Detection And Genetic Mapping Of Quantitative Trait Loci Influencing Stem Growth Efficiency In Radiata Pine

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Declaration

The work presented in this thesis is my own. Assistance and specific contributions by others are referred to in the text and acknowledgments.

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Abstract

Needle-to-stem unit rate (NESTUR) is a stem growth index of conifer seedling trees that measures the efficiency of stemwood production per unit of needle growth. Five experiments were carried out in this thesis using progenies of two unrelated full-sib radiata pine crosses. The initial experiment (experiment 1) applied the bulked segregant analysis technique to determine whether RAPD analysis could be successfully extended to the development of molecular markers for NESTUR in radiata pine. The NESTUR values of 174 progenies of the full-sib family 12038 x 10946 were determined. Based on the genotypic analysis of the individuals, two quantitative trait loci (QTL) controlling NESTUR were identified at ANOVA P-levels of 0.01-0.001. An absence of RAPD fragment markers generated by primers OPE-06 and OPA-10 was associated with low NESTUR values, while primer UBC-333 generated a 550 bp band that was associated with high NESTUR values. Linkage to components of NESTUR (increments in stem diameter and stem volume) was demonstrated for one of the QTL, while the other was unique to NESTUR, and not shared with the components. There was a significant interaction between the two QTLs. Presence of OPA-10_{1200} locus appeared to inhibit expression of the QTL linked to UBC-333_{550}.

To further analyse the quantitative trait loci (QTLs) controlling NESTUR, a linkage map was constructed from RAPD markers segregating in 93 haploid progeny of another full sib cross (30040 x 80121) (experiment 2). Two hundred and sixty-two (262) markers were mapped to 14 linkage groups of at least 7 markers, ranging in size from 39 to 183 cM. The 14 linkage groups covered approximately 1511 cM of genetic map distance.

In experiment 3, the linkage map was used to map QTLs controlling NESTUR, as well as increments in seedling stem diameter, volume, and height and needle volume. Altogether, five putative QTLs were detected for NESTUR, with explained variation ranging from 9 to 22%. Of the five QTLs detected, 3 were coincidental with those for stem growth in height, diameter and volume. The two QTL positions that were unique to NESTUR were flanked by QTLs for the component traits. Together, effects of the five QTLs explained 48% of the total phenotypic variation for NESTUR.

Ability of identified markers to predict the phenotype and seedlings with growth potential was assessed in the cross 30040 x 80121, using six RAPD markers associated with NESTUR at ANOVA P-levels of 0.01-0.001 (experiment 4). The correlation between observed NESTUR and predicted values was 0.70. Differences in observed vs. predicted values were not large and did not indicate serious misclassifications, such as classification of an upper ranking individual into the lower group, or vice versa.

Over a two-year growth period, the ability of NESTUR to predict stem growth was strongly affected by seedling age. In contrast, markers linked to NESTUR showed a consistent ability to predict stem growth, irrespective of seedling age. Compared with the top 1% of the original population, seedlings selected for their genotypic values showed a higher stem volume growth of 103% in the first year, and 76% in the second year.

The expression of QTLs for stem volume, stem diameter, height, number of branches, number of whorls, and branches/whorl were compared at 5, 12, and 24 months of age. Two QTLs detected for height showed contrasting expression over two years, one was gradually reduced from LOD of 2.70 to 0.43 and the other

increased from 1.12 to 2.45. Compared with the pattern observed for height, LOD scan profiles for diameter and volume showed less temporal change of peaks, suggesting that the genetic control for height growth is probably more unstable than that of diameter. QTLs controlling the phenotype at the time of measurement (ie the final phenotype) showed similar magnitude of effects on that trait's respective increments (or growth rate).

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