RAPD MARKER VARIATION IN MEAT QUALITY TRAITS OF POLL DORSET SECOND-CROSS LAMBS SELECTED FOR MUSCLE OR GROWTH

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Introduction

Crossbreeding has long been recognised as a powerful tool for exploiting genetic differences between two or more breeds to harness hybrid vigour in the offspring as a means of improving traits of economic importance. The growth and carcass merit of crossbred lambs is significant to the efficiency of production in the Australian meat sheep industry because the national flock is predominantly based on Merino. The development of DNA-based genetic markers has had a revolutionary impact on animal genetics in that genetic variation can be observed and exploited in the entire genome at the molecular level. Applications of DNA markers include investigations of genetic variability and inbreeding, species and strain identification, parentage assignment, the construction of high-resolution genetic linkage maps and identification of major genes for use in marker-assisted selection (Liu and Cordes 2004). Molecular markers can be classified into type I and type II markers. The former are markers associated with genes of known function, while the latter are associated with anonymous genomic segments. Random amplified polymorphic DNA (RAPD) markers are type II markers because their bands are amplified from anonymous genomic regions via the polymerase chain reaction. This research focuses on the prospects of RAPD markers distinguishing between Poll Dorset crossbred progeny carrying the genes for muscle or growth on the basis of their rams selected for high estimated breeding values (EBV) for the two traits.

Materials and Methods

One hundred and ninety six Poll Dorset x (Border Leicester x Merino) lambs from the Kirby Research Station in Armidale, New South Wales were used in a 3 x 2 experimental design for this study. They were progeny from 3 sire types selected on the basis of their EBVs for growth, muscle or control and accorded two levels of nutrition; low or high. Details of the pasture compositions of the nutrition levels, EBVs, sire selection, lambing, post lambing management, pasture assessment, live animal assessment, slaughter and abattoir assessment have been described (Hegarty *et al.* 2006). DNA was extracted from the muscle tissue and screened with nine RAPD markers whose primer sequences had been published (Malau-Aduli *et al.* 2006). Standard laboratory procedures of genomic DNA extraction, polymerase chain reaction assays, gel electrophoresis, RAPD band scoring and analyses were utilised (Sambrook and Russell, 2001).

Results and Discussion

Fat depth at the GR and C sites was significantly ($P<0.05$) influenced by level of nutrition and nutrition level x siretype interaction (Figure 1) in that fat depths were greater in crossbred lambs fed at high levels of nutrition than those fed low nutrition levels. Lambs selected for growth and fed high level of nutrition produced carcasses with the least KNIFE GR fat depth of 11.4mm, a significant reduction from 18.1mm in the control group fed low level nutrition (Figure 1). KNIFE GR fat depth was not affected by low levels of nutrition in crossbred lambs whose sires had been selected for growth or muscle. In Figure 2, all muscle measurements were similar except for slight differences in eye muscle depth (EMD) where high level of nutrition in groups selected for muscle and growth led to higher values than the control groups. All organisms are subject to mutations as a result of normal cellular operations or interactions with the environment, leading to genetic variation (polymorphism). In conjunction with selection and genetic drift, there arises genetic variation within and among individuals and species. For this variation to be useful to geneticists, it must be heritable and discernable whether as a recognisable phenotypic variation or as a genetic mutation distinguishable through molecular techniques. PCR amplification and gel electrophoresis resolution of products using RAPD primer A_2 in Figure 3 shows polymorphism of up to 5 bands was evident. It also demonstrates that at the molecular level, there are banding differences that can be picked up between crossbred progeny sired by rams with high genetic merit for growth or muscle. It would be interesting in further association studies to investigate if these differences can be significantly linked to QTL for inclusion in marker-assisted selection.

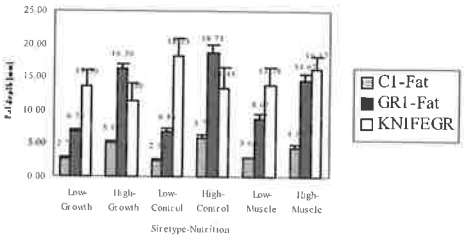

Figure 1: Fat depth variation at the C1 (CFAT), GR1 (GR1-Fat) sites and KnifeGR in mm.

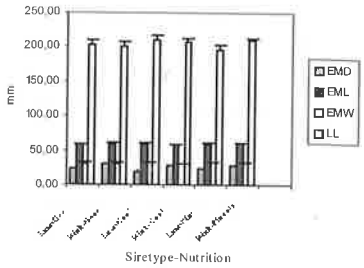

Figure 2: Siretype-nutrition variation in eye muscle depth (EMD), length (EML), width (EMW) and loin length (LL) in mm.

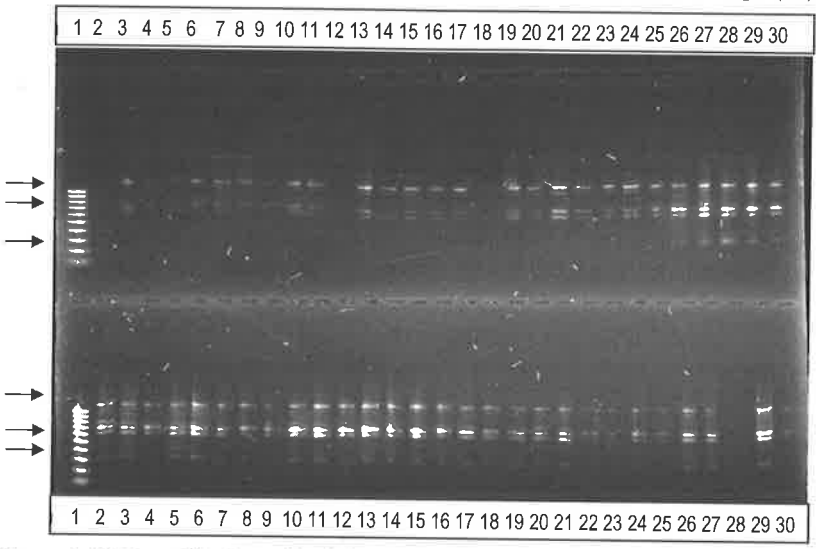

Figure 3: PCR amplification and gel electrophoresis resolution of products using RAPD primer A_2 in Poll Dorset x (Border Leicester x Merino) crossbred sheep. Upper Row Lane 12 and Lower Row Lane 28 controls without any band. 600-700bp and 1.1kb fragments produced bright fragments in all samples (except in the control lanes) indicating they were all crossbreds. At 300bp fragment in the upper row, a band is present in Lanes 26-29 (crossbreds sired by rams selected for high muscle EBVs) as distinct from Lanes 1-25 that did not have any band (crossbreds sired by either unselected rams or those selected for high growth EBVs).

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