

**Quantitative Trait Loci Mapping in Merino Sheep and
Effect of Accuracy of QTL Parameter Estimation on
Marker Assisted Selection**

By

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University of New England, April 2008*



I certify that the substance of this thesis has not already been submitted for any other degree and is not currently being submitted for any other degree or qualification.

I certify that any help received in preparing this thesis, and all sources used, have been acknowledged in this thesis.

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Signature

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Dedication

*To Huna, Fahimeh
and my family*

Abstract

The objectives of this thesis were to perform a genome scan for important production traits in Australian Merino sheep and to investigate issues related to the prediction of marker assisted selection (MAS) response in single and multiple trait selection schemes in animal breeding programs.

In the first experimental chapter, a genome scan was performed for 4 growth and 7 fleece traits in Australian Merino sheep. Quantitative trait loci (QTL) parameters were estimated through single QTL interval mapping within and across four paternal half-sib families. The genome scan yielded 21 significant QTL for all traits at the 1% chromosome wise significance threshold level in within family analysis. Across family analysis supported most of the highly significant results from single family analysis but did not show any common significant QTL at the 1% chromosome wise significance threshold level across all families. Because of the relatively small progeny group sizes the power and the precision of the analysis are probably low and the QTL allele substitution effects are overestimated.

In the subsequent three chapters some important issues related to the application of QTL information in MAS, including efficient prediction of MAS response and effect of the accuracy of estimated QTL effect in single and multiple trait selection, were investigated.

In the second experimental chapter the efficiency of two deterministic methods in prediction of MAS response were compared to a stochastic simulation method. The

advantage of deterministic methods in prediction of MAS response is that they are fast and can be easily applied in optimization of breeding programs. The prediction of MAS response in two deterministic methods was based on selection index methodology, but in method II MAS response was predicted across genotypic groups, according to a truncation selection and selection differentials for polygenic effects in each group. The results showed that the prediction of non-MAS response was similar in all three methods. In case of MAS, all three methods showed that additional MAS over non-MAS response of a specific QTL effect was dependant on the initial QTL allele frequency. The standard selection approach (deterministic method I) provides acceptable prediction of MAS response at intermediate QTL allele frequencies but can lead to inaccurate prediction of MAS response in other cases. This method underestimates and overestimates MAS response under low or high QTL allele frequencies, respectively. Furthermore, prediction method I incorrectly predicts the same MAS response for a QTL with low or high allele frequencies, it can not clearly provide separate prediction of polygenic and QTL response and can not predict the changes in QTL allele frequency due to selection. This method shows the maximum MAS response when the QTL allele frequency is intermediate. Results from the deterministic method II, which were very close to outcomes obtained by stochastic simulation, didn't have the limitations of the prediction method I. Prediction method II shows higher MAS response when QTL allele frequency is lower. It can separate the MAS response due to QTL and polygenic effect and provides changes in QTL allele frequency. This method showed the maximum MAS response of one generation of selection when the favourable QTL allele frequency is 0.3 to 0.4, which was supported by stochastic simulation.

In the third experimental chapter we investigated the effect of the accuracy of estimated QTL effects on relative efficiency of expected MAS response over non-MAS response in a single trait selection scheme. The results showed that the realized MAS to non-MAS response of a QTL associated with some error was always less than expected, because of incorrect estimation of response due to QTL and also not optimal exploitation of polygenic effect. The probability of realized MAS to non-MAS response being less than expected increased with bigger standard error associated with estimated QTL effects. This probability was significantly higher for bigger QTL effects and/or lower heritability and MAS response could be equal or even less than non-MAS when a QTL with high standard error constitutes a considerable proportion of overall genetic variance. By taking into account a correct prior distribution of QTL effects, it is possible to have unbiased estimation of MAS responses using Bayes theorem.

In the last experimental chapter, first the effect of the accuracy level of non-MAS due to different sources of phenotypic information, such as own performance or some combination of own and relative performance, on additional MAS response was studied in a single trait (ST) selection scheme. Then in the second part the effect of the accuracy of estimated QTL effect was evaluated in multiple trait (MT) MAS considering QTL without or with some estimation errors in either one or two traits and the results were compared to ST MAS response. The results of the first part showed that the additional MAS over non-MAS response in ST selection was higher when the original non-MAS accuracy was lower (due to either low heritability or limited phenotypic sources of information). In the second part the index response of

MT_MAS was larger than non-MAS but the QTL information shifted the emphasis of selection response toward the trait with QTL information at the cost of the trait without QTL information. This change of emphasis of selection was larger with bigger QTL effect, lower non-MAS accuracy and an unfavourable correlation among traits. However, the additional MAS response for individual traits was higher in ST selection compared to response of traits with QTL in MT_MAS. Pleiotropic QTL resulted in higher MAS response particularly with an unfavourable correlation between traits. Considering the standard error associated with estimated QTL effect, the realized index response and the QTL trait response, which were obtained by incorporating prior distribution of QTL effects and applying a Bayesian approach, was less than expected and response of the trait without QTL information was more than expected, especially for larger QTL effect, higher standard error and an unfavourable correlation among traits. This study also showed that the inaccuracy associated with estimated QTL effects gives larger upward biased prediction of MAS index response in MT selection than in ST selection.

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