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**DETECTION AND UTILISATION OF ASSOCIATIONS
BETWEEN GENETIC MARKERS AND QUANTITATIVE
TRAIT LOCI IN RADIATA PINE**

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ABSTRACT

This thesis focuses on the detection of quantitative trait loci (QTL) and utilisation of marker-trait associations in tree breeding programs. Theoretical expressions of variance components for single-marker ANOVA were derived and were used in deterministic simulations to determine the power of two-generation QTL mapping experiments in an outbred population containing full-sib or self families. Analysis of one linkage group for mapping QTL for wood density is presented. Genetic markers that are linked to the QTL can be used for selection purposes. The effect of using genetic markers to assist in different selection and deployment schemes was studied. The additional response to selection was computed using stochastic simulation. Most of the studies on MAS are concentrated on expected genetic progress for a single trait. However, in practice, the commercial breeding objective is nearly always composed of several traits. For a conventional breeding framework, a method is proposed to reduce the effect of sampling errors on the estimates of multivariate genetic parameters and thus increasing the efficiency of index selection. The general discussion of this thesis addresses QTL analysis methods, various aspects of QTL mapping designs and implementation of MAS in the radiata pine breeding program in New Zealand.

Dedicated to Mum, Dad and Sandhya

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