide level, respectively.

Linkage groups 3, 13 and 14 contain a single QTL attaining the suggestive level 0f significance and linkage group 7 contains a single QTL at the significant level. The effect 0f the QTL on linkage group 7 accounts for 8% of the residual variance in the progeny. The estimates of the effect of this QTL suggest that both parents are heterozygous at this locus and that the alleles are not additive. Linkage groups 2 and 3 both showed evidence at the suggestive level for two QTLs. In each case, the allele with a relative positive effect for 0ne QTL originated from the same parental gamete as the allele with the negative effect at the second QTL (thereby cancelling the effects of each other under a single QTL model). The conclusion of these analyses is that the current data does not support the presence of single QTLs with large effect for WSG, although there is evidence for QTLs with small effect (KNOTT *et al.* in press).

Recently, new phenotypic trait data has been collected for this pedigree to study components of wood specific gravity (eg, earlywood SG, latewood SG, a weighted average 0f early- and latewood SG, percent volume of latewood, and ring width). This data was collected ring by ring for years 3-11. The results from a preliminary single QTL analysis 0f these new traits were compared to those of KNOTT *et al.* (in press). For each of the following QTLs from this preliminary analysis, the genetic effects for the mother, father and interaction term were in the same direction as those found in KNOTT *et al.* (in press). On linkage group 3 for both latewood SG and weighted average SG at ring 11, a single QTL attaining the suggestive level of significance was found within 30 cM of that found in KNOTT *et al.* (in press). Both studies detected a single QTL (for earlywood SG at ring 4 which accounted f0r 10% of the residual variation in the preliminary study) at the significant level on linkage group 7, although they are at opposite ends of the linkage group. However, at ring 10, each of the five new traits showed evidence for a single QTL on linkage groups 13 and 14. On linkage group 14, four of the five new traits exceeded the significant threshold and each accounted for approximately 13% of the residual variance. For these two linkage groups, the new traits reside within 14 cM of those found in KNOTT *et al.* (in press). Although other single QTLs were detected at the suggestive level for this preliminary analysis (results n0t discussed), the results from this study and those of KNOTT *et al.* (in press) show that for the most part the findings are comparable among these different but related traits.

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