DETECTION OF GENE MARKERS LINKED TO CARCASS AND MEAT QUALITY TRAITS IN A TROPICAL BEEF HERD.

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SUMMARY
Gene markers were used to detect genes responsible for genetic variation in carcass and meat quality traits in a tropical beef herd. Progeny from first cross Charolais x Brahman sires were grass finished to export specifications and a range of carcass and meat quality traits were measured. A total of 153 markers providing 81% genome coverage were analysed on 311 progeny from two sire families. Significant effects for one or more gene markers were detected for most traits with the estimated size of effect ranging from 0.8 to 1.7 phenotypic SD. In particular, gene markers were detected for tenderness, marbling, and predicted yield. The markers are currently being evaluated in industry herds to assess their utility in genetic evaluation schemes and breeding programs.

Keywords: Gene markers, QTL, meat quality

INTRODUCTION
Gene markers that detect the different forms of genes responsible for genetic variation in a herd will be a powerful tool for animal breeders. The development of gene markers requires the mapping or isolation of the genes responsible for individual differences for a particular trait. In recent years markers have been developed for many of the common genetic disorders in cattle (Healy 1996). Other genes with major effects on growth and development which have been localised using gene markers include double muscling in cattle (Charlier et al, 1994), muscular hypertrophy in sheep (Cockett et al, 1994) and meat quality in pigs (Milan et al, 1995).

Quantitative traits represent a major challenge for molecular genetic analysis. Variation in quantitative traits is due to the action of many genes or quantitative trait loci (QTL) and for some traits, environmental effects can be large. The goal is to identify the genes with medium to large effects, develop gene marker tests and incorporate them into genetic evaluation schemes and breeding programs. This task has been facilitated by the development of tools for genome analysis. In particular, the construction of genetic and physical maps for cattle (eg Barendse et al, 1994; Bishop et al, 1994) has made panels of mapped markers available. These markers can be used to systematically search the genome for QTL which are segregating in a population. Early successes have identified QTL affecting milk yield and composition in dairy cattle (Georges et al, 1995) and growth and carcass characteristics in pigs (Andersson et al, 1994). In this paper, we provide an interim report on a study to detect QTL for carcass and meat quality traits in a herd of tropical beef.
cattle. The family design, measurements and genotyping are briefly described and some interim results are presented. The research required to complete the study is indicated and future research projects to evaluate the broad utility of gene markers and isolate genes responsible for some of the effects detected are outlined.

MATERIALS AND METHODS

Animals. Three large half-sib (same sire) families were bred from F1 Charolais x Brahman bulls mated to a composite (AXBX) herd of dams. Their calves, designated CBX, were weaned in 1992, 1993 and 1994. The AXBX originated from equal contributions of the Africander, Hereford, Brahman, and Shorthorn breeds and were the progeny of three selection lines (Mackinnon et al. 1990). Families with 237, 166 and 170 offspring were generated by artificial insemination and natural mating for the three sires. All calves were born and grown out until 18 months-of-age on ‘Belmont’, the National Cattle Breeding Research Station 20km north of Rockhampton in Central Queensland. The 1992 and 1994 cohorts were transferred to the QDPI’s ‘Brigalow Research Station’ at Theodore in southern Central Queensland to be finished whilst the 1993 cohort were finished at the property leased by the CRC for Meat Quality ‘Duck Ponds’ near Emerald in Central Queensland. Animals were slaughtered on reaching target weights at abattoirs in Rockhampton and Biloela. Export market specifications of 270kg carcass weight for steers and 250kg for heifers with between 7 and 22mm of subcutaneous fat at the P8 site were targeted.

Markers. DNA was extracted from blood collected from calves at branding. Beginning in July 1992, DNA markers have been progressively genotyped on each cohort of progeny. Markers were chosen from available maps, but principally the map produced on the International Bovine Reference Panel (Barendse et al. 1994, Barendse et al. 1996). Marker selection, which is based on map position and heterozygosity in the F1 sires, aims for 95% genome coverage in each of the three sire families. The majority of the markers typed were microsatellites (97%) though some single-strand conformation polymorphisms (SSCP) and restriction fragment length polymorphisms (RFLP) were also analysed.

Traits. Carcass and meat quality traits are the focus of the CBX study though a large number of growth and morphological traits have been assessed on each of the progeny slaughtered. All animals followed a standard pre-slaughter protocol. At the abattoir, a range of commercial carcass traits were measured. After chilling, the Longissimus dorsi (LD) and Semitendinosus muscles (ST) were dissected out for meat quality assessment. Other traits were derived using published equations including predicted saleable meat yield (Fenwick 1991) and a tenderness index (Harris and Shorthose 1988).

Analysis. The most recent analysis of the CBX study used data from two sire families and offspring from the 1992 and 1993 cohorts. There were a total of 192 and 119 offspring from each sire respectively across the two cohorts. Each animal had a total of 54 carcass and meat quality traits measured on them. A total of 152 and 136 markers had been typed in the 1992 and 1993 cohorts respectively. A marker map was constructed for the CBX animals using maximum likelihood techniques (Georges et al., 1995). Multipoint interval mapping and linkage analysis was used to
detect QTL. A univariate maximum likelihood interval mapping analysis (IM) was used for continuously variable traits (Georges et al., 1995) whilst pair-wise linkage analysis was employed for qualitative traits such as marbling. Quantitative traits were pre-analysed to account for effects of contemporary group (cohort/sex/slaughter group), dentition, dam selection line, and both age and kill sequence within contemporary group. Residuals for each animal obtained from this analysis were utilised in the IM analysis. Each family x chromosome x trait combination was analysed independently. The IM analysis calculates a lod score at 2cM locations along an interval between markers separated by a defined distance. Information from all markers on a chromosome contributes to the analysis at each location. The lod score is the ratio of the log-odds of the likelihood of a QTL with an estimated allele substitution effect=α, relative to the likelihood where α=0. The analysis produces a lod score profile along each chromosome for every trait. The presence of a QTL is indicated when the maximum lod score in the profile surpasses a critical value. Critical values for lod scores were determined for genome-wise type I and type II error rates by simulation (Davis and DeNise, unpublished). These were used to assign gross probability statements to each QTL detected. A lod score threshold of 2.5 corresponding to a Type I genome-wise error rate of 5% was chosen.

RESULTS
QTL were detected for 18 of the 54 carcass and meat quality traits. A selection of those above the lod score threshold of 2.5 are summarised in Table 1. One, or in some cases two (data not shown), QTL were detected for most of these traits. The size of effect (α) ranged from 0.8 to 1.7 standard deviations (SD), with a mode of around one SD. Estimates of effect size may be biased upwards due to use of the IM technique with families of less than 150 animals.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Herd mean</th>
<th>Estimated QTL effect (a)</th>
<th>Standard Deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carcass weight</td>
<td>268 kg</td>
<td>9</td>
<td>1.5</td>
</tr>
<tr>
<td>Dressing percentage</td>
<td>50.5%</td>
<td>1.5</td>
<td>1.0</td>
</tr>
<tr>
<td>Predicted saleable meat yield</td>
<td>196 kg</td>
<td>8</td>
<td>1.1</td>
</tr>
<tr>
<td>Eye muscle area</td>
<td>69.8 cm²</td>
<td>6.5</td>
<td>0.9</td>
</tr>
<tr>
<td>Marbling score</td>
<td>1.2 units</td>
<td>0.4</td>
<td>1.1</td>
</tr>
<tr>
<td>Peak force</td>
<td>5.8 kg</td>
<td>0.4</td>
<td>1.1</td>
</tr>
<tr>
<td>Rump fat depth</td>
<td>10.5 mm</td>
<td>2.5</td>
<td>0.8</td>
</tr>
<tr>
<td>Subcutaneous fat colour (LD)</td>
<td>16.0 units</td>
<td>2.4</td>
<td>1.4</td>
</tr>
<tr>
<td>Tenderness index (ST)</td>
<td>8.4 units</td>
<td>0.6</td>
<td>1.0</td>
</tr>
</tbody>
</table>

DISCUSSION
The results show that after an analysis at an interim stage of the detection phase of the experiment significant QTL were found for carcass and meat quality traits. This phase of the experiment will be
completed in mid-1997. Power calculations conducted prior to the study determined that a minimum half-sib family size of 150 with an average marker spacing of 20cM was required to detect QTL and adequately estimate their effect. The results reported in this paper were obtained with a dataset significantly below that which will be achieved on completion of the detection phase. Simulation studies suggest that QTL with effects as low as 0.4 SD should be detected at a genome-wise type I error rate of 5% when this phase is complete. Although the probability of detecting all segregating QTL within each family is relatively low, the use of three families derived from F1 sires will ensure a higher power overall.

Gene markers for the QTL detected in this study are potentially useful as genetic predictors for traits. However, since the markers are only linked to the genes, the specific marker type associated with the positive allele may differ from one family to another. Furthermore, it is not known whether the QTL are segregating within other Charolais x Brahman sires or herds. Finally, it remains to be shown that the gene markers for the QTL detected in this study are useful predictors in other breeds or crosses. The next phase of this study is to evaluate the markers in industry relevant breeds and crosses. This will be carried out in selected herds involved in the core breeding program of the CRC for Meat Quality where seven breeds are represented. Markers will be evaluated to determine the increase in accuracy of Estimated Breeding Value (EBV) compared with EBV’s calculated solely on the performance records of related animals. It is envisaged that linked markers of this type will generally be used in combination with other records in genetic evaluation schemes such as BREEDPLAN. The ultimate goal of the study is to isolate some of the genes responsible for differences in carcass and meat quality traits. Once QTL have been mapped to a specific chromosome segment the region to search for the gene is narrowed. From this situation the positional candidate approach (Collins 1995) can be used in which genes previously mapped to the segment in cattle (or to homologous regions in other organisms) can be tested as candidate genes. This approach offers the best hope in the short term of isolating the genes identified in this study. Once a gene is isolated, a gene marker test can be developed based on the allelic variant responsible for a specific effect. Such tests can be used without knowledge of an animal’s pedigree and thus will be easier to use in practice.

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