USE OF MOLECULAR MARKERS IN GENETIC EVALUATION OF ANIMALS WITH APPLICATIONS IN AUSTRALIAN MERINOS

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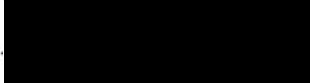
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I certify that the substance of this thesis has not already been submitted for any degree and is not currently being submitted for any other degree or qualification.

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

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Acknowledgments

Abstract

This thesis has examined aspects of detection and utilisation of genetic marker technology in animal breeding systems. Models have been proposed to include genetic marker information into mixed model equations for estimating major gene, or Quantitative Trait Loci (QTL) effects. These involve building a Gametic Relationship Matrix (GRM) with probabilities of identity by descent of QTL alleles between gametes. Algorithms to build the GRM were compared and a further method was proposed to build the GRM based on simulated QTL information. The simulated QTL method was identified as an approximation of the true GRM, as it involved simulating all possible QTL–marker genotype combinations.

Detection of linkage between genetic markers and QTL is usually based on data collected from animals in the field which are assumed to be unselected. The effect of this assumption on parameter estimates is unknown. Results from use of a restricted maximum likelihood detection method and a granddaughter design population, show that in the presence of within family (or sire) selection, large underestimates of variance occur and QTL position and effect estimates are inaccurate. However, selection of grandsires only has little effect on estimation of variance.

A non-iterative method for estimating genotype probabilities using genetic marker information is proposed. Random QTL effects are estimated using best linear unbiased prediction and genotype probabilities are calculated conditional on each possible QTL genotype. Stochastic simulated used to compare the non-iterative method with an iterative method, which incorporates segregation analysis, showed that the non-iterative method does not provide as accurate estimates, however, it is able to handle complex pedigrees. making it feasible over any pedigree structure.

A practical application of the use of genotype probability estimates is in mate selection decisions. Strategies for including genotype information on the recessive gene for black lambs in a sheep breeding program using mate selection were evaluated. Results show that for an observable trait, such as the gene for black lambs, there is little benefit in genotyping all animals. Similar gains can be made by use of genotype probability estimates or by selective genotyping and using mate selection to optimise genetic value of the progeny.

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